

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:35:00 ; Search time 1016.15 Seconds
(without alignments)
118.796 Million cell updates/sec

Title:	US-10-800-926-3
Perfect score:	20
Sequence:	1 agguacagccaggaucgca 20

scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

```
Searched:      5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766283
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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database

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1:  gm_ba:*
2:  gm_in:*
3:  gm_env:*
4:  gm_om:*
5:  gm_ov:*
6:  gm_pat:*
7:  gm_ph:*
8:  gm_pr:*
9:  gm_ro:*
10: gm_stc:*
11: gm_sy:*
12: gm_un:*
13: gm_vl:*
14: gm_hng:*
15: gm_pl:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	100.0	20	6	AX104199	AX104199 Sequence
2	20	100.0	20	6	AX355040	AX355040 Sequence
3	20	100.0	20	6	AX547252	AX547252 Sequence
4	18	90.0	5253	9	AB012214	AB012214 Rattus ra
5	18	90.0	192617	14	AC123751	AC123751 Mus muscu
6	18	90.0	24311	14	AC135310	AC135310 Rattus no
7	17.4	87.0	265	8	HS48HR	Z61246 H.sapiens C
8	17.4	87.0	276	8	HS70GSF	Z66016 H.sapiens C
9	17.4	87.0	172415	8	AC073834	AC073834 Homo sapi
10	17.4	87.0	200966	9	AL596108	AL596108 Mouse DNA
11	17	85.0	598	3	AY547816	AY547816 Unculture
12	17	85.0	700	3	AY164354	AY164354 Unculture
13	17	85.0	700	3	AY164380	AY164380 Unculture
14	17	85.0	1908	2	AF011463	AF011463 Monophyloc
15	17	85.0	177687	14	AC160912	AC160912 Rhinophor
16	17	85.0	191592	14	AC118070	AC118070 Rattus no
17	17	85.0	193801	9	AC154620	AC154620 Mus muscu
18	17	85.0	194439	14	CT025535	CT025535 Mus muscu

19	17	85.0	252467	14	AC108255	AC108255 <i>Rattus n</i>
20	16.8	84.0	720	1	PSE1ASRA1	D30812 <i>Pseudomnas</i>
21	16.8	84.0	720	1	PSE1ASRB	D30813 <i>Pseudomnas</i>
22	16.8	84.0	720	6	BD224017	BD224017 <i>Gene swit</i>
23	16.8	84.0	720	6	CQ839858	CQ839858 <i>Sequence</i>
24	16.8	84.0	720	6	CQ839862	CQ839862 <i>Sequence</i>
25	16.8	84.0	720	11	AY658192	AY658192 <i>Synthetic</i>
26	16.8	84.0	802	10	BV658915	BV658915 <i>S216P6135</i>
27	16.8	84.0	1725	1	PSE1ASR	M59425 <i>Pseudomnas</i>
28	16.8	84.0	3444	2	ABGYOYC	X12874 <i>Sea urchin</i>
29	16.8	84.0	10238	1	AE004572	AE004572 <i>Pseudomn</i>
30	16.8	84.0	36255	14	AC016208	AC016208 <i>Homo sapi</i>
31	16.8	84.0	93714	14	AL161651	AL161651 <i>Homo sapi</i>
32	16.8	84.0	111051	14	AL161675	AL161675 <i>Homo sapi</i>
33	16.8	84.0	118395	8	AC007138	AC007138 <i>Bos tauru</i>
34	16.8	84.0	131972	8	AC008794	AC008794 <i>Homo sapi</i>
35	16.8	84.0	132063	14	AC142244	AC142244 <i>Homo sapi</i>
36	16.8	84.0	147815	8	HS99896	AL031687 <i>Human DNA</i>
37	16.8	84.0	149208	14	AC164137	AC164137 <i>Bos tauru</i>
38	16.8	84.0	160241	14	AC148601	AC148601 <i>Gasterocyt</i>
39	16.8	84.0	165241	8	AC104460	AC104460 <i>Homo sapi</i>
40	16.8	84.0	162701	14	AC0073317	AC0073317 <i>Homo sapi</i>
41	16.8	84.0	163385	8	AC015723	AC015723 <i>Homo sapi</i>
42	16.8	84.0	166703	8	AL133378	AC015372 <i>Homo sapi</i>
43	16.8	84.0	168087	14	AC157818	AL133378 <i>Human DNA</i>
44	16.8	84.0	187700	14	AC131061	AC157818 <i>Mus muscu</i>
45	16.8	84.0	192104	14	AC011114	AC131061 <i>Mus muscu</i>
46	16.8	84.0	195041	9	AC15809	AC011141 <i>Homo sapi</i>
47	16.8	84.0	195767	9	AC127377	AC15809 <i>Mus muscu</i>
48	16.8	84.0	201745	9	AC104205	AC127377 <i>Mus muscu</i>
49	16.8	84.0	204393	14	AC145989	AC14205 <i>Mus muscu</i>
50	16.8	84.0	206775	9	AC158309	AC145989 <i>Pan trogl</i>
51	16.8	84.0	209285	14	AC013517	AC158309 <i>Mus muscu</i>
52	16.8	84.0	219033	14	AC159839	AC013517 <i>Homo sapi</i>
53	16.8	84.0	231764	14	AC119470	AC159839 <i>Bos tauru</i>
54	16.8	84.0	233445	9	AC129662	AC119470 <i>Rattus no</i>
55	16.8	84.0	235705	9	AC113970	AC129662 <i>Rattus no</i>
56	16.8	84.0	303855	1	AE017230	AC113970 <i>Mus muscu</i>
57	16.4	82.0	243	6	HS47B1R	AE017230 <i>Mycobacte</i>
58	16.4	82.0	246	6	AE673655	Z61175 <i>H. sapiens C</i>
59	16.4	82.0	487	3	AY124609	AE673655 <i>Sequence</i>
60	16.4	82.0	606	10	GE95328	AY124609 <i>Unculture</i>
61	16.4	82.0	1044	6	CQ741984	GE95328 <i>S208P6750FA</i>
62	16.4	82.0	17237	9	AP463761	CQ741984 <i>Sequence</i>
63	16.4	82.0	25379	1	CP000011	AP463761 <i>Mus muscu</i>
64	16.4	82.0	31632	6	AK659262	CP000011 <i>Confination (24 o</i>
65	16.4	82.0	46826	14	AC160847	AK659262 <i>Sequence</i>
66	16.4	82.0	71047	15	NCB23174	AC160847 <i>Homo sapi</i>
67	16.4	82.0	73005	1	BX571966	BX284746 <i>Neurospor</i>
68	16.4	82.0	96599	6	AK695824	AX695824 <i>Sequence</i>
69	16.4	82.0	110000	1	CR626937	AK695824 <i>Sequence</i>
70	16.4	82.0	110000	1	AP006841	CR626937 <i>Confination (37 o</i>
71	16.4	82.0	110000	14	AC0744221	AP006841 <i>Confination (38 o</i>
72	16.4	82.0	134388	14	AC141344	AC0744221 <i>Confination (2 of</i>
73	16.4	82.0	135541	9	AC138108	AC141344 <i>Rattus no</i>
74	16.4	82.0	138211	9	AL607078	AC138108 <i>Mus muscu</i>
75	16.4	82.0	139619	14	AC074028	AL607078 <i>Mus muscu</i>
76	16.4	82.0	142047	8	AL0526708	AC074028 <i>Mus muscu</i>
77	16.4	82.0	142565	9	AL5925545	AL0526708 <i>Homo sapi</i>
78	16.4	82.0	143739	9	AC154817	AL5925545 <i>Mus muscu</i>
79	16.4	82.0	149109	14	AC101018	AC154817 <i>Mus muscu</i>
80	16.4	82.0	152618	14	AC058811	AC101018 <i>Rattus no</i>
81	16.4	82.0	155689	14	AC149117	AC058811 <i>Homo sapi</i>
82	16.4	82.0	156580	8	AP003493	AC149117 <i>Homo sapi</i>
83	16.4	82.0	162456	14	AC044846	AP003493 <i>Homo sapi</i>
84	16.4	82.0	162530	9	AC124439	AC044846 <i>Mus muscu</i>
85	16.4	82.0	165339	14	AC149880	AC124439 <i>Mus muscu</i>
86	16.4	82.0	166537	14	AC139896	AC149880 <i>Mus muscu</i>
87	16.4	82.0	168794	9	AC134569	AC139896 <i>Olelemur</i>
88	16.4	82.0	171930	14	AC118687	AC134569 <i>Mus muscu</i>
89	16.4	82.0	175552	14	AC027475	AC118687 <i>Mus muscu</i>
90	16.4	82.0	175582	9	AC023590	AC027475 <i>Homo sapi</i>
91	16.4	82.0	176011	9	AL645862	AC023590 <i>Homo sapi</i>
						AL645862 <i>Mus muscu</i>

92	16.4	82.0	179705	9	AL627087	AL627087 Mouse DNA	c 165	16	80.0	1265	3	AY592491	AY592491 Unculture
93	16.4	82.0	183582	14	AC158891	AC158891 Bos tauru	c 166	16	80.0	1279	3	AP355045	AP355045 Unculture
94	16.4	82.0	183905	9	AC022682	AC022682 Mus muscu	c 167	16	80.0	1446	3	AP355044	AP355044 Unculture
95	16.4	82.0	186464	14	AC142067	AC142067 Rattus no	c 168	16	80.0	1564	6	AR507944	AR507944 Sequence
96	16.4	82.0	188292	9	AC156639	AC156639 Mus muscu	c 169	16	80.0	1734	3	AF092445	AF092445 Sequence
97	16.4	82.0	188519	8	AC104041	AC104041 Homo sapi	c 170	16	80.0	2052	3	DQ009429	DQ009429 Unculture
98	16.4	82.0	189732	8	AC023034	AC023034 Homo sapi	c 171	16	80.0	2238	2	AY061199	AY061199 Drosophill
99	16.4	82.0	190256	9	AC121302	AC121302 Mus muscu	c 172	16	80.0	2335	2	BT001775	BT001775 Drosophill
100	16.4	82.0	191710	9	AC122489	AC122489 Mus muscu	c 173	16	80.0	2550	6	CQ599994	CQ599994 Sequence
101	16.4	82.0	191798	14	AC123952	AC123952 Mus muscu	c 174	16	80.0	2668	6	CQ584337	CQ584337 Sequence
102	16.4	82.0	192761	14	AC135939	AC135939 Rattus no	c 175	16	80.0	4972	6	CQ599993	CQ599993 Sequence
103	16.4	82.0	192872	9	AC140374	AC140374 Mus muscu	c 176	16	80.0	4989	6	CQ584336	CQ584336 Sequence
104	16.4	82.0	193572	9	AC140268	AC140268 Mus muscu	c 177	16	80.0	5987	14	AC138671_3	AC138671_3
105	16.4	82.0	193934	14	AL616287	AL616287 Rattus no	c 178	16	80.0	65987	14	AC101565	AC101565
106	16.4	82.0	197658	14	AL646094	AL646094 Mus muscu	c 179	16	80.0	74753	14	AC008477	AC008477
107	16.4	82.0	199318	14	AC156543	AC156543 Mus muscu	c 180	16	80.0	87865	14	AC095424_3	AC095424_3
108	16.4	82.0	199422	9	AC124180	AC124180 Mus muscu	c 181	16	80.0	89437	14	AC095424_3	AC095424_3
109	16.4	82.0	199604	9	AC133902	AC133902 Mus muscu	c 182	16	80.0	96600	6	AX695710	AX695710
110	16.4	82.0	203073	9	AC122322	AC122322 Mus muscu	c 183	16	80.0	110000	14	AC095424_2	AC095424_2
111	16.4	82.0	208625	14	AC164605	AC164605 Mus muscu	c 184	16	80.0	112643	14	AC11637_1	AC11637_1
112	16.4	82.0	208765	9	EX004985	EX004985 Mouse DNA	c 185	16	80.0	127883	9	AC114434	AC114434
113	16.4	82.0	209751	9	AC154733	AC154733 Mus muscu	c 186	16	80.0	128760	9	AC153843	AC153843
114	16.4	82.0	212974	14	AC110466	AC110466 Rattus no	c 187	16	80.0	129957	8	HS41562	HS41562
115	16.4	82.0	212974	14	AC124578	AC124578 Mus muscu	c 188	16	80.0	133499	14	AC141969	AC141969
116	16.4	82.0	213229	8	AC026782	AC026782 Homo sapi	c 189	16	80.0	145263	13	AF030027	AF030027
117	16.4	82.0	214025	9	AC131081	AC131081 Mus muscu	c 190	16	80.0	146201	9	AC153942	AC153942
118	16.4	82.0	215532	14	AC131081	AC131081 Mus muscu	c 191	16	80.0	148167	9	AC141879	AC141879
119	16.4	82.0	215532	14	AC131081	AC131081 Mus muscu	c 192	16	80.0	148555	14	AC126921	AC126921
120	16.4	82.0	218085	14	AC094952	AC094952 Rattus no	c 193	16	80.0	148650	5	EX323829	EX323829
121	16.4	82.0	218127	14	AC132713	AC132713 Bos tauru	c 194	16	80.0	148675	9	AL631769	AL631769
122	16.4	82.0	218872	14	AC126232	AC126232 Bos tauru	c 195	16	80.0	151596	9	AL669859	AL669859
123	16.4	82.0	221159	14	AC163666	AC163666 Mus muscu	c 196	16	80.0	156905	14	AC020006	AC020006
124	16.4	82.0	221256	14	AC122104	AC122104 Rattus no	c 197	16	80.0	160034	9	AC131986	AC131986
125	16.4	82.0	222640	14	AC148797	AC148797 Crolemur	c 198	16	80.0	162472	14	AC114460	AC114460
126	16.4	82.0	224623	14	AC118994	AC118994 Rattus no	c 199	16	80.0	166983	8	AC020894	AC020894
127	16.4	82.0	224778	9	AC116071	AC116071 Rattus no	c 200	16	80.0	167822	14	AC155592	AC155592
128	16.4	82.0	228201	5	AC15914	AC15914 Gallus ga	c 201	16	80.0	170059	14	AC150005	AC150005
129	16.4	82.0	230212	14	AC095694	AC095694 Rattus no	c 202	16	80.0	170499	8	AC008653	AC008653
130	16.4	82.0	230845	14	AC098415	AC098415 Rattus no	c 203	16	80.0	173049	8	AC0022142	AC0022142
131	16.4	82.0	231754	14	AC133804	AC133804 Rattus no	c 204	16	80.0	174186	9	AC155294	AC155294
132	16.4	82.0	232885	14	AC106163	AC106163 Rattus no	c 205	16	80.0	175195	9	AC131066	AC131066
133	16.4	82.0	233144	14	AC110317	AC110317 Rattus no	c 206	16	80.0	175716	9	AC117245	AC117245
134	16.4	82.0	233303	14	AC110317	AC110317 Rattus no	c 207	16	80.0	177775	9	AC161447	AC161447
135	16.4	82.0	234217	14	AC162551	AC162551 Bos tauru	c 208	16	80.0	182569	9	AC117206	AC117206
136	16.4	82.0	234300	14	AC162551	AC162551 Bos tauru	c 209	16	80.0	183585	16	AC117130	AC117130
137	16.4	82.0	236344	14	AC116431	AC116431 Rattus no	c 210	16	80.0	184209	14	AC117130	AC117130
138	16.4	82.0	240125	9	AL669982	AL669982 Mouse DNA	c 211	16	80.0	184794	14	AC129582	AC129582
139	16.4	82.0	242728	14	AC154647	AC154647 Mus muscu	c 212	16	80.0	185466	9	AC160464	AC160464
140	16.4	82.0	250169	14	AC095874	AC095874 Rattus no	c 213	16	80.0	185967	9	AC161888	AC161888
141	16.4	82.0	254483	14	AC095874	AC095874 Rattus no	c 214	16	80.0	189540	9	AL772264	AL772264
142	16.4	82.0	256132	14	AC136623	AC136623 Rattus no	c 215	16	80.0	191017	14	AC034286	AC034286
143	16.4	82.0	256367	14	AC124207	AC124207 Rattus no	c 216	16	80.0	191513	9	AC139335	AC139335
144	16.4	82.0	257714	14	AC096219	AC096219 Rattus no	c 217	16	80.0	192812	9	AC133805	AC133805
145	16.4	82.0	267067	14	AC096559	AC096559 Rattus no	c 218	16	80.0	195625	14	AC105486	AC105486
146	16.4	82.0	270699	14	AC133821	AC133821 Rattus no	c 219	16	80.0	195887	9	AC139335	AC139335
147	16.4	82.0	273595	14	AC095278	AC095278 Rattus no	c 220	16	80.0	195887	9	AC139335	AC139335
148	16.4	82.0	298970	14	AC119651	AC119651 Rattus no	c 221	16	80.0	195887	9	AC139335	AC139335
149	16.4	82.0	303008	14	AC158959	AC158959 Mus muscu	c 222	16	80.0	195887	9	AC139335	AC139335
150	16.4	82.0	318959	14	AY657023	AY657023 Mus muscu	c 223	16	80.0	195887	9	AC139335	AC139335
151	16.4	82.0	335283	14	AC020865	AC020865 Mus muscu	c 224	16	80.0	195887	9	AC139335	AC139335
152	16.4	82.0	348971	1	BX572594	BX572594 Rhodopseu	c 225	16	80.0	195887	9	AC139335	AC139335
153	16.4	82.0	348971	1	AY165971	AY165971 Unculture	c 226	16	80.0	195887	9	AC139335	AC139335
154	16.4	82.0	348971	1	AB046181	AB046181 Unculture	c 227	16	80.0	195887	9	AC139335	AC139335
155	16.4	82.0	348971	1	AB046181	AB046181 Unculture	c 228	16	80.0	195887	9	AC139335	AC139335
156	16.4	82.0	348971	1	AB046181	AB046181 Unculture	c 229	16	80.0	195887	9	AC139335	AC139335
157	16.4	82.0	348971	1	AB046181	AB046181 Unculture	c 230	16	80.0	195887	9	AC139335	AC139335
158	16.4	82.0	348971	1	AB046181	AB046181 Unculture	c 231	16	80.0	195887	9	AC139335	AC139335
159	16.4	82.0	348971	1	AB046181	AB046181 Unculture	c 232	16	80.0	195887	9	AC139335	AC139335
160	16.4	82.0	348971	1	AB046181	AB046181 Unculture	c 233	16	80.0	195887	9	AC139335	AC139335
161	16.4	82.0	348971	1	AB046181	AB046181 Unculture	c 234	16	80.0	195887	9	AC139335	AC139335
162	16.4	82.0	348971	1	AB046181	AB046181 Unculture	c 235	16	80.0	195887	9	AC139335	AC139335
163	16.4	82.0	348971	1	AB046181	AB046181 Unculture	c 236	16	80.0	195887	9	AC139335	AC139335
164	16.4	82.0	348971	1	AB046181	AB046181 Unculture	c 237	16	80.0	195887	9	AC139335	AC139335

238	16	80.0	204312	9	AL669943	AL669943	Mouse DNA	311	16	80.0	300940	14	AC134267	AC134267	Rattus no
239	16	80.0	205599	9	AC137156	AC137156	Mus muscu	312	16	80.0	303008	14	AC158959	AC158959	Mus muscu
240	16	80.0	205702	9	AC140190	AC140190	Mus muscu	313	16	80.0	307435	1	AE016914	AE016914	Chromobac
241	16	80.0	206230	9	AC084272	AC084272	Mus muscu	314	15.8	79.0	542	6	CQ484046	CQ484046	Sequence
242	16	80.0	206741	2	AE003747	AE003747	Drosophila	315	15.8	79.0	568	10	BV050995	BV050995	Sequence
243	16	80.0	207157	9	AC147634	AC147634	Mus muscu	316	15.8	79.0	576	6	AR506666	AR506666	Sequence
244	16	80.0	207239	9	AC113107	AC113107	Mus muscu	317	15.8	79.0	592	6	CO513874	CO513874	Sequence
245	16	80.0	208715	14	AC158176	AC158176	Rattus no	318	15.8	79.0	628	10	BV370636	BV370636	Sequence
246	16	80.0	209071	14	AC134109	AC134109	Rattus no	319	15.8	79.0	965	5	AY633582	AY633582	Hemilamph
247	16	80.0	209211	14	AC084883	AC084883	Mus muscu	320	15.8	79.0	965	5	AY633583	AY633583	Hemilamph
248	16	80.0	209799	9	AL671117	AL671117	Mouse DNA	321	15.8	79.0	969	8	AH007006S1	AH007006S1	Homo sapien
249	16	80.0	209838	9	AC102505	AC102505	Mus muscu	322	15.8	79.0	978	6	CO575691	CO575691	Sequence
250	16	80.0	210204	14	AC158174	AC158174	Rattus no	323	15.8	79.0	1003	6	AF012467	AF012467	Colobus a
251	16	80.0	210257	14	AC135865	AC135865	Rattus no	324	15.8	79.0	1023	11	AY659219	AY659219	Synthetic
252	16	80.0	210959	9	AC109606	AC109606	Mus muscu	325	15.8	79.0	1057	6	BD209546	BD209546	Compositi
253	16	80.0	211317	14	AC114505	AC114505	Rattus no	326	15.8	79.0	1057	6	BD209546	BD209546	Compositi
254	16	80.0	212221	14	AC136126	AC136126	Rattus no	327	15.8	79.0	1140	4	AF338683	AF338683	Pteronotu
255	16	80.0	213476	14	AC114589	AC114589	Mus muscu	328	15.8	79.0	1140	4	AF338684	AF338684	Pteronotu
256	16	80.0	213482	9	AC154633	AC154633	Mus muscu	329	15.8	79.0	1140	4	AY604461	AY604461	Pteronotu
257	16	80.0	216169	9	AC109608	AC109608	Mus muscu	330	15.8	79.0	1288	2	AY089582	AY089582	Pteronotu
258	16	80.0	218758	9	AC131712	AC131712	Mus muscu	331	15.8	79.0	1408	3	AY922139	AY922139	Unculture
259	16	80.0	219379	9	AL627083	AL627083	Mouse DNA	332	15.8	79.0	2004	6	BD209680	BD209680	Compositi
260	16	80.0	220622	9	AC111085	AC111085	Mus muscu	333	15.8	79.0	2004	6	AR341486	AR341486	Sequence
261	16	80.0	220742	14	AC105644	AC105644	Rattus no	334	15.8	79.0	2040	6	BD158578	BD158578	Primer fo
262	16	80.0	221599	14	AC094756	AC094756	Rattus no	335	15.8	79.0	2040	8	AK023694	AK023694	Sequence
263	16	80.0	221805	9	AC105515	AC105515	Rattus no	336	15.8	79.0	2040	8	AK023694	AK023694	Sequence
264	16	80.0	222544	14	AC127923	AC127923	Rattus no	337	15.8	79.0	2151	8	GG86LOP	GG86LOP	Sequence
265	16	80.0	222775	9	AC084069	AC084069	Mus muscu	338	15.8	79.0	2368	15	SCU62525	SCU62525	Saccharomy
266	16	80.0	223344	14	AC106193	AC106193	Rattus no	339	15.8	79.0	3026	13	MCU02500	MCU02500	Murine cyto
267	16	80.0	223541	9	AC125010	AC125010	Mus muscu	340	15.8	79.0	3074	2	BT011433	BT011433	Drosophila
268	16	80.0	224703	14	AC115510	AC115510	Rattus no	341	15.8	79.0	3215	9	AF245476	AF245476	Mus muscu
269	16	80.0	224933	14	AC085378	AC085378	Rattus no	342	15.8	79.0	3215	9	AF245476	AF245476	Mus muscu
270	16	80.0	225308	14	AC098918	AC098918	Rattus no	343	15.8	79.0	3265	6	CO575690	CO575690	Sequence
271	16	80.0	225308	14	AC098918	AC098918	Rattus no	344	15.8	79.0	3461	5	AY303542	AY303542	Takifugu
272	16	80.0	226538	9	AC153909	AC153909	Mus muscu	345	15.8	79.0	3540	5	AB182274	AB182274	Takifugu
273	16	80.0	227833	14	AC128446	AC128446	Rattus no	346	15.8	79.0	7055	8	GORHBBG	GORHBBG	Gorilla bet
274	16	80.0	228191	14	AC094451	AC094451	Rattus no	347	15.8	79.0	8476	8	GIBRGLOP	GIBRGLOP	H. lar pel-e
275	16	80.0	228296	14	AL831751	AL831751	Mus muscu	348	15.8	79.0	11593	1	AE004678	AE004678	Pseudom
276	16	80.0	229761	14	AC123314	AC123314	Rattus no	349	15.8	79.0	12046	1	AE005017	AE005017	Halobacte
277	16	80.0	229976	14	AC166359	AC166359	Mus muscu	350	15.8	79.0	13961	1	AE004984	AE004984	Halobacte
278	16	80.0	230212	14	AC095694	AC095694	Rattus no	351	15.8	79.0	15051	6	CO575081	CO575081	Sequence
279	16	80.0	230394	14	AC098017	AC098017	Rattus no	352	15.8	79.0	15769	1	AY026914	AY026914	Pseudom
280	16	80.0	230447	9	AL671866	AL671866	Mouse DNA	353	15.8	79.0	16440	1	AE001993	AE001993	Delinococ
281	16	80.0	231295	14	AC097286	AC097286	Rattus no	354	15.8	79.0	22566	8	CERGLORIN	CERGLORIN	Cebus albit
282	16	80.0	231822	14	AC129612	AC129612	Rattus no	355	15.8	79.0	25913	15	SC9910	SC9910	S. cerevisia
283	16	80.0	233094	14	AC128479	AC128479	Rattus no	356	15.8	79.0	27256	9	AF240003	AF240003	Mus muscu
284	16	80.0	234351	14	AC135903	AC135903	Rattus no	357	15.8	79.0	45562	8	AL358512	AL358512	Human DNA
285	16	80.0	235453	9	AC133910	AC133910	Mus muscu	358	15.8	79.0	49197	15	AP006349	AP006349	Human DNA
286	16	80.0	235938	14	AC121469	AC121469	Rattus no	359	15.8	79.0	67987	9	AL672157	AL672157	Mus muscu
287	16	80.0	236159	14	AC125553	AC125553	Rattus no	360	15.8	79.0	73920	9	AC091397	AC091397	Rattus no
288	16	80.0	236502	14	AC098186	AC098186	Rattus no	361	15.8	79.0	74507	8	AC004031	AC004031	Homo sapi
289	16	80.0	236933	14	AC111937	AC111937	Rattus no	362	15.8	79.0	90801	8	AC025033	AC025033	Homo sapi
290	16	80.0	237754	9	AC125576	AC125576	Rattus no	363	15.8	79.0	93156	8	AY640177	AY640177	Homo sapi
291	16	80.0	240411	14	AC162491	AC162491	Bos tauru	364	15.8	79.0	95537	14	AC0021512	AC0021512	Homo sapi
292	16	80.0	245853	14	AC125965	AC125965	Rattus no	365	15.8	79.0	100120	8	AC090454	AC090454	Homo sapi
293	16	80.0	246229	14	AC096184	AC096184	Rattus no	366	15.8	79.0	101736	14	AC166132	AC166132	Bos tauru
294	16	80.0	247144	14	AC111654	AC111654	Rattus no	367	15.8	79.0	102234	14	AC161116	AC161116	Mus muscu
295	16	80.0	247177	14	AC121402	AC121402	Rattus no	368	15.8	79.0	104939	14	AC138556	AC138556	Takifugu
296	16	80.0	247452	14	AC115242	AC115242	Rattus no	369	15.8	79.0	105393	8	AL713859	AL713859	Human DNA
297	16	80.0	248040	14	AC136279	AC136279	Rattus no	370	15.8	79.0	107857	8	AC008631	AC008631	Homo sapi
298	16	80.0	252689	14	AC079433	AC079433	Mus muscu	371	15.8	79.0	110000	1	AP006716	AP006716	Sequence
299	16	80.0	252788	14	AC135436	AC135436	Rattus no	372	15.8	79.0	110000	1	BA000035	BA000035	Sequence
300	16	80.0	252958	14	AC126832	AC126832	Rattus no	373	15.8	79.0	110000	1	CP000058	CP000058	Sequence
301	16	80.0	254734	14	AC134631	AC134631	Rattus no	374	15.8	79.0	110000	14	AC109729	AC109729	Sequence
302	16	80.0	262325	14	AC107280	AC107280	Rattus no	375	15.8	79.0	110000	15	AE016820	AE016820	Sequence
303	16	80.0	264321	9	AL807762	AL807762	Mouse DNA	376	15.8	79.0	110000	15	AE016820	AE016820	Sequence
304	16	80.0	278760	14	AC110842	AC110842	Rattus no	377	15.8	79.0	110000	15	AE016820	AE016820	Sequence
305	16	80.0	278760	14	AC110842	AC110842	Rattus no	378	15.8	79.0	110970	9	AC004807	AC004807	Mus muscu
306	16	80.0	284150	14	AC119130	AC119130	Rattus no	379	15.8	79.0	123430	8	AP001824	AP001824	Homo sapi
307	16	80.0	285748	14	AC106055	AC106055	Rattus no	380	15.8	79.0	128638	8	AC015968	AC015968	Homo sapi
308	16	80.0	290052	14	AC106649	AC106649	Rattus no	381	15.8	79.0	131796	14	AC138558	AC138558	Takifugu
309	16	80.0	293771	14	AC127156	AC127156	Rattus no	382	15.8	79.0	135369	14	AC090557	AC090557	Homo sapi
310	16	80.0	293834	14	AC135528	AC135528	Rattus no	383	15.8	79.0	138033	14	AP002339	AP002339	Homo sapi

C 384	15.8	79.0	139619	14	AC074028	AC074028 Mus muscu	457	15.8	79.0	219769	9	AC067964	AC067964 Mus Muscu
C 385	15.8	79.0	140956	8	AC023058	AC023058 Homo sapi	458	15.8	79.0	219913	14	AC120967	AC120967 Rattus no
C 386	15.8	79.0	142534	14	AC156364	AC156364 Gallicabu	459	15.8	79.0	225212	9	AC162183	AC162183 Mus muscu
C 387	15.8	79.0	143028	14	CR749173	CR749173 Dario rex	460	15.8	79.0	226112	14	AC162526	AC162526 Mus muscu
C 388	15.8	79.0	144391	14	AC055823	AC055823 Homo sapi	461	15.8	79.0	227406	14	AC118439	AC118439 Rattus no
C 389	15.8	79.0	149453	9	AC084109	AC084109 Mus muscu	462	15.8	79.0	227507	14	AC091310	AC091310 Mus muscu
C 390	15.8	79.0	150986	14	AC023802	AC023802 Mus muscu	463	15.8	79.0	228085	14	AC154375	AC154375 Mus muscu
C 391	15.8	79.0	153343	14	AC139739	AC139739 Felle cat	464	15.8	79.0	228645	9	AL450397	AL450397 Mouse DNA
C 392	15.8	79.0	156724	14	AC016306	AC016306 Homo sapi	465	15.8	79.0	230278	13	MGU68299	MGU68299 Mouse cysom
C 393	15.8	79.0	158696	8	AC007502	AC007502 Homo sapi	466	15.8	79.0	230492	14	AC097250	AC097250 Rattus no
C 394	15.8	79.0	160982	14	AC128945	AC128945 Rattus no	467	15.8	79.0	232050	2	AE003779	AE003779 Drosophill
C 395	15.8	79.0	161566	8	AC008060	AC008060 Homo sapi	468	15.8	79.0	232562	14	AC164640	AC164640 Mus muscu
C 396	15.8	79.0	162695	8	AL353580	AL353580 Human DNA	469	15.8	79.0	233422	9	AL591070	AL591070 Mouse DNA
C 397	15.8	79.0	164565	14	AC158728	AC158728 Rhinoloph	470	15.8	79.0	234220	14	AC128874	AC128874 Rattus no
C 398	15.8	79.0	169799	9	AC158995	AC158995 Mus muscu	471	15.8	79.0	235326	14	AC105592	AC105592 Rattus no
C 399	15.8	79.0	171615	14	AC089988	AC089988 Homo sapi	472	15.8	79.0	238367	14	AC094187	AC094187 Rattus no
C 400	15.8	79.0	172363	9	AL672105	AL672105 Mouse DNA	473	15.8	79.0	239598	14	AC073733	AC073733 Mus muscu
C 401	15.8	79.0	172655	14	AC140975	AC140975 Papio ham	474	15.8	79.0	243462	14	AC096174	AC096174 Rattus no
C 402	15.8	79.0	173505	14	AC016323	AC016323 Homo sapi	475	15.8	79.0	243676	14	AC055521	AC055521 Rattus no
C 403	15.8	79.0	176388	14	AC162494	AC162494 Bos tauru	476	15.8	79.0	243628	14	AC131627	AC131627 Rattus no
C 404	15.8	79.0	177411	14	AC092223	AC092223 Homo sapi	477	15.8	79.0	250313	14	AC103170	AC103170 Rattus no
C 405	15.8	79.0	178209	14	AC160528	AC160528 Bos tauru	478	15.8	79.0	250849	14	AC103463	AC103463 Rattus no
C 406	15.8	79.0	178361	9	AL645471	AL645471 Mouse DNA	479	15.8	79.0	251052	14	AC130129	AC130129 Rattus no
C 407	15.8	79.0	178473	8	HSJ749H19	HSJ749H19 Human DNA	480	15.8	79.0	253403	14	AC115243	AC115243 Rattus no
C 408	15.8	79.0	179342	8	AC158620	AC158620 Mus muscu	481	15.8	79.0	256348	14	AC095686	AC095686 Rattus no
C 409	15.8	79.0	179372	14	AC040922	AC040922 Homo sapi	482	15.8	79.0	257339	14	AC128869	AC128869 Rattus no
C 410	15.8	79.0	181214	15	CR391923	CR391923 Zebrafish	483	15.8	79.0	260253	14	AC126971	AC126971 Rattus no
C 411	15.8	79.0	181262	14	AC129783	AC129783 Rattus no	484	15.8	79.0	260468	14	AC109419	AC109419 Rattus no
C 412	15.8	79.0	181446	14	AC007469	AC007469 Drosophill	485	15.8	79.0	270086	14	AC128132	AC128132 Rattus no
C 413	15.8	79.0	181464	14	AC154167	AC154167 Rhinoloph	486	15.8	79.0	274863	14	AC118370	AC118370 Rattus no
C 414	15.8	79.0	181835	8	AC146227	AC146227 Pan trogl	487	15.8	79.0	277815	14	AC163589	AC163589 Bos tauru
C 415	15.8	79.0	181923	8	AC022872	AC022872 Homo sapi	488	15.8	79.0	278876	14	AC120936	AC120936 Rattus no
C 416	15.8	79.0	182785	8	AC145937	AC145937 Pan trogl	489	15.8	79.0	295058	14	AC153544	AC153544 Mus muscu
C 417	15.8	79.0	183179	14	AL133212	AL133212 Homo sapi	490	15.8	79.0	301536	14	AC134158	AC134158 Rattus no
C 418	15.8	79.0	183252	14	AC023637	AC023637 Homo sapi	491	15.8	79.0	305584	14	AE016920	AE016920 Chromodac
C 419	15.8	79.0	185405	8	AC121248	AC121248 Homo sapi	492	15.8	77.0	317	10	G01279	G01279 Fruit fly S
C 420	15.8	79.0	186404	8	AC121248	AC121248 Homo sapi	493	15.4	77.0	372	10	AF047240	AF047240 Rattus no
C 421	15.8	79.0	190076	8	AC008403	AC008403 Homo sapi	494	15.4	77.0	375	8	AF103097	AF103097 Homo sapi
C 422	15.8	79.0	191626	9	AC102262	AC102262 Mus muscu	495	15.4	77.0	448	6	BD223798	BD223798 Modificat
C 423	15.8	79.0	192292	9	AL671875	AL671875 Mouse DNA	496	15.4	77.0	453	3	AB154538	AB154538 Unculture
C 424	15.8	79.0	192355	14	AC012727	AC012727 Drosophill	497	15.4	77.0	533	10	BV157453	BV157453 RPMMSE00
C 425	15.8	79.0	193440	9	AL669915	AL669915 Mouse DNA	498	15.4	77.0	544	3	AB127628	AB127628 Unculture
C 426	15.8	79.0	194695	14	AC026375	AC026375 Mus muscu	499	15.4	77.0	557	10	BV060692	BV060692 Rattus no
C 427	15.8	79.0	195286	9	AC102856	AC102856 Mus muscu	500	15.4	77.0	561	3	AF195423	AF195423 Unculture
C 428	15.8	79.0	195505	5	BX537287	BX537287 Zebrafish	501	15.4	77.0	561	3	AF507882	AF507882 Unculture
C 429	15.8	79.0	195505	5	BX537287	BX537287 Zebrafish	502	15.4	77.0	635	10	BV034844	BV034844 S209P6376
C 430	15.8	79.0	195905	9	AC165086	AC165086 Mus muscu	503	15.4	77.0	699	10	BV069431	BV069431 Unculture
C 431	15.8	79.0	196346	14	AC151242	AC151242 Bos tauru	504	15.4	77.0	700	3	AY547801	AY547801 Unculture
C 432	15.8	79.0	196399	9	AC152943	AC152943 Mus muscu	505	15.4	77.0	759	3	ACF555197	ACF555197 Unculture
C 433	15.8	79.0	196484	14	AC129435	AC129435 Rattus no	506	15.4	77.0	769	3	AY226294	AY226294 Rattus no
C 434	15.8	79.0	197080	9	AC108434	AC108434 Mus muscu	507	15.4	77.0	847	10	BV063667	BV063667 Rattus no
C 435	15.8	79.0	197273	9	AC024607	AC024607 Mus muscu	508	15.4	77.0	859	3	AY5617842	AY5617842 Unculture
C 436	15.8	79.0	197273	9	AC024607	AC024607 Mus muscu	509	15.4	77.0	861	3	AY542580	AY542580 Unculture
C 437	15.8	79.0	197356	9	AL929275	AL929275 Mouse DNA	510	15.4	77.0	863	1	AY524140	AY524140 Halorarcha
C 438	15.8	79.0	197853	14	AC114423	AC114423 Rattus no	511	15.4	77.0	899	3	DO110111	DO110111 Unculture
C 439	15.8	79.0	198463	9	AC125038	AC125038 Mus muscu	512	15.4	77.0	902	3	DO088233	DO088233 Unculture
C 440	15.8	79.0	199312	14	AC156543	AC156543 Mus muscu	513	15.4	77.0	911	3	DO110098	DO110098 Unculture
C 441	15.8	79.0	199612	9	AC147098	AC147098 Mus muscu	514	15.4	77.0	940	15	AB099930	AB099930 MaJus x d
C 442	15.8	79.0	200266	9	AC111202	AC111202 Mus muscu	515	15.4	77.0	952	3	DO053885	DO053885 Unculture
C 443	15.8	79.0	200830	9	AC153845	AC153845 Mus muscu	516	15.4	77.0	974	15	AY343085	AY343085 Unculture
C 444	15.8	79.0	201187	9	AC116494	AC116494 Mus muscu	517	15.4	77.0	1005	3	AF1424507	AF1424507 Unculture
C 445	15.8	79.0	201379	8	AC121764	AC121764 Homo sapi	518	15.4	77.0	1005	3	AF142810	AF142810 Unculture
C 446	15.8	79.0	203717	8	AC157658	AC157658 Mus muscu	519	15.4	77.0	1008	4	SMJ4431	SMJ4431 Sorex min
C 447	15.8	79.0	204289	9	AC091263	AC091263 Mus muscu	520	15.4	77.0	1045	15	AF164325S1	AF164325 Entophlyc
C 448	15.8	79.0	204552	14	AC152625	AC152625 Bos tauru	521	15.4	77.0	1045	15	AF164327S1	AF164327 Physocled
C 449	15.8	79.0	206919	5	BX005076	BX005076 Zebrafish	522	15.4	77.0	1076	15	AB093034	AB093034 Pyrus com
C 450	15.8	79.0	212677	9	AC077689	AC077689 Mus muscu	523	15.4	77.0	1076	15	AB093034	AB093034 Pyrus com
C 451	15.8	79.0	212677	9	AC077689	AC077689 Mus muscu	524	15.4	77.0	1112	15	AF164323S1	AF164323 Chyrtiomy
C 452	15.8	79.0	213462	9	AC148894	AC148894 Oroleumr	525	15.4	77.0	1141	3	AY331783	AY331783 Unculture
C 453	15.8	79.0	215632	14	AC150697	AC150697 Bos tauru	526	15.4	77.0	1168	15	DO100329	DO100329 Eucalyptu
C 454	15.8	79.0	218484	14	CT0059713	CT0059713 Mus muscu	527	15.4	77.0	1312	15	AF516880	AF516880 Glycine m
C 455	15.8	79.0	218928	14	CT0059713	CT0059713 Mus muscu	528	15.4	77.0	1367	6	AX695969	AX695969 Sequence
C 456	15.8	79.0	219695	9	AC122252	AC122252 Mus muscu	529	15.4	77.0	1367	6	AX695969	AX695969 Sequence

C 530	15.4	77.0	1411	3	DQ067002	Unculture	C 603	15.4	77.0	103836	9	AC125670	AC125670 Rattus no
C 531	15.4	77.0	1424	3	AY921745	Unculture	C 604	15.4	77.0	106784	14	AC136250	AC136250 Rattus no
C 532	15.4	77.0	1435	6	C0722238	Sequence	C 605	15.4	77.0	107704	15	BX640523	BX640523 Zebrafish
C 533	15.4	77.0	1448	3	AF507879	Unculture	C 606	15.4	77.0	107740	15	AC069558	AC069558 Genomic S
C 534	15.4	77.0	1454	1	NSP16684	Unculture	C 607	15.4	77.0	107819	8	AL589685	AL589685 Human DNA
C 535	15.4	77.0	1472	3	AJ853628	Unculture	C 608	15.4	77.0	110000	1	BA000030	BA000030 03
C 536	15.4	77.0	1474	3	AF290065	Unculture	C 609	15.4	77.0	110000	1	CP000075	CP000075 51
C 537	15.4	77.0	1485	3	AJ853543	Unculture	C 610	15.4	77.0	110000	1	CP000075	CP000075 08
C 538	15.4	77.0	1485	3	DQ125868	Unculture	C 611	15.4	77.0	110000	14	AC091352	AC091352 0
C 539	15.4	77.0	1515	6	AK695973	Sequence	C 612	15.4	77.0	110000	14	AC091352	AC091352 03
C 540	15.4	77.0	1519	3	AY180041	Unculture	C 613	15.4	77.0	110000	14	AC091371	AC091371 03
C 541	15.4	77.0	1519	3	AY180041	Unculture	C 614	15.4	77.0	110000	14	AC091371	AC091371 04
C 542	15.4	77.0	1531	3	AY196681	Unculture	C 615	15.4	77.0	110000	14	AC098559	AC098559 0
C 543	15.4	77.0	1531	3	AY196681	Unculture	C 616	15.4	77.0	110000	14	AC105643	AC105643 2
C 544	15.4	77.0	1531	3	AY196681	Unculture	C 617	15.4	77.0	110000	14	AC105643	AC105643 3
C 545	15.4	77.0	1531	3	AY196681	Unculture	C 618	15.4	77.0	110000	14	AC110831	AC110831 1
C 546	15.4	77.0	1531	3	AY196681	Unculture	C 619	15.4	77.0	110000	14	AC112324	AC112324 2
C 547	15.4	77.0	1543	2	AY587129	Unculture	C 620	15.4	77.0	110000	14	AC132018	AC132018 2
C 548	15.4	77.0	1548	2	AY587129	Unculture	C 621	15.4	77.0	110000	14	AC151898	AC151898 4
C 549	15.4	77.0	1548	2	AY587129	Unculture	C 622	15.4	77.0	110000	14	AC153648	AC153648 0
C 550	15.4	77.0	1548	2	AY587129	Unculture	C 623	15.4	77.0	110000	14	AC157600	AC157600 3
C 551	15.4	77.0	1548	2	AY587129	Unculture	C 624	15.4	77.0	110000	14	AY819658	AY819658 0
C 552	15.4	77.0	1548	2	AY587129	Unculture	C 625	15.4	77.0	110000	15	AP008218	AP008218 205
C 553	15.4	77.0	1548	2	AY587129	Unculture	C 626	15.4	77.0	110000	15	AP008218	AP008218 206
C 554	15.4	77.0	1548	2	AY587129	Unculture	C 627	15.4	77.0	110000	15	AP008218	AP008218 207
C 555	15.4	77.0	1548	2	AY587129	Unculture	C 628	15.4	77.0	110000	15	AP008218	AP008218 207
C 556	15.4	77.0	1548	2	AY587129	Unculture	C 629	15.4	77.0	110000	15	AP008218	AP008218 207
C 557	15.4	77.0	1548	2	AY587129	Unculture	C 630	15.4	77.0	110000	15	AP008218	AP008218 207
C 558	15.4	77.0	1548	2	AY587129	Unculture	C 631	15.4	77.0	110000	15	AP008218	AP008218 207
C 559	15.4	77.0	1548	2	AY587129	Unculture	C 632	15.4	77.0	110000	15	AP008218	AP008218 207
C 560	15.4	77.0	1548	2	AY587129	Unculture	C 633	15.4	77.0	110000	15	AP008218	AP008218 207
C 561	15.4	77.0	1548	2	AY587129	Unculture	C 634	15.4	77.0	110000	15	AP008218	AP008218 207
C 562	15.4	77.0	1548	2	AY587129	Unculture	C 635	15.4	77.0	110000	15	AP008218	AP008218 207
C 563	15.4	77.0	1548	2	AY587129	Unculture	C 636	15.4	77.0	110000	15	AP008218	AP008218 207
C 564	15.4	77.0	1548	2	AY587129	Unculture	C 637	15.4	77.0	110000	15	AP008218	AP008218 207
C 565	15.4	77.0	1548	2	AY587129	Unculture	C 638	15.4	77.0	110000	15	AP008218	AP008218 207
C 566	15.4	77.0	1548	2	AY587129	Unculture	C 639	15.4	77.0	110000	15	AP008218	AP008218 207
C 567	15.4	77.0	1548	2	AY587129	Unculture	C 640	15.4	77.0	110000	15	AP008218	AP008218 207
C 568	15.4	77.0	1548	2	AY587129	Unculture	C 641	15.4	77.0	110000	15	AP008218	AP008218 207
C 569	15.4	77.0	1548	2	AY587129	Unculture	C 642	15.4	77.0	110000	15	AP008218	AP008218 207
C 570	15.4	77.0	1548	2	AY587129	Unculture	C 643	15.4	77.0	110000	15	AP008218	AP008218 207
C 571	15.4	77.0	1548	2	AY587129	Unculture	C 644	15.4	77.0	110000	15	AP008218	AP008218 207
C 572	15.4	77.0	1548	2	AY587129	Unculture	C 645	15.4	77.0	110000	15	AP008218	AP008218 207
C 573	15.4	77.0	1548	2	AY587129	Unculture	C 646	15.4	77.0	110000	15	AP008218	AP008218 207
C 574	15.4	77.0	1548	2	AY587129	Unculture	C 647	15.4	77.0	110000	15	AP008218	AP008218 207
C 575	15.4	77.0	1548	2	AY587129	Unculture	C 648	15.4	77.0	110000	15	AP008218	AP008218 207
C 576	15.4	77.0	1548	2	AY587129	Unculture	C 649	15.4	77.0	110000	15	AP008218	AP008218 207
C 577	15.4	77.0	1548	2	AY587129	Unculture	C 650	15.4	77.0	110000	15	AP008218	AP008218 207
C 578	15.4	77.0	1548	2	AY587129	Unculture	C 651	15.4	77.0	110000	15	AP008218	AP008218 207
C 579	15.4	77.0	1548	2	AY587129	Unculture	C 652	15.4	77.0	110000	15	AP008218	AP008218 207
C 580	15.4	77.0	1548	2	AY587129	Unculture	C 653	15.4	77.0	110000	15	AP008218	AP008218 207
C 581	15.4	77.0	1548	2	AY587129	Unculture	C 654	15.4	77.0	110000	15	AP008218	AP008218 207
C 582	15.4	77.0	1548	2	AY587129	Unculture	C 655	15.4	77.0	110000	15	AP008218	AP008218 207
C 583	15.4	77.0	1548	2	AY587129	Unculture	C 656	15.4	77.0	110000	15	AP008218	AP008218 207
C 584	15.4	77.0	1548	2	AY587129	Unculture	C 657	15.4	77.0	110000	15	AP008218	AP008218 207
C 585	15.4	77.0	1548	2	AY587129	Unculture	C 658	15.4	77.0	110000	15	AP008218	AP008218 207
C 586	15.4	77.0	1548	2	AY587129	Unculture	C 659	15.4	77.0	110000	15	AP008218	AP008218 207
C 587	15.4	77.0	1548	2	AY587129	Unculture	C 660	15.4	77.0	110000	15	AP008218	AP008218 207
C 588	15.4	77.0	1548	2	AY587129	Unculture	C 661	15.4	77.0	110000	15	AP008218	AP008218 207
C 589	15.4	77.0	1548	2	AY587129	Unculture	C 662	15.4	77.0	110000	15	AP008218	AP008218 207
C 590	15.4	77.0	1548	2	AY587129	Unculture	C 663	15.4	77.0	110000	15	AP008218	AP008218 207
C 591	15.4	77.0	1548	2	AY587129	Unculture	C 664	15.4	77.0	110000	15	AP008218	AP008218 207
C 592	15.4	77.0	1548	2	AY587129	Unculture	C 665	15.4	77.0	110000	15	AP008218	AP008218 207
C 593	15.4	77.0	1548	2	AY587129	Unculture	C 666	15.4	77.0	110000	15	AP008218	AP008218 207
C 594	15.4	77.0	1548	2	AY587129	Unculture	C 667	15.4	77.0	110000	15	AP008218	AP008218 207
C 595	15.4	77.0	1548	2	AY587129	Unculture	C 668	15.4	77.0	110000	15	AP008218	AP008218 207
C 596	15.4	77.0	1548	2	AY587129	Unculture	C 669	15.4	77.0	110000	15	AP008218	AP008218 207
C 597	15.4	77.0	1548	2	AY587129	Unculture	C 670	15.4	77.0	110000	15	AP008218	AP008218 207
C 598	15.4	77.0	1548	2	AY587129	Unculture	C 671	15.4	77.0	110000	15	AP008218	AP008218 207
C 599	15.4	77.0	1548	2	AY587129	Unculture	C 672	15.4	77.0	110000	15	AP008218	AP008218 207
C 600	15.4	77.0	1548	2	AY587129	Unculture	C 673	15.4	77.0	110000	15	AP008218	AP008218 207
C 601	15.4	77.0	1548	2	AY587129	Unculture	C 674	15.4	77.0	110000	15	AP008218	AP008218 207
C 602	15.4	77.0	1548	2	AY587129	Unculture	C 675	15.4	77.0	110000	15	AP008218	AP008218 207

C 676	15.4	77.0	153767	9	AC124981	AC124981 Mus muscu	749	15.4	77.0	187418	14	AC156240	AC156240 Bos tauru
C 677	15.4	77.0	154298	9	AL831773	AL831773 Mouse DNA	C 750	15.4	77.0	187600	14	AC140360	AC140360 Mus muscu
C 678	15.4	77.0	154447	8	AC146056	AC146056 Pan trogl	C 751	15.4	77.0	188880	9	AC092203	AC092203 Mus muscu
C 679	15.4	77.0	154542	14	AC079040	AC079040 Mus muscu	C 752	15.4	77.0	189296	9	AC122336	AC122336 Mus muscu
C 680	15.4	77.0	155034	9	AL662803	AL662803 Mouse DNA	C 753	15.4	77.0	189454	14	AC141044	AC141044 Mus muscu
C 681	15.4	77.0	156280	14	AC079595	AC079595 Homo sapi	C 754	15.4	77.0	189458	9	AC134908	AC134908 Mus muscu
C 682	15.4	77.0	158255	8	AC025695	AC025695 Homo sapi	C 755	15.4	77.0	189892	14	AC091425	AC091425 Mus muscu
C 683	15.4	77.0	158972	14	AC160538	AC160538 Mus muscu	C 756	15.4	77.0	189932	14	AC146117	AC146117 Mus muscu
C 684	15.4	77.0	160367	8	AC009542	AC009542 Homo sapi	C 757	15.4	77.0	190048	14	AL591126	AL591126 Mouse DNA
C 685	15.4	77.0	160697	14	AC003457	AC003457 Homo sapi	C 758	15.4	77.0	190149	9	AL713913	AL713913 Mouse DNA
C 686	15.4	77.0	161647	8	AC079080	AC079080 Homo sapi	C 759	15.4	77.0	190485	9	AL713913	AL713913 Mouse DNA
C 687	15.4	77.0	161652	9	AC140353	AC140353 Mus muscu	C 760	15.4	77.0	190937	14	AC103477	AC103477 Mus muscu
C 688	15.4	77.0	162087	14	AC115938	AC115938 Mus muscu	C 761	15.4	77.0	191328	9	AC159886	AC159886 Mus muscu
C 689	15.4	77.0	162455	9	AC125540	AC125540 Mus muscu	C 762	15.4	77.0	191723	9	AC121792	AC121792 Mus muscu
C 690	15.4	77.0	163800	9	AC122510	AC122510 Mus muscu	C 763	15.4	77.0	191904	9	AC158524	AC158524 Mus muscu
C 691	15.4	77.0	165012	14	AC117782	AC117782 Mus muscu	C 764	15.4	77.0	191920	14	AC129843	AC129843 Mus muscu
C 692	15.4	77.0	165241	9	AC161455	AC161455 Mus muscu	C 765	15.4	77.0	192062	9	AC121855	AC121855 Mus muscu
C 693	15.4	77.0	165781	9	AC101542	AC101542 Mus muscu	C 766	15.4	77.0	192200	14	AC163629	AC163629 Mus muscu
C 694	15.4	77.0	167145	9	AC158748	AC158748 Mus muscu	C 767	15.4	77.0	192367	8	AC010424	AC010424 Mus muscu
C 695	15.4	77.0	167418	9	AC133944	AC133944 Mus muscu	C 768	15.4	77.0	192282	14	AC121410	AC121410 Mus muscu
C 696	15.4	77.0	167526	14	AC121622	AC121622 Rattus no	C 769	15.4	77.0	192586	9	AL645972	AL645972 Mouse DNA
C 697	15.4	77.0	167691	14	AC103349	AC103349 Mus muscu	C 770	15.4	77.0	192586	14	AC129244	AC129244 Mus muscu
C 698	15.4	77.0	167775	9	AC112268	AC112268 Mus muscu	C 771	15.4	77.0	192687	14	AC097960	AC097960 Mus muscu
C 699	15.4	77.0	168107	9	AC124326	AC124326 Mus muscu	C 772	15.4	77.0	193147	14	AC097960	AC097960 Mus muscu
C 700	15.4	77.0	168482	9	AC145082	AC145082 Mus muscu	C 773	15.4	77.0	193469	9	AC128125	AC128125 Mus muscu
C 701	15.4	77.0	169059	14	AC009790	AC009790 Homo sapi	C 774	15.4	77.0	193811	9	AC142098	AC142098 Mus muscu
C 702	15.4	77.0	170292	9	AC132229	AC132229 Mus muscu	C 775	15.4	77.0	194189	8	AC103705	AC103705 Mus muscu
C 703	15.4	77.0	170321	9	AC108484	AC108484 Mus muscu	C 776	15.4	77.0	194209	9	AL928249	AL928249 Mouse DNA
C 704	15.4	77.0	170737	9	AC129180	AC129180 Mus muscu	C 777	15.4	77.0	194307	14	AC132042	AC132042 Mus muscu
C 705	15.4	77.0	171697	14	AC119116	AC119116 Rattus no	C 778	15.4	77.0	194593	9	AC116470	AC116470 Mus muscu
C 706	15.4	77.0	172499	8	AC146031	AC146031 Pan trogl	C 779	15.4	77.0	194616	14	AC186629	AC186629 Mus muscu
C 707	15.4	77.0	172595	9	AC145297	AC145297 Mus muscu	C 780	15.4	77.0	194627	9	AC150685	AC150685 Mus muscu
C 708	15.4	77.0	173022	9	AC140275	AC140275 Mus muscu	C 781	15.4	77.0	195017	9	AC154667	AC154667 Mus muscu
C 709	15.4	77.0	173472	9	AC131760	AC131760 Mus muscu	C 782	15.4	77.0	195129	9	AC105958	AC105958 Mus muscu
C 710	15.4	77.0	173493	14	AC136016	AC136016 Rattus no	C 783	15.4	77.0	195305	9	AC140233	AC140233 Mus muscu
C 711	15.4	77.0	173810	9	AC083815	AC083815 Mus muscu	C 784	15.4	77.0	196053	14	AC130953	AC130953 Mus muscu
C 712	15.4	77.0	174768	8	AC009330	AC009330 Homo sapi	C 785	15.4	77.0	196249	14	AC154418	AC154418 Mus muscu
C 713	15.4	77.0	174882	9	AC127273	AC127273 Mus muscu	C 786	15.4	77.0	196260	14	AC112606	AC112606 Mus muscu
C 714	15.4	77.0	175144	14	AC010415	AC010415 Homo sapi	C 787	15.4	77.0	196783	9	AC137855	AC137855 Mus muscu
C 715	15.4	77.0	175245	9	AC129188	AC129188 Mus muscu	C 788	15.4	77.0	196783	9	AC137855	AC137855 Mus muscu
C 716	15.4	77.0	176038	15	AC135915	AC135915 Oryza sat	C 789	15.4	77.0	197462	8	AL844592	AL844592 Mouse DNA
C 717	15.4	77.0	176092	9	AC129329	AC129329 Mus muscu	C 790	15.4	77.0	197639	8	AC009554	AC009554 Mus muscu
C 718	15.4	77.0	176354	14	BX855600	BX855600 Mus muscu	C 791	15.4	77.0	197658	14	AC124208	AC124208 Mus muscu
C 719	15.4	77.0	177047	14	AC138613	AC138613 Mus muscu	C 792	15.4	77.0	198374	14	AC118519	AC118519 Mus muscu
C 720	15.4	77.0	177336	14	AC128487	AC128487 Rattus no	C 793	15.4	77.0	198621	9	AC122828	AC122828 Mus muscu
C 721	15.4	77.0	177733	14	AC113908	AC113908 Rattus no	C 794	15.4	77.0	198621	9	AC139243	AC139243 Mus muscu
C 722	15.4	77.0	177885	14	AC141947	AC141947 Rattus no	C 795	15.4	77.0	198921	14	AC159972	AC159972 Mus muscu
C 723	15.4	77.0	178098	14	AC040955	AC040955 Mus muscu	C 796	15.4	77.0	199035	14	AB088420	AB088420 Pseudom
C 724	15.4	77.0	178562	14	AC152854	AC152854 Oryctolag	C 797	15.4	77.0	199098	14	AC156302	AC156302 Mus muscu
C 725	15.4	77.0	178868	14	AC160124	AC160124 Mus muscu	C 798	15.4	77.0	199204	14	AC131298	AC131298 Mus muscu
C 726	15.4	77.0	179162	14	AC132076	AC132076 Bos tauru	C 799	15.4	77.0	199207	9	AC124762	AC124762 Mus muscu
C 727	15.4	77.0	179927	9	AC154616	AC154616 Mus muscu	C 800	15.4	77.0	199240	9	AC124549	AC124549 Mus muscu
C 728	15.4	77.0	180079	9	AC114678	AC114678 Mus muscu	C 801	15.4	77.0	199341	14	AC112386	AC112386 Mus muscu
C 729	15.4	77.0	180136	9	AL773257	AL773257 Mouse DNA	C 802	15.4	77.0	199789	15	ATCRH1V89	ATCRH1V89 Mouse DNA
C 730	15.4	77.0	180353	14	AC128288	AC128288 Rattus no	C 803	15.4	77.0	200057	14	AC073810	AC073810 Mus muscu
C 731	15.4	77.0	180560	9	AC137605	AC137605 Mus muscu	C 804	15.4	77.0	200412	14	AC115666	AC115666 Mus muscu
C 732	15.4	77.0	181111	14	AC166857	AC166857 Oryctolag	C 805	15.4	77.0	200653	14	CT025540	CT025540 Mus muscu
C 733	15.4	77.0	182058	9	AC154412	AC154412 Mus muscu	C 806	15.4	77.0	200935	14	AC148834	AC148834 Mus muscu
C 734	15.4	77.0	182058	9	AC137950	AC137950 Mus muscu	C 807	15.4	77.0	201075	14	AC166870	AC166870 Oryctolag
C 735	15.4	77.0	182309	9	AC121846	AC121846 Mus muscu	C 808	15.4	77.0	201441	14	AC111527	AC111527 Mus muscu
C 736	15.4	77.0	182439	9	AL805955	AL805955 Mouse DNA	C 809	15.4	77.0	202404	9	AC115295	AC115295 Mus muscu
C 737	15.4	77.0	182439	9	AL805955	AL805955 Mouse DNA	C 810	15.4	77.0	202554	8	AC104447	AC104447 Homo sapi
C 738	15.4	77.0	182445	14	AC132717	AC132717 Rattus no	C 811	15.4	77.0	202554	14	AC163076	AC163076 Mus muscu
C 739	15.4	77.0	182962	14	AC132511	AC132511 Rattus no	C 812	15.4	77.0	202686	14	AC104447	AC104447 Homo sapi
C 740	15.4	77.0	182990	14	AC141383	AC141383 Rattus no	C 813	15.4	77.0	202768	9	AL589870	AL589870 Mouse DNA
C 741	15.4	77.0	183129	9	AC133282	AC133282 Mus muscu	C 814	15.4	77.0	203558	9	AL670464	AL670464 Mouse DNA
C 742	15.4	77.0	184074	14	AC148560	AC148560 Oryctolag	C 815	15.4	77.0	204031	14	AC093354	AC093354 Mus muscu
C 743	15.4	77.0	184174	9	AC121570	AC121570 Mus muscu	C 816	15.4	77.0	204313	14	AC126304	AC126304 Mus muscu
C 744	15.4	77.0	185232	9	AC127266	AC127266 Mus muscu	C 817	15.4	77.0	205084	9	AC121859	AC121859 Mus muscu
C 745	15.4	77.0	185321	14	AC110324	AC110324 Rattus no	C 818	15.4	77.0	206093	9	AC087330	AC087330 Mus muscu
C 746	15.4	77.0	185938	9	AC122037	AC122037 Mus muscu	C 819	15.4	77.0	206924	9	AC087780	AC087780 Mus muscu
C 747	15.4	77.0	186673	14	AL5590713	AL5590713 Homo sapi	C 820	15.4	77.0	206924	9	AC087780	AC087780 Mus muscu
C 748	15.4	77.0	187181	9	AL591854	AL591854 Mouse DNA	C 821	15.4	77.0	206924	9	AC087780	AC087780 Mus muscu

822	15.4	77.0	207429	9	AC150312	AC150312 Mus muscu	895	15.4	77.0	223497	14	AC15162	AC15162 Rattus no
823	15.4	77.0	207823	14	AC145542	AC145542 Oryctolag	896	15.4	77.0	223520	9	AC155636	AC155636 Mus muscu
824	15.4	77.0	208376	9	AC155160	AC155160 Mus muscu	897	15.4	77.0	223658	14	AC095283	AC095283 Rattus no
825	15.4	77.0	208483	9	AC107757	AC107757 Mus muscu	898	15.4	77.0	224019	14	AC131146	AC131146 Rattus no
826	15.4	77.0	208652	14	EX324228	EX324228 Mus muscu	899	15.4	77.0	224181	9	AC139671	AC139671 Mus muscu
827	15.4	77.0	208848	14	AC139608	AC139608 Rattus no	900	15.4	77.0	224344	14	AC108294	AC108294 Rattus no
828	15.4	77.0	208848	14	AC139608	AC139608 Rattus no	901	15.4	77.0	224522	14	AC106627	AC106627 Rattus no
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835	15.4	77.0	209907	9	AC118038	AC118038 Mus muscu	908	15.4	77.0	227026	14	AC136659	AC136659 Rattus no
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838	15.4	77.0	210891	14	AC153356	AC153356 Mus muscu	911	15.4	77.0	227679	9	AC109807	AC109807 Mus muscu
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851	15.4	77.0	213625	14	AC140950	AC140950 Rattus no	924	15.4	77.0	230026	14	AC109847	AC109847 Rattus no
852	15.4	77.0	213817	14	AC123649	AC123649 Mus muscu	925	15.4	77.0	230116	9	AL732620	AL732620 Mouse DNA
853	15.4	77.0	214121	14	AC136708	AC136708 Mus muscu	926	15.4	77.0	230168	14	AC091604	AC091604 Mus muscu
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866	15.4	77.0	215722	9	AC140457	AC140457 Mus muscu	939	15.4	77.0	232175	14	AC115380	AC115380 Rattus no
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871	15.4	77.0	217636	9	AC127411	AC127411 Mus muscu	944	15.4	77.0	233367	9	AC118931	AC118931 Mus muscu
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884	15.4	77.0	221906	14	AC117634	AC117634 Mus muscu	957	15.4	77.0	236337	14	AC161806	AC161806 Mus muscu
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888	15.4	77.0	222398	9	AC151838	AC151838 Mus muscu	961	15.4	77.0	236778	14	AC129110	AC129110 Rattus no
889	15.4	77.0	222536	14	AC117919	AC117919 Rattus no	962	15.4	77.0	237067	14	AC118339	AC118339 Rattus no
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892	15.4	77.0	223152	14	AC114994	AC114994 Mus muscu	965	15.4	77.0	237421	14	AC099103	AC099103 Rattus no
893	15.4	77.0	223292	14	AC133790	AC133790 Rattus no	966	15.4	77.0	237549	14	AC112451	AC112451 Rattus no
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968 15.4 77.0 237779 14 AC095321 Rattus no
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 C 1000 15.4 77.0 245907 14 AC095162 Rattus no

ALIGNMENTS

RESULT 1

AX104199 20 bp DNA linear PAT 30-APR-2001
 LOCUS AX104199
 DEFINITION Sequence 391 from Patent WO0122972.
 ACCESSION AX104199
 VERSION AX104199.1 GI:13920396
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Krieg, A.M., Schletter, C. and Vollmer, J.C.
 TITLE Immunostimulatory nucleic acids
 JOURNAL Patent: WO 0122972-A 391 05-APR-2001;
 UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
 GmbH (DE)
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 /db_xref="taxon:32630"

ORIGIN

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 Best Local Similarity 90.0%; Pred. No. 83;
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGUAAGCCAGACUACGA 20
 DB 1 AGGTAAGCCAGACUACGA 20

RESULT 2
 AX355040 20 bp DNA linear PAT 06-FEB-2002
 LOCUS AX355040



DEFINITION Sequence 68 from Patent WO0197843.
 ACCESSION AX355040
 VERSION AX355040.1 GI:18619707
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Weiner, G. and Hartmann, G.
 TITLE Methods for enhancing antibody-induced cell lysis and creating
 cancer
 JOURNAL Patent: WO 0197843-A 68 27-DEC-2001;
 UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
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RESULT 3

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 LOCUS AX547252
 DEFINITION Sequence 391 from Patent WO02053141.
 ACCESSION AX547252
 VERSION AX547252.1 GI:25812396
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Bratzler, R.L.
 TITLE Inhibition of angiogenesis by nucleic acids
 JOURNAL Patent: WO 02053141-A 391 11-JUL-2002;
 Coley Pharmaceutical Group, Inc. (US)
 FEATURES
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 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Synthetic Sequence"

ORIGIN

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 Best Local Similarity 90.0%; Pred. No. 83;
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RESULT 4

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 DEFINITION Rattus rattus mRNA for DNA cytosine 5 methyltransferase, complete
 cds.

ACCESSION AB012214
 VERSION AB012214.1 GI:4160669
 KEYWORDS DNA cytosine 5 methyltransferase.
 SOURCE Rattus rattus (black rat)
 ORGANISM Rattus rattus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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QY      2  GGUACAGCCAGGACTUACG  19
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Db     2679  GGTAACAGCCAGGACTTACG  2696

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Smlt, A.F.A. & Green, P. (1996-1997) . . .

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

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----- Genome Center
Center: Broad Institute of MIT and Harvard
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence\_submissions@broad.mit.edu
Project Information
Center project name: L26564
Center clone name: 187_P_1

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* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES
SOURCE

Query Match	Score	DB	Length
90.0%	18	14	192617

QY 3 GUACAGCCAGGACTUACGA 20
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Db 24573 GTACAGCCAGGACTACGA 24556

RESULT 6				
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LOCUS	Rattus norvegicus clone CH230-11C16,	*** SEQUENCING IN PROGRESS		
DEFINITION	*** 5 unordered pieces.			
ACCESSION	ACI35310			
VERSION	ACI35310.2 GI:24941813			
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.			
SOURCE	Rattus norvegicus (Norway rat)			
ORGANISM	Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
REFERENCE	1 (bases 1 to 243411)			

AUTHORS

Muzny, D. Marine, Metzker, M. Lee, Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Anyalebech, V., Aoyagi, A., Ayodeji, I. M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bubay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Cessari, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Demson, S., Deamo, C., Ding, Y., Dinh, H., Diya, K., Draper, H., Dugan-Rochs, S., Dunn, A., Dudbin, K., Duval, B., Eaves, K., Egan, A., Becotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Galbis, A., Gante, R., Garcia, A., Garner, T., Garza, M., Gebregregios, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Healand, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Haylak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladin, S. L., Hodgson, A., Hogues, J., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Kackapathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, T., Lewis, L., Li, Z., Liu, J., Liu, U., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenzshewna, L., Louissegh, H., Loyado, R. J., Lu, X., Ma, J., Mangun, B. M., Mahndartine, M., Mahmood, M., Malloy, K., Mangum, A., Manishwari, M., Martin, K., Martin, R., Martinez, E., Manu, B., Mapua, P., Martin, K., Mehall, T. Z., Meenan, E., Mahoney, S., McLeod, M. P., McNell, T. Z., Montenor, J., Milosavljevic, A., Miner, G., Morris, N., Mundasa, M., Murphy, M., Nair, L., Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Nair, L., Nakeriya, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokotemeh, O., Okwomou, G., Olampunsaagoun, A., Pal, S., Parks, K., Paternack, S., Paul, H., Perez, A., Perez, L., Pfamknoch, C., Poldner, F., Poldner, A., Popovic, D., Primus, E., Pu, L., T., Rieves, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Sanders, W., Savatsky, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajic, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorrelle, R., Sosa, T., Steinle, M., Strong, R., Sutton, A., Svetek, A., Taber, P., Taylor, T., Thomas, N., Thomas, S., Tinney, A., Trejos, Z., Umanan, K., Vals, R., Verz, V., Villaseana, D., Waldron, L., Walker, B., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczky, R., Wooden, H., Wotley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yan, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Neiderhausen, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstein, G., and Gibbs, R. A.

COMMENT

REFERENCE AUTHORS TITLE JOURNAL	COMMENT
3 (bases 1 to 243411) Rat Genome Sequencing Consortium. Direct Submission Submitted (13-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 13, 2002 this sequence version replaced gi:23915440.	combination of BAC based reads

genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GEMP

Center clone name: CH230-11C16

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 217795 bases at least Q40

Consensus quality: 222117 bases at least Q30

Consensus quality: 224860 bases at least Q20

Estimated insert size: 223813; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces

* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

```
1 24504: contig of 24504 bp in length
* 24505 24604: gap of unknown length
* 24605 24605: contig of 72591 bp in length
* 97196 97295: gap of unknown length
* 97296 210508: contig of 113213 bp in length
* 210509 210608: gap of unknown length
* 210609 228026: contig of 17418 bp in length
* 228027 228126: gap of unknown length
* 228127 243411: contig of 15285 bp in length.
```

FEATURES

source

1..243411

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-11C16"

5084..5594

/note="clone_boundary"

clone_end:17

site:

end_sequence:BH320807"

complement(22562..23010)

/note="clone_boundary"

clone_end:5p6

site:

end_sequence:BH320808"

23397..24504

/note="wgs_end_extension"

clone_end:5p6"

24505..24604

/estimated_length=unknown

24605..26284

/note="wgs_end_extension"

clone_end:5p6"

97196..97295

/estimated_length=unknown

101862..103349

/note="wgs_end_extension"

clone_end:5p6"

188174..190069

/note="wgs_end_extension"

clone_end:5p6"

210509..210608

/estimated_length=unknown

221883..223151

/note="wgs_end_extension
clone_end:5p6"
228027..228126
/estimated_length=unknown

gap

ORIGIN

Query Match

Best Local Similarity 88.9%; Pred. No. 4.4e+02; Length 243411;

Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy

2 GGUACGCCAGCAGCAGC 19

Db 163253 GGTACAGCCAGCAGCAGC 163270

RESULT 7

HS48H8R

LOCUS

DEFINITION

H.sapiens Cpg island DNA genomic Meel fragment, clone 48h8, reverse

read cp948h8.rta.

Z61248.1 GI:1033626

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1

Cross, S.H., Charlton, J.A., Nan, X., and Bird, A.P.

Purification of Cpg islands using a methylated DNA binding column

Nat. Genet. 6 (3), 236-244 (1994)

8012384

2 (bases 1 to 266)

MacDonald, M., Huckle, E., Wilkinson, P. and Micklem, G.

Direct Submission

Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire,

CB10 1RQ, England. E-mail contact: humquerry@sanger.ac.uk

Vector: pGEM-5Zf(-)

Clones are available from the UK MRC Human Genome Mapping Project

Resource Centre, Hinxton, Cambridgeshire CB10 1RQ, UK. See URL:

<http://www.hgmp.mrc.ac.uk/> for details

or contact: biobelp@hmp.mrc.ac.uk.

location/Qualifiers

1..266

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="48h8"

/sex="male"

/tissue_type="blood"

/clone_id="CGI-1"

/dev_stage="adult"

ORIGIN

Query Match

Best Local Similarity 87.0%; Score 17.4; DB 8; Length 266;

Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGUACAGCCAGCAGCAGC 19

Db 54 AGTACAGCCAGCAGCAGC 72

RESULT 8

HS70G5F

LOCUS

DEFINITION

H.sapiens Cpg island DNA genomic Meel fragment, clone 70g5, forward

read cp970g5.ftdb.

Z66016

VERSION

KEYWORDS

SOURCE

266016.1 GI:1038838
Cpg island; genomic Meel fragment.
Homo sapiens (human)

```

ORGANISM
Homo sapiens
Mammalia: Eutheria, Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

REFERENCE
AUTHORS Cross,S.H., Charlton,J.A., Nan,X. and Bird,A.P.
TITLE Purification of CpG islands using a methylated DNA binding column
JOURNAL Nat. Genet. 6 (3), 236-244 (1994)
PUBMED 8012384

COMMENT
2 (bases 1 to 275)
MacDonald,M., Huckle,E., Wilkinson,P. and Mickleam,G.
Direct Submission
Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire,
CB10 1RQ, England. E-mail contact: humquery@sanger.ac.uk
Vector: pGEM-5Zf(-)
Clones are available from the UK MRC Human Genome Mapping Project
Resource Centre, Hinxton, Cambridgeshire CB10 1RQ, UK. See URL:
http://www.hgmp.mrc.ac.uk/ for details
or contact: biocentre@hgmp.mrc.ac.uk.
location/Qualifiers
1..275
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="70g5"
/sex="male"
/tissue_type="blood"
/clone_id="CGI-1"
/dev_stage="adult"

ORIGIN

Query Match 87.0%; Score 17.4; DB 8; Length 275;
Best Local Similarity 84.2%; Pred. No. 1.3e+03;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY
1 AGGACGACGACGACGACG 19
|||||:|||||:|||||
54 AGGTACAGCCGCGACTACG 72

RESULT 9
AC073834/c 172415 bp DNA linear PRI 16-Apr-2005
LOCUS AC073834
DEFINITION Homo sapiens BAC clone RP11-250N10 from 2, complete sequence.
ACCESSION AC073834
VERSION AC073834.6 GI:13677134
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 172415)
Cordum,H., Belter,E. and Mishra,S.
The sequence of Homo sapiens BAC clone RP11-250N10
Unpublished (2001)
2 (bases 1 to 172415)
Waterston,R.H.
Direct Submission
Submitted (29-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
3 (bases 1 to 172415)
Waterston,R.H.
Direct Submission
Submitted (23-MAY-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 172415)
Waterston,R.
Direct Submission
Submitted (07-NOV-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

```

```

REFERENCE 5 (bases 1 to 172415)
AUTHORS Wilson R.K.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2005) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Apr 19, 2001 this sequence version replaced gi:13491268.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@wustl.wustl.edu
----- Summary Statistics
Center project name: H_NH0250N10
-----

NOTICE:
This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
http://genome.wustl.edu

SOURCE INFORMATION:
The RPc1-11 human BAC library was made from the blood of one male
donor, as described by Ossegewa, K., Moon, P.Y., Zhao, B., Frengen, B.,
Tateno, M., Catanehe, J.J., and de Jong, P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at http://www.chori.org
VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-540F24; the clone sequenced
to the right is RP11-91J18. Actual start of this clone is at base
position 1 of RP11-250N10; actual end is at base position 172415 of
RP11-250N10.

FEATURES
source      Location/Qualifiers
            1..172415
             /organism="Homo sapiens"
             /mol_type="Genomic DNA"
             /db_xref="taxon:9606"
             /chromosome="2"
             /clone="RP11-250N10"
             /clone_1fb="RPc1-11"
            1066..31373
             /gene="AGPS"
             /join(1066..1127,6915..7004,14365..14464,16844..16901,
            31170..31373)
             /gene="AGPS"
             /join(1066..1127,6915..7004,14365..14464,16844..16901,
            31170..31373)
             /gene="AGPS"
             /note="Homo sapiens alkylglycerone phosphate synthase
            (AGPS), mRNA.; H_NH0250N10.1
            This gene was based on gi(4501992)
            Continued from H_NH0540F24.1"
             /codon_start=1
             /product="unknown"
             /protein_id="AAK93112.1"
             /db_xref="GI:62702186"
             /translation="DIALEHYVLGHSFETSPAMRWVDLCNVERITRCKEKGQVF
            APTSCRVLTQYDAGACIYFAFAYRGIISDPLTVFETQEAARERILLANGSLSHRH

```

```

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sw:
SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-326K2 is
from the RPCT-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBAC3.6.

FEATURES
SOURCE
    location/Qualifiers
        1..200966
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10090"
            /chromosome="11"
            /clone="RP23-326K2"
            /clone_1id="RPCT-23"

ORIGIN
Query Match      87.0%; Score 17.4; DB 9; Length 200966;
Best Local Similarity 89.5%; Pred. No. 8,7e+02;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy      1 AGGACGACCGCAGACGACG 19
        ||| ||||| ||||| |||
Db      166365 AGGACGACCGCAGACTACG 166347

RESULT 11      598 bp      DNA      linear      ENV 20-MAR-2004
LOCUS      AY547816/c
DEFINITION      Uncultured bacterium clone B42-25.04 16S ribosomal RNA gene,
partial sequence.
ACCESSION      AY547816
VERSION      AY547816.1 GI:45439624
KEYWORDS      ENV.
ORGANISM      uncultured bacterium
                uncultured bacterium
                Bacteria; environmental samples.
REFERENCE      1 (bases 1 to 598)
AUTHORS      van der Wielen, P.W.J.J.
TITLE      Prokaryotic communities in the interface of the deep hypersaline
                anoxic Bannock basin, Eastern Mediterranean
JOURNAL.      Unpublished
REFERENCE      2 (bases 1 to 598)
AUTHORS      van der Wielen, P.W.J.J.
TITLE      Direct Submissions
SUBMITTER      Submitted (13-FEB-2004) Microbial Ecology, University of Groningen,
                Kercklaan 30, Haren 9751 NN, The Netherlands
FEATURES
SOURCE      location/Qualifiers
        1..598
            /organism="uncultured bacterium"
            /mol_type="genomic DNA"
            /isolation_source="Drine interface of Bannock basin,
                Eastern Mediterranean"
            /db_xref="taxon:77133"
            /clone="B42-25.04"
            /environmental_sample
            <1..598
                /product="16S ribosomal RNA"

```

ORIGIN

Query Match 85.0%; Score 17; DB 3; Length 598;
 Best Local Similarity 88.2%; Pred. No. 2e+03;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 UACAGCCAGGACUACGA 20
 :|||||:|||||:
 Db 57 TACAGCCAGGACTACGA 41

RESULT 12
 AY164354/c 700 bp DNA linear ENV 28-DEC-2004
 LOCUS Uncultured Verrucomicrobia bacterium clone ALIB-68 16S ribosomal
 DEFINITION RNA gene, partial sequence.

ACCESSION AY164354
 VERSION AY164354.1 GI:27371648
 KEYWORDS ENV.

SOURCE uncultured Verrucomicrobia bacterium
 ORGANISM Bacteria; Verrucomicrobia; environmental samples.

REFERENCE 1 (bases 1 to 700)
 AUTHORS van der Wielen, P.W.J.J., Brons, J.K. and Bolhuis, H.
 TITLE Bacterial and Archaeal Communities of 4 Deep-Sea Hypersaline Anoxic Basins in the Mediterranean Sea

JOURNAL Unpublished
 2 (bases 1 to 700)
 REFERENCES van der Wielen, P.W.J.J., Brons, J.K. and Bolhuis, H.
 AUTHORS Direct Submission
 TITLE Submitted (14-OCT-2002) CEES, University of Groningen, Laboratory of Microbial Ecology, Kerklaan 30, Haren 9751 NN, The Netherlands

FEATURES
 source location/Qualifiers
 1..700
 /organism="uncultured Verrucomicrobia bacterium"
 /mol_type="genomic DNA"
 /isolation_source="hypersaline anoxic basin; brine interface of L'Atalante, Mediterranean Sea"
 /db_xref="taxon:156588"
 /clone="ALIB-68"
 /environmental_sample
 <1..>700
 /product="16S ribosomal RNA"

ORIGIN
 rRNA

Query Match 85.0%; Score 17; DB 3; Length 700;
 Best Local Similarity 88.2%; Pred. No. 1.9e+03;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 UACAGCCAGGACUACGA 20
 :|||||:|||||:
 Db 129 TACAGCCAGGACTACGA 113

RESULT 13
 AY164380 700 bp DNA linear ENV 28-DEC-2004
 LOCUS Uncultured Verrucomicrobia bacterium clone BLIB-55 16S ribosomal
 DEFINITION RNA gene, partial sequence.

ACCESSION AY164380
 VERSION AY164380.1 GI:27371674
 KEYWORDS ENV.

SOURCE uncultured Verrucomicrobia bacterium
 ORGANISM Bacteria; Verrucomicrobia; environmental samples.

REFERENCE 1 (bases 1 to 700)
 AUTHORS van der Wielen, P.W.J.J., Brons, J.K. and Bolhuis, H.
 TITLE Bacterial and Archaeal Communities of 4 Deep-Sea Hypersaline Anoxic Basins in the Mediterranean Sea

JOURNAL Unpublished
 2 (bases 1 to 700)
 REFERENCES van der Wielen, P.W.J.J., Brons, J.K. and Bolhuis, H.
 AUTHORS Direct Submission
 TITLE

JOURNAL Submitted (14-OCT-2002) CEES, University of Groningen, Laboratory of Microbial Ecology, Kerklaan 30, Haren 9751 NN, The Netherlands
 Location/Qualifiers

FEATURES

source
 1..700
 /organism="uncultured Verrucomicrobia bacterium"
 /mol_type="genomic DNA"
 /isolation_source="hypersaline anoxic basin; brine interface of Bannock, Mediterranean Sea"
 /db_xref="taxon:156588"
 /clone="BLIB-55"
 /environmental_sample
 <1..>700
 /product="16S ribosomal RNA"

ORIGIN

Query Match 85.0%; Score 17; DB 3; Length 700;
 Best Local Similarity 88.2%; Pred. No. 1.9e+03;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 UACAGCCAGGACUACGA 20
 :|||||:|||||:
 Db 134 TACAGCCAGGACTACGA 118

RESULT 14
 AF011463/c 1908 bp rRNA linear INV 05-APR-2004
 LOCUS Monopylocystis viresvarai small subunit ribosomal RNA, complete
 DEFINITION sequence.

ACCESSION AF011463
 VERSION AF011463
 KEYWORDS AF011463.1 GI:4102252

SOURCE Monopylocystis viresvarai
 ORGANISM Monopylocystis viresvarai
 Monopylocystis viresvarai
 Eukaryota; Heterolobosea; Monopylocystis.

REFERENCE 1 (bases 1 to 1908)
 AUTHORS O'Kelly, C.J., Silberman, J.D., Amaral Zettler, L.A., Nerd, T.A. and Sogin, M.L.
 TITLE Monopylocystis viresvarai N. Gen., N. Sp. and Sawyeria marylandensis N. Gen., N. Sp.: Two New Amoebozoan Heterolobosean Amoeboae from Anoxic Environments

JOURNAL Unpublished
 2 (bases 1 to 1908)
 REFERENCES Silberman, J.D., Roger, A.J., Nerd, T.A., Gunderson, J.H. and Sogin, M.L.
 AUTHORS Direct Submission
 TITLE Submitted (30-JUN-1997) Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, 7 MBL St., Woods Hole, MA 02543, USA

JOURNAL Unpublished
 2 (bases 1 to 1908)
 REFERENCES Silberman, J.D., Roger, A.J., Nerd, T.A., Gunderson, J.H. and Sogin, M.L.
 AUTHORS Direct Submission
 TITLE Submitted (30-JUN-1997) Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, 7 MBL St., Woods Hole, MA 02543, USA

FEATURES

source location/Qualifiers
 1..1908
 /organism="Monopylocystis viresvarai"
 /mol_type="rRNA"
 /strain="ATCC 50576"
 /db_xref="ATCC:50576"
 /db_xref="taxon:63603"
 1..1908
 /product="small subunit ribosomal RNA"

ORIGIN

Query Match 85.0%; Score 17; DB 2; Length 1908;
 Best Local Similarity 88.2%; Pred. No. 1.8e+03;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 UACAGCCAGGACUACGA 20
 :|||||:|||||:
 Db 1107 TACAGCCAGGACTACGA 1091

RESULT 15
 AC160912 177687 bp DNA linear HTG 04-MAY-2005
 LOCUS Rhinolphus ferrugineum clone VWRCT-253D3, WORKING DRAFT
 DEFINITION

FEATURES	SEQUENCE, 8 unordered pieces.
ACCESSION	AC160912
VERSION	HTG_0912.1 GI:63025317
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE	Rhinolophus ferrumequinum (greater horseshoe bat)
ORGANISM	Rhinolophus ferrumequinum
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Chiroptera; Microchiroptera; Rhinolophidae; Rhinolophinae; Rhinolophus.
AUTHORS	Antonacci, A., Ayele, K., Benjamin, B., Blakesley, R.W., Boakye, A., Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, H., Engle, J., Fukeenko, T., Gesto, M., Greene, A., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hunter, G., Hult, B., Idol, J.R., Kwong, P., Latic, P., Larson, S., Lee-Lin, S.-Q., Legaaspi, R., Madden, M., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Maestri, C., Maekker, B., McDowell, J., Mojidi, H.A., Mullikin, J.C., Oestreicher, J.S., Park, M., Portnoy, M.B., Prasad, A., Puri, O., Reddi-Dugue, N., Schandler, K., Schueler, M.G., Sison, C., Stanttirop, S., Stephen, B., Teye, A., Thomas, J.W., Thomas, P.J., Tsipouri, V., Ung, L., Vogt, J.L., Wetherby, K.D., Young, A. and Green, B.D.
TITLE	NISC Comparative Sequencing Initiative
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 176687)
AUTHORS	Green, B.D.
TITLE	Direct Submission
JOURNAL	Submitted (04-MAY-2005) NIH Intramural Sequencing Center, 5625 Fishers Lane, Rockville, MD 20852, USA
COMMENT	----- Genome Center
	Center: NIH Intramural Sequencing Center
	Center code: NISC
	Web site: http://www.nisc.nih.gov
	Contact: nisc.zoo@nih.gov
	----- Project Information
	Center project name: ifr
	Center clone name: 253D03
	----- Summary Statistics
	Sequencing vector: plasmid; n/a; 100% of reads
	Chemistry: Dye-terminator Big Dye, 100% of reads
	Assembly program: Phrap; Version 0.990319
	Consensus quality: 174630 bases at least Q40
	Consensus quality: 175229 bases at least Q20
	Consensus quality: 175664 bases at least Q20
	Insert size: 192000; agarose-fp
	Insert size: 176987; sum-of-contigs
	Quality coverage: 9.86x in Q20 bases; agarose-fp
	Quality coverage: 10.69x in Q20 bases; sum-of-contigs

	* NOTE: This is a 'working draft' sequence. It currently
	* consists of 8 contigs. The true order of the pieces
	* is not known and their order in this sequence record is
	* arbitrary. Gaps between the contigs are represented as
	* runs of N, but the exact sizes of the gaps are unknown.
	* This record will be updated with the finished sequence
	* as soon as it is available and the accession number will
	* be preserved.

	1 9793: contig of 9793 bp in length
	* 9794 9893: gap of unknown length
	* 9894 21264: contig of 11371 bp in length
	* 21265 21364: gap of unknown length
	* 21365 33884: contig of 12520 bp in length
	* 33885 33984: gap of unknown length
	* 33985 48903: contig of 14919 bp in length
	* 48904 49003: gap of unknown length
	* 49004 69905: contig of 20902 bp in length
	* 69906 70005: gap of unknown length
	* 70006 97843: contig of 27837 bp in length
	* 97843 135962: gap of unknown length
	* 135963 136062: contig of 38020 bp in length
	* 136063 176687: gap of unknown length
	* 176687: contig of 41625 bp in length.

	Location/Qualifiers

```

source
1. 177687
/organism="Rhinolophus ferrumequinum"
/mol_type="genomic DNA"
/db_xref="taxon:59479"
/clone="VMRC7-253D3"
/clone_id="VMRC7"
/notes="TAC resource: http://bacpac.chori.org/"
1. 9793
/notes="assembly_fragment"
9794. .9893
/estimated_length=unknown
9894. 21254
/notes="assembly_fragment"
21255. 21364
/estimated_length=unknown
21365. 33884
/notes="assembly_fragment"
33885. 33984
/estimated_length=unknown
33985. 48903
/notes="assembly_fragment"
48904. 49003
/estimated_length=unknown
49004. 69305
/notes="assembly_fragment"
clone_end:SP6
vector_side:right"
69306. 70005
/estimated_length=unknown
70006. 97842
/notes="assembly_fragment"
97843. 97942
/estimated_length=unknown
97943. 135962
/notes="assembly_fragment"
135963. 136062
/estimated_length=unknown
136063. 177687
/notes="assembly_fragment"

ORIGIN
Query Match 85.0%; Score 17; DB 14; Length 177687;
Best Local Similarity 88.2%; Pred. No. 1.4e+03;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGUACAGCGACGACUAC 18
||:|||||:||||:|
Db 56007 GGTACAGCGACGACTAC 55991

RESULT 16
AC118070 191592 bp DNA linear HTG 11-OCT-2002
AC118070 Rattus norvegicus clone CH230-377A5, *** SEQUENCING IN PROGRESS
***, 5 unordered pieces.
AC118070
AC118070.6 GI:23813463
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Rattus.
1 (bases 1 to 191592)
Muzny,D,Marle, Metzker,M,Lee, Abramson,S, Adams,C, Alder,J,
Allen,C, Allen,H, Alsbrooks,S, Amin,A, Angiano,D,
Anyalebechi,V, Aoyagi,A, Ayodeji,M, Baca,E, Baden,H,
Baldwin,D, Bandaranaike,D, Barber,M, Barnstead,M, Bernabed,F,
Blawie,K, Blair,J, Blankensbury,K, Blyth,P, Brown,M,
Bryant,N, Buhey,C, Burch,P, Burrell,K, Calderon,E,
Cardenas,V, Carter,K, Cavazos,I, Ceasar,H, Center,A,
Chacko,J, Chavez,D, Chen,G, Chen,R, Chen,Y, Chen,Z, Chu,J,
Cleveland,C, Cockrell,R, Cox,C, Coyle,M, Cree,A, D'Souza,L,

```


DEFINITION Mus musculus BAC clone RP23-323M20 from chromosome 13, complete sequence.

ACCESSION AC154620 AC120857

VERSION AC154620.2 GI:71725589

KEYWORDS HTG.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 193801)

AUTHORS Tiran, L. and Cotton, M.

TITLE The sequence of Mus musculus BAC clone RP23-323M20

JOURNAL Unpublished (2001)

REFERENCE 2 (bases 1 to 193801)

AUTHORS Wilson, R.K.

TITLE Direct Submission

JOURNAL Submitted (30-DEC-2004) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 3 (bases 1 to 193801)

AUTHORS Wilson, R.K.

TITLE Direct Submission

JOURNAL Submitted (12-JAN-2005) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 4 (bases 1 to 193801)

AUTHORS Wilson, R.K.

TITLE Direct Submission

JOURNAL Submitted (03-AUG-2005) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

COMMENT On Aug 3, 2005 this sequence version replaced gi:5690246.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu>

Contact: submissions@wustl.wustl.edu

----- Summary Statistics

Center project name: M_BA0323M20

Drafting center: WTB

NOTICE:

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e. phred quality >30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone, fosmid clone or direct clone walk sequence. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to obtain the consensus sequence. The assembly was confirmed by restriction digest.

This finishing standard has slightly changed from the previous human standard. Specifically, standards for regions of low sequence complexity (such as dinucleotide repeats and small unit tandem repeats) have been relaxed. These regions are very prevalent in the mouse genome, and the return on extended finishing efforts is minimal.

If a sequence meets the criteria of the above statement, it needs no comments or tags. If the criteria are not met, such as ambiguous bases, then the region is duly annotated.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

SOURCE INFORMATION:

The BAC library has been constructed by Kazutoyo Osegawa and Minako Terezo in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (<http://www.resgen.com>) or

FEATURES

source

Pieter de Jong and coworkers at <http://www.chori.org>

This sequence is the entire insert of the clone.

Location/Qualifiers

1..193801

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/chromosome="13"

/clone="RP23-323M20"

/clone_1id="RPC1-23"

125240..125409

/note="Unresolved simple sequence repeat."

125410..125453

/note="Sequence derived from one plasmid subclone."

168907..168928

/note="Unresolved homopolymeric repeat."

172159..172248

/note="Unresolved simple sequence repeat."

ORIGIN

Query Match 85.0%; Score 17; DB 9; Length 193801;

Best Local Similarity 88.2%; Pred. No. 1.4e+03;

Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GUACGCCAGACGACG 19

Db 61853 GTACAGCCAGACTACG 61837

RESULT 18

LOCUS CT025535

DEFINITION Mus musculus chromosome 14 clone RP23-35905, *** SEQUENCING IN PROGRESS ***

ACCESSION CT025535

VERSION CT025535.3 GI:71793992

KEYWORDS HTG; HTGS PHASE1.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLR

JOURNAL

COMMENT

CT025535 194439 bp DNA linear HTG 03-AUG-2005

Mus musculus chromosome 14 clone RP23-35905, *** SEQUENCING IN PROGRESS ***

CT025535

CT025535.3 GI:71793992

HTG; HTGS PHASE1.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

1 (bases 1 to 194439)

Stma,S.

Direct Submission

Submitted (02-AUG-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk

Clone requests: clonerequest@sanger.ac.uk

On Aug 3, 2005 this sequence version replaced gi:71793983.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: vegas@sanger.ac.uk

----- Project Information

Center project name: BM35905

----- Summary Statistics

Assembly program: XGAP4; version 4.5

Chemistry: Dye-terminator; 100% of reads

Consensus quality: 192076 bases at least Q40

Consensus quality: 192699 bases at least Q30

Consensus quality: 193232 bases at least Q20

Insert size: 193739; sum-of-contigs

Insert size: 193745; 4.7% error; agarose-fp

Quality coverage: 7.84x in Q20 bases; sum-of-contigs Quality coverage: 7.84x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 1 43304: contig of 43304 bp in length
 * 43305 43404: gap of 100 bp
 * 43405 70409: contig of 27005 bp in length
 * 70410 70509: gap of 100 bp
 * 70510 77402: contig of 6893 bp in length
 * 77403 77502: gap of 100 bp
 * 77503 86407: contig of 8905 bp in length
 * 86408 86507: gap of 100 bp
 * 86508 166030: contig of 79523 bp in length
 * 166031 166130: gap of 100 bp
 * 166131 177242: contig of 11112 bp in length
 * 177243 177342: gap of 100 bp
 * 177343 187735: contig of 10393 bp in length
 * 187736 187835: gap of 100 bp
 * 187836 194439: contig of 6604 bp in length.

FEATURES

source
 1. 194439
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /chromosome="14"
 /clone="RP23-35905"
 /clone_11b="RPC1-23"
 1. 43304
 /note="assembly_fragment:00748
 fragment_chain:1
 clone_end:SP6
 vector_side:left"

misc_feature

43405..70409
 /note="assembly_fragment:00476
 fragment_chain:1"

misc_feature

70510..77402
 /note="assembly_fragment:00073
 fragment_chain:1"

misc_feature

77503..86407
 /note="assembly_fragment:00152
 fragment_chain:1"

misc_feature

86508..166030
 /note="assembly_fragment:01224
 fragment_chain:1"

misc_feature

166131..177242
 /note="assembly_fragment:00235
 fragment_chain:1"

misc_feature

177343..187735
 /note="assembly_fragment:00354
 fragment_chain:1"

misc_feature

187836..194439
 /note="assembly_fragment:00001
 fragment_chain:1
 clone_end:T7
 vector_side:right"

ORIGIN

Query Match 85.0%; Score 17; DB 14; Length 194439;
 Best Local Similarity 88.2%; Pred. No. 1.4e+03;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GUNACGACGAGACUACG 19
 |:|||||:|||||:|||||
 Db 166983 GTACAGCCAGACTACG 166999

RESULT 19
 AC108255 AC108255 252467 bp DNA linear HTG 13-MAY-2003
 LOCUS Rattus norvegicus clone CH230-2952, *** SEQUENCING IN PROGRESS ***
 DEFINITION 4 unordered pieces.
 AC108255
 AC108255 5 GI:30580587
 VERSION
 KEYWORDS HTG, HTGS_PHASE1, HTGS_DRAFT, HTGS_ENRICHED.

SOURCE

ORGANISM

Rattus norvegicus (Norway rat)
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Rattus.
 1 (bases 1 to 252467)

REFERENCE

Muzny D, Marie, Metzker M, Lee, Abramson S, Adams C, Alder J,
 Allen C, Allen H, Alperin S, Amin A, Anguiano D,
 Anyalebech V, Ayegbi A, Ayodeji M, Baca E, Baden H,
 Baldwin D, Bandaranaike D, Barber M, Barnstead M, Benhamed F,
 Biswal N, Blair J, Blankenburg K, Blyth P, Brown M,
 Bryant N, Buhay C, Burch P, Butrell K, Calderon E,
 Cardenas V, Carter K, Cavazos I, Caesar H, Center A,
 Chacko J, Chavez D, Chen G, Chen Y, Chen Z, Chu J,
 Cleveland C, Cockrell R, Cox C, Coyle M, Cree A, D'Souza L,
 Davila M, Davis C, Deramo C, Ding Y, Dinh H, Diya K,
 Delgado O, Denson S, Dunn A, Durbin K, Duval B, Eaves K,
 Draper H, Dugan-Rocha S, Dunn A, Durbin K, Duval B, Eaves K,
 Egan A, Escotto M, Eugene C, Evans C, Falls T, Fan G,
 Fernandez S, Finley M, Flagg N, Forbes L, Foster P,
 Fraser C, Gabriel A, Ganta R, Garcia A, Garner T, Garza M,
 Gebregeorgis E, Geier K, Gill R, Grady M, Guerra M, Guevara W,
 Gunaratne P, Haaland W, Hamill C, Hamilton C, Hamilton K,
 Harvey Y, Havlak P, Hawes A, Henderson N, Hernandez J,
 Hernandez R, Hines S, Hladun S, Hodgson A, Hogue M,
 Hollins B, Howell S, Hulik S, Hume J, Idelbird D, Jackson A,
 Jackson L, Jacob L, Jiang S, Khan Z, King L, Kovar C,
 Karpachy S, Kelly S, Kelly S, Khan Z, Lewis L, Liu J,
 Kowalski C, Krafic C, Lebow H, Levan J, Lopez J,
 Liu J, Liu W, Liu Y, London P, Longacre S, Lopez J,
 Lorenshewa L, Louisedge H, Lozano R, Lu X, Ma J,
 Maheshwari M, Mahindaratne M, Mahmood M, Malloy K, Mangum A,
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 Mangum B, Mapus P, McNeill T, Meenan E,
 Mawlawi S, McLeod M, McNeill T, Meenan E,
 Milosavljevic A, Miner G, Minja S, Montemayor J, Moore S,
 Morgan M, Morris K, Morris S, Munidasa N, Murphy M, Nair L,
 Narkerys C, Neal D, Newton N, Nguyen N, Norris S,
 Nwankweli O, Okunolu G, Olajunsgun A, Pal S, Parks K,
 Paatelnak S, Paul H, Perez A, Perez L, Pfankuch C,
 Plopper F, Polidexter A, Popovic D, Primus B, Pu L, L,
 Puzo M, Qutro J, Rachlin B, Reeves K, Regier M, A, Reigh R,
 Reilly B, Reilly M, Ren Y, Reuter M, Richards S, Riggs F,
 Rives C, Rodkey T, Rojas A, Rose M, Rose R, Ruiz S, J,
 Sanders M, Savery G, Scherer S, Scott G, Shatman S, Shen H,
 Shetty J, Shvartsbeyn A, Sisson I, Sitter C, D, Smajic D,
 Sneed A, Sodergren E, Song X, Z, Sorlie R, Sosa J,
 Steimle M, Strong R, Sutton A, Svatek A, Thor P, Taylor C,
 Taylor T, Thomas N, Thomas S, Tingey A, Trejos Z, Umant K,
 Vals R, Vera V, Villaseana D, Waldron L, Walker B, Wang J,
 Wang Q, Wang S, Warren R, Wiczek R, Wooden H, Wozniak K,
 Williams G, Wilson R, Wiczek R, Wozniak K, Wozniak K,
 Wright D, Wright R, Wu J, Yakub S, Yan J, Yoon L, Yoon V,
 Yu F, Zhang J, Zhou J, Zhou X, Zhao S, Dunn D, von
 Niederhusern A, Weiss R, Smith D, Holt R, A, Smith H, O.,
 Weinstein G, and Gibbs R, A.

TITLE

Direct Submission

JOURNAL

Unpublished
 2 (bases 1 to 252467)

REFERENCE

Worley K.C.
 Direct Submission
 Submitted (27-JAN-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

JOURNAL

3 (bases 1 to 252467)

REFERENCE

Rat Genome Sequencing Consortium.

AUTHORS

Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

JOURNAL

On May 13, 2003 this sequence version replaced gi:23111072.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Arctis
 (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described

COMMENT

Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

In the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GRP

Center clone name: CH230-29E2

----- Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 232152 bases at least Q40

Consensus quality: 234728 bases at least Q30

Estimated insert size: 242175; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_drafc_data.html).
* NOTE: This is a working draft sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 247030: contig of 247030 bp in length
* 247031 247130: gap of unknown length
* 247131 248423: contig of 1293 bp in length
* 248424 248523: gap of unknown length
* 248524 250348: contig of 1825 bp in length
* 250349 250448: gap of unknown length
* 250449 252467: contig of 2019 bp in length.

FEATURES
source
Location/Qualifiers
1..252467
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-29E2"

misc_feature

1..1489
/note="wgs contig"

gap
247031..247130
/estimated_length=unknown

gap
248424..248523
/estimated_length=unknown

gap
250349..250448
/estimated_length=unknown

ORIGIN

Query Match 85.0%; Score 17; DB 14; Length 252467;
Best Local Similarity 88.2%; Pred. No. 1.4e+03;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GUACGCGACGACGACG 19

Db 69203 GTACAGCCAGACGACG 69219

RESULT 20
PSELASRA1 720 bp DNA linear BCT 21-JAN-2003
DEFINITION Pseudomonas aeruginosa gene for laeR, complete cds.
ACCESSION D30812 GI:541656
VERSION D30812.1 GI:541656

KEYWORDS
SOURCE
ORGANISM

Pseudomonas aeruginosa
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

REFERENCE
AUTHORS
TITLE
Gambello, M.J. and Igleski, B.H.
Cloning and characterization of the Pseudomonas aeruginosa laeR
gene, a transcriptional activator of elastase expression.

JOURNAL
PUBMED
1902216
J. Bacteriol. 173 (9), 3000-3009 (1991)

REFERENCE
AUTHORS
TITLE
2 (bases 1 to 720)
Fukushima, J., Ishiwata, T., Kurata, M., You, Z. and Okuda, K.
Intracellular receptor-type transcription factor, laeR, contains a
highly conserved amphipathic region which precedes the putative
helix-turn-helix DNA binding motif

JOURNAL
PUBMED
7937080
Nucleic Acids Res. 22 (18), 3706-3707 (1994)

REFERENCE
AUTHORS
TITLE
3 (bases 1 to 720)
Fukushima, J.
Direct Submission
Submitted (25-MAY-1994) Jun Fukushima, Yokohama City University
School of Medicine, Department of Bacteriology, 3-9 Fukura,
Kanazawa-ku, Yokohama, Kanagawa 236, Japan
(E-mail: jfukushima@med.yokohama-cu.ac.jp, Tel: 81-45-787-2602,
Fax: 81-45-787-2509)

FEATURES
source
Location/Qualifiers
1..720
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="F03455"
/db_xref="taxon:287"
/clone="pFae3455"
1..720
/note="transcriptional activator"

CDS

1..720
/codon_start=1
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/product="laeR"
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/db_xref="GI:541657"
/translation="MALVDGFLERSSGKLERSALIKKASDLPGLPLKPS
ODVENAIVGNYPAAAREHYDRAGVADPTVCHQOSVLPFMBSIYGTROHPR
ERASAGIYVGLTMRPLHARGELGALSISYRANRANRPFISVPTLMLDYALQ
SGAGLAPHPVSPVAVTSRKEVILQWALGKTSWEISVLCNCSKANVNFHKNIRK
FGVTSRRVAIVMNVGLITL"
432
/gene="laeR"
432
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/replace="g"

variation

ORIGIN

Query Match 84.0%; Score 16.8; DB 1; Length 720;
Best Local Similarity 85.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGUACGCGACGACGACG 20

Db 124 AAGGACGCGACGACGACG 143

RESULT 21
PSELASRB 720 bp DNA linear BCT 21-JAN-2003
DEFINITION Pseudomonas aeruginosa gene for laeR, complete cds.
ACCESSION D30813 GI:541658
KEYWORDS
SOURCE
ORGANISM
Pseudomonas aeruginosa
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

REFERENCE 1 (bases 1 to 720)
 AUTHORS Fukushima, J., Ishiwata, T., Kurata, M., You, Z. and Okuda, K.
 TITLE Intracellular receptor-type transcription factor, LasR, contains a highly conserved amphipathic region which precedes the putative helix-turn-helix DNA binding motif
 JOURNAL Nucleic Acids Res. 22 (18), 3706-3707 (1994)
 PUBMED 7937080
 REFERENCE 2 (bases 1 to 720)
 AUTHORS Fukushima, J.
 TITLE Direct Submission
 JOURNAL Submitted (25-MAY-1994) Jun Fukushima, Yokohama City University School of Medicine, Department of Bacteriology, 3-9 Fukuoka, Kanazawa-ku, Yokohama, Kanagawa 236, Japan
 (E-mail: fukushima@med.yokohama-cu.ac.jp, Tel:81-45-787-2602, Fax:81-45-787-2503)
 FEATURES
 source Location/Qualifiers
 1..720
 /organism="Pseudomonas aeruginosa"
 /mol_type="genomic DNA"
 /strain="PA103"
 /db_xref="taxon:287"
 /clone="pBtaClasR103"
 1..720
 /note="transcriptional activator"
 /codon_start=1
 /transl_table=11
 /product="lasR"
 /protein_id="BA06490.1"
 /db_xref="GI:541659"
 /translation="MALVDGFLERSSGKLEMSALIQKMSDYGFSKILFGLPKDS ODYENAFIVGNYPAMREHYDAGYARDPVVSHCTOSVLIPIFMSPIYQTRKHFF EASAGAGLVGGLTPELHARGELGALISVBAENBAZANRPIESVLTPLMMLKAYALQ SGAGLAFEPVSKPVLTLSRKEVYLQWCAIGKTSWEISVICNCSBANVPFMGNIRK FGVTSRVAAIMAVNLGLITL"
 CDS
 1 AGGACAGCCAGGACUACGA 20
 |||||
 124 AAGGACAGCCAGGACTACGA 143
 |||||
 ORIGIN
 Query Match 84.0%; Score 16.8; DB 1; Length 720;
 Best Local Similarity 85.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 RESULT 22
 LOCUS BD224017 720 bp DNA linear PAT 17-JUL-2003
 DEFINITION Gene switch.
 ACCESSION BD224017
 VERSION BD224017.1 GI:33033787
 KEYWORDS JP 2002522079-A/16.
 SOURCE Pseudomonas aeruginosa
 ORGANISM Pseudomonas aeruginosa
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
 1 (bases 1 to 720)
 Martinez, A., Jepson, I. and Fray, R.G.
 Gene switch
 Patent: JP 2002522079-A 16 23-JUL-2002;
 SYNGENTA LTD
 OS Pseudomonas aeruginosa
 PN JP 2002522079-A/16
 PD 23-JUL-2002
 PF 12-AUG-1999 JP 2000565139
 PR 13-AUG-1998 GB 9817704.1
 PI ALBERTO MARTINEZ, IAN JEPSON, ROBERT GEORGE FRAY PC
 C1A1N15/09, A01H5/00, C12N5/10, C12O1/02// (C12N5/10, C12R1:91) CC
 (C12O1/02, C12R1:91), C12N15/00, C12N5/00, (C12N5/00, C12R1:91) CC
 Gene switch
 FH Key
 FT source Location/Qualifiers
 1..720
 /organism="Pseudomonas aeruginosa".

FEATURES
 source Location/Qualifiers
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 /organism="Pseudomonas aeruginosa"
 /mol_type="genomic DNA"
 /db_xref="taxon:287"
 ORIGIN
 Query Match 84.0%; Score 16.8; DB 6; Length 720;
 Best Local Similarity 85.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 RESULT 23
 LOCUS CO839858 720 bp DNA linear PAT 29-JUL-2004
 DEFINITION Sequence 4 from Patent WO2004058996.
 ACCESSION CO839858
 VERSION CO839858.1 GI:50837795
 KEYWORDS
 SOURCE Pseudomonas aeruginosa
 ORGANISM Pseudomonas aeruginosa
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
 1
 Feesche, J., Stumpe, S., Maurer, K.H., Breves, R. and Hoven, N.
 Method for controlling processes based on microbial interaction
 Patent: WO 2004058996-A 4 15-JUL-2004;
 Henkel Kommanditgesellschaft auf Aktien (DE)
 Location/Qualifiers
 1..720
 /organism="Pseudomonas aeruginosa"
 /mol_type="unassigned DNA"
 /db_xref="taxon:287"
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 /note="unnamed protein product"
 /codon_start=1
 /transl_table=11
 /protein_id="CAH05768.1"
 /db_xref="GI:50837796"
 /translation="MALVDGFLERSSGKLEMSALIQKMSDYGFSKILFGLPKDS ODYENAFIVGNYPAMREHYDAGYARDPVVSHCTOSVLIPIFMSPIYQTRKHFF EASAGAGLVGGLTPELHARGELGALISVBAENBAZANRPIESVLTPLMMLKAYALQ SGAGLAFEPVSKPVLTLSRKEVYLQWCAIGKTSWEISVICNCSBANVPFMGNIRK FGVTSRVAAIMAVNLGLITL"
 CDS
 1 AGGACAGCCAGGACUACGA 20
 |||||
 124 AAGGACAGCCAGGACTACGA 143
 |||||
 ORIGIN
 Query Match 84.0%; Score 16.8; DB 6; Length 720;
 Best Local Similarity 85.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 RESULT 24
 LOCUS CO839862 720 bp DNA linear PAT 29-JUL-2004
 DEFINITION Sequence 8 from Patent WO2004058996.
 ACCESSION CO839862
 VERSION CO839862.1 GI:50837799
 KEYWORDS
 SOURCE Pseudomonas aeruginosa
 ORGANISM Pseudomonas aeruginosa
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
 1
 Feesche, J., Stumpe, S., Maurer, K.H., Breves, R. and Hoven, N.
 Method for controlling processes based on microbial interaction

CDS

1. .>72

Contact: Michael C. Zody
Broad Institute of MIT and Harvard
320 Charles Street, Cambridge, MA 02141, USA
Tel: 6172580933
Fax: 6172580903
Email: mczody@broad.mit.edu
Primer A: No sequence submitted
Primer B: No sequence submitted
STS size: 802

Protocol:
23,021,928 chimpanzee whole genome shotgun reads were aligned to the Human genome NCBI Build 34 (hg16, July 2003). Chimp WGS reads were from 9 donors, including Clint (Pan troglodytes verus), 3 other Pan troglodytes versus chimps (Donald, Karlsen, Yvonne), 3 Pan troglodytes troglodytes chimps (Noemie, Masuku, Clara) and 2 chimps of unknown origin (Gon, Unknown Chimp). Common names: Pan troglodytes versus is the western chimp and Pan troglodytes troglodytes is the central chimp. To be included in chimpanzee SNP discovery, a read must be at least 500bp in length, at least 50% of its base calls must have Phred score >= 20, at least 30% of its base calls must satisfy SNQS(30,25) (single strand NQS, the base in question has Phred score >= 30, the surrounding 10 bases in the read have Phred score >= 25), and the read must have at least 200 bp SNQS(30,25) bases. Reads not uniquely

placed in the genome and read pairs whose two ends were not consistently placed were discarded. After above filtering, NGS(30.25) standard was applied to all pairs of overlapping reads to call NGS bases and SNPs. Alignments (between two reads) with less than 100 NGS bases or with SNP rate > 0.01 were discarded. To exclude alignment between two reads that share 95% of their genome alignments (>95% bases of read A and >95% bases of read B were placed at the same locus

Location/Qualifiers
1. 802
/organism="Pan troglodytes troglodytes"
/mol_type="genomic DNA"
/sub_species="troglodytes"
/db_xref="taxon:37011"
/clone_id="Masuku"
<1..>802

FEATURES

SOURCE

Query Match 84.0%; Score 16.8; DB 10; Length 802;
Best Local Similarity 85.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

ORIGIN
Query Match 84.0%; Score 16.8; DB 10; Length 802;
Best Local Similarity 85.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 27
PSEULSR 1725 bp DNA linear BCT 31-MAR-1999
LOCUS Pseudomonas aeruginosa lasR (lasR) and virulence gene repressor
DEFINITION RsaI (rsal) gene, complete cde.
ACCESSION M59425
VERSION M59425.1 GI:151325
KEYWORDS
SOURCE Pseudomonas aeruginosa
ORGANISM Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

REFERENCE
AUTHORS 1 (bases 1 to 1725)
TITLE Gambello, M.J. and Igilewski, B.H.
JOURNAL Cloning and characterization of the Pseudomonas aeruginosa lasR
PUBMED gene, a transcriptional activator of elastase expression
AUTHORS J. Bacteriol. 173 (9), 3000-3009 (1991)
TITLE 1902216

REFERENCE
AUTHORS 2 (bases 1138 to 1380)
TITLE de Kievit, T., Seed, P.C., Nezezon, J., Passador, L. and Igilewski, B.H.
JOURNAL Real, a novel repressor of virulence gene expression in Pseudomonas
PUBMED aeruginosa
AUTHORS J. Bacteriol. 181 (7), 2175-2184 (1999)
TITLE 10094696

REFERENCE
AUTHORS 3 (bases 1 to 1725)
TITLE Gambello, M.J. and Igilewski, B.H.
JOURNAL Submitted (09-MAY-1991) Microbiology and Immunology, University of
PUBMED Rochester Medical Center, 601 Elmwood Ave., Rochester, NY 14642,
TITLE USA

FEATURES
SOURCE Location/Qualifiers
1. 1725
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="PA01"
/db_xref="taxon:287"
429. 1148
/gene="lasR"
429. 1148
/gene="lasR"
CDS
/function="activate elastase expression"

ORIGIN

Query Match 84.0%; Score 16.8; DB 1; Length 1725;
Best Local Similarity 85.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

ORIGIN
Query Match 84.0%; Score 16.8; DB 1; Length 1725;
Best Local Similarity 85.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 28
APGUCYC 3444 bp mRNA linear INV 31-MAR-1995
LOCUS See urchin (Arbacia punctulata) mRNA for guanylate cyclase.
DEFINITION X12874
ACCESSION X12874.1 GI:5648
VERSION X12874.1 GI:5648
KEYWORDS cell surface glycoprotein; glycoprotein; guanylate cyclase;
receptor; transmembrane protein.

REFERENCE
AUTHORS 1 (bases 1 to 3444)
TITLE Singh, S., Lowe, D.G., Thorpe, D.S., Rodriguez, H., Kuang, W.J.,
JOURNAL Dangot, L.J., Chinkers, M., Goeddel, D.V. and Garbers, D.L.
PUBMED Membrane guanylate cyclase is a cell-surface receptor with homology
AUTHORS Nature 334 (6184), 708-712 (1988)
TITLE 2901039

REFERENCE
AUTHORS 1 (bases 1 to 3444)
TITLE Singh, S., Lowe, D.G., Thorpe, D.S., Rodriguez, H., Kuang, W.J.,
JOURNAL Dangot, L.J., Chinkers, M., Goeddel, D.V. and Garbers, D.L.
PUBMED Membrane guanylate cyclase is a cell-surface receptor with homology
AUTHORS Nature 334 (6184), 708-712 (1988)
TITLE 2901039

REFERENCE
AUTHORS 1 (bases 1 to 3444)
TITLE Singh, S., Lowe, D.G., Thorpe, D.S., Rodriguez, H., Kuang, W.J.,
JOURNAL Dangot, L.J., Chinkers, M., Goeddel, D.V. and Garbers, D.L.
PUBMED Membrane guanylate cyclase is a cell-surface receptor with homology
AUTHORS Nature 334 (6184), 708-712 (1988)
TITLE 2901039

FEATURES
SOURCE Location/Qualifiers
1. 3444
/organism="Arbacia punctulata"
/mol_type="mRNA"
/db_xref="taxon:7641"
/cbase_type="testes"
/clone_id="lambda-ZAP"
141. 3101
/codon_start=1
/product="guanylate cyclase (AA -21 to 965)"
/protein_id="CAA31367.1"
/db_xref="GI:5649"
/db_xref="GO:01528"
/db_xref="UniProt/Swiss-Prot:P11528"
/translation="NATYRLPLVAVWITWRSATLHNTPTVINDLRGRLTGM
LTSWTNADNSQGTGTPSAGAFPLAIVYANDMDIAGDIINFVDTCHINDGMAI
SDWKRGLFVIGPGCGCTEGLASLAPMIDVACDERPVSNEKEPPTFLTIPS
IOVVDSTLITLDMVQVAVVENITKRVNVTNKEQPMSEBETLHRYVAGAVT
PMDPDAEPFTDIORTKTRIVYFGSGSDIROPALSDVGLNSGVAIVGAVT
DLIRDSQDHSHTLEADYIEQINQAVEQFKLREYRTDDEALFMKSLVLT

GEPVLRSGAMHIYSAIVIDNALDEPFGTLEKTDIDMAVYIFDATTLLKALDALT
 QAGGIMYDGSQVSNLFTNTSYRSKAKADYOPDENGDDKSVYLHRIPIPYDGGMP
 GSPGMYPIGTVRABSGHMSFNKDPDLADYVHNDPDDPLMDPVGFGHCLCTNNGLYL
 GTLIPAFIIRGGIGYIKRAYEALDLSVWKPDKETQTSBETNSGQFSKSKM
 VLSAIVSINAEKQOIFATITGRTKSTICAHVKNHIDLTRAVTELTAKRMDHND
 ICPGTACIDRPHICILMHYCAKSLDQIMENDIKLDSMFLASLIDLVLGLYLHS
 SEIKSHGLKSNKNCVDNRWVLTQIDYGHFRKQKEDVDLGHAKLARLMTAPER
 LREKSMHFGTSPKGDYISFSLITLMTYRQSPHENDLADLIARVSKGVPYRP
 VLVNVEAPDPCVLTALPACVDEMBRPNTIIVRTMAPLOKPLKPYLLDMTAME
 RYTNVLELDERQELQEKAKTRQHLRLPSIASOLIKGISVLPETDMSITF
 SDIYGLIFHSLSGCRFLCSQVPLVLPVHLSLTLPLHLPLIMMPLISSFAQPSW
 SALSHTSCSLAHSS"

sig_peptide
 /note="signal peptide (AA -21 to -1)"
 141..203
 204..3098
 /product="guanylate cyclase (AA 1 - 965)"

Query Match 84.0%; Score 16.8; DB 2; Length 3444;
 Best Local Similarity 85.0%; Pred. No. 2.2e+03;
 Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1 AGGACAGCCGAGACUACGA 20
 981 AGGACAGCCGAGACTACCA 1000

RESULT 29
 AB004572 10238 bp DNA linear BCT 19-FEB-2003
 LOCUS Pseudomonas aeruginosa PA01, section 133 of 529 of the complete
 DEFINITION genome.
 ACCESSION AB004572 AB004091
 VERSION AB004572.1 GI:9947372
 KEYWORDS
 SOURCE
 ORGANISM Pseudomonas aeruginosa PA01
 Pseudomonas aeruginosa PA01
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Pseudomonadaceae; Pseudomonas.
 1 (bases 1 to 10238)
 Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrenner, P.,
 Hickey, M.J., Brinkman, F.S.L., Hutnagle, W.O., Kowalik, D.J.,
 Lagrou, M., Garber, R.L., Goltzy, L., Tolentino, B.,
 Westbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N.,
 Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H.,
 Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reiter, J., Salter, M.H.,
 Complete genome sequence of Pseudomonas aeruginosa PA01, an
 opportunistic pathogen
 Nature 406 (6799), 959-964 (2000)
 10984043
 2 (bases 1 to 10238)
 Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrenner, P.,
 Hickey, M.J., Brinkman, F.S.L., Hutnagle, W.O., Kowalik, D.J.,
 Lagrou, M., Garber, R.L., Goltzy, L., Tolentino, B.,
 Westbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N.,
 Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H.,
 Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reiter, J., Salter, M.H.,
 Hancock, R.E.W., Lory, S. and Olson, M.V.
 Direct Submission
 Submitted (16-MAY-2000) Department of Medicine and Genetics,
 University of Washington Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA
 3 (bases 1 to 10238)

REFERENCE
 JOURNAL PUBMED
 PSEUDOMONAS AERUGINOSA Community Annotation Project (PseudoCAP)
 AUTHORS
 CONSTRM
 TITLE
 JOURNAL
 COMMENT

This represents the February 3, 2003 version of the continually
 updated, reviewed, Pseudomonas aeruginosa PA01 genome annotation,
 from PseudocAP (see <http://www.pseudomonas.com> for latest updates

and links to alternate annotations). PseudocAP is coordinated by
 Fiona S.L. Brinkman (Simon Fraser University, Canada) and Robert
 E.W. Hancock (University of British Columbia, Canada). We welcome
 submission through www.pseudomonas.com of any proposed changes.

'Protein name confidence' is used to rate our confidence of the
 accuracy of the protein name.

Class 1: Function experimentally demonstrated in *P. aeruginosa*.
 Class 2: Function of highly similar gene experimentally
 demonstrated in another organism (and gene context consistent
 in terms of pathways its involved in, if known).
 Class 3: Function proposed based on presence of conserved amino
 acid motif, structural feature or limited sequence similarity
 to an experimentally studied gene.
 Class 4: Homologs of previously reported genes of unknown function,
 or no similarity to any previously reported sequences.

Location/Qualifiers
 1..10238
 /organism="Pseudomonas aeruginosa PA01"
 /mol_type="genomic DNA"
 /strain="PA01"
 /db_xref="taxon:208964"
 179..790
 /locus_tag="PA1424"
 179..790
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 /note="Protein name confidence: Class 4 (homologs of
 previously reported genes of unknown function, or no
 similarity to any previously reported sequences)"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"
 /protein_id="AG04813.1"
 /db_xref="GI:9947373"
 /translation="MPRIKCEKCARPASHQICALIPSLPRTVVLQHPSEVGHAN
 TAGLAVIGCMELRIGERPAERTWAPVGRACILPGROARLAEAAAEAPILL
 VPDGTRKARKLHNPALALPRISLABGASRYRLKAPGEGALSTTEALAAAD
 ELKAPTHEALPFPDALIRGQTAANGEDTYRRNHLSEKRRR"
 1280..2896
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 /note="Protein name confidence: Class 3 (function proposed
 based on presence of conserved amino acid motif,
 structural feature or limited sequence similarity to an
 experimentally studied gene)"
 /codon_start=1
 /transl_table=11
 /product="probable ATP-binding component of ABC
 transporter"
 /protein_id="AG04814.1"
 /db_xref="GI:9947374"
 /translation="MNTSTLTLDGVSPQLPDGSILFSPDLDEPDRHGVGNRGV
 KSLARLAVGLQPSGSGVRRGRVYLAQLEPRADYVADLAGRPMELARLEA
 GSILADADYCLGRWDITRDLADLAAGGSHRDVTSERISGSGCKVALGAVLD
 DADPLIDSPNPDLGPAPALRLRLAANDGILLVSHRRLLEGQRLVEISSTGLR
 SYGGGSFYAQSREBARERLDQRLERKQTLAMEQOORCORSCAGSGRBEKT
 ANOAKILGGFRSEVSAGKLRNAAQERLDRVRAAEVESAFLILDSPAR
 LAAORIVELKAVYPLHAGPLREIDILGSPRLAVGNGSGKSTTLRLAGCGAP
 LAGCAVYGAAYLQRLSVLDHGRGVLEQLLEVRNRSRGSWTRLRLQGLPARILA
 OPTATSGSERIKKALALVLYADRPQQLLDLDEPNDHLARQALSMGOYRGALL
 VVSHDVFPLRLALDGLRLATGAAGMLBDR"
 2937..3293
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 2937..3293
 /locus_tag="PA1426"
 /note="Protein name confidence: Class 4 (homologs of
 previously reported genes of unknown function, or no
 similarity to any previously reported sequences)"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"

gene
 CDS
 /locus_tag="PA1426"
 2937..3293
 /locus_tag="PA1426"
 /note="Protein name confidence: Class 4 (homologs of
 previously reported genes of unknown function, or no
 similarity to any previously reported sequences)"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"

* * * * *

* NOTE: This is a 'working draft' sequence. It currently

* consists of 5 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

*	5294:	cont:ig of 5294 bp	in length
*	5394:	gap of 100 bp	
*	5395:	cont:ig of 5487 bp	in length
*	10881:	gap of 100 bp	
*	10982:	cont:ig of 6185 bp	in length
*	17167:	gap of 100 bp	
*	24683:	cont:ig of 7417 bp	in length
*	24684:	gap of 100 bp	
*	36255:	cont:ig of 11472 bp	in length

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FEATURES
source
location/Qualifiers
1..36255
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RP11-2511"
/clone_id="RCCR11 Human Male BAC"
1..5394
misc_feature
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misc_feature    /estimated_length=100
5395.    .10881
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gap          10882. 10981
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            10982. 17166
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gap          17167. 17266  
            /estimated_length=100  
misc_feature 17267. 24683
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gap	/note="assembly_fragment 24684.24783
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	/note="assembly_fragment

ORIGIN

Query Match	84.0%;	Score 16.8;	DB 14;	Length 36255;
Best Local Similarity	80.0%;	Pred. No. 1.9e+03;		
Matches 16;	Conservative 2;	Mismatches 2;	Indels 0;	Gaps 0;

```

QY      1 AGGUAACGCCAGGACUACGA 20
          |||:|||||||:||||
Db      14190 AGGTACAGCCAGGAGTAAGA 14209

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RESULT 31
AL161661

LOCUS	AL161661	93714 bp	DNA	linear	HTG 13-JUN-2003
DEFINITION	Homo sapiens chromosome 20 clone RP5-984123.				
ACCESSION	AL161661				

ALCESSION	AL161661
VERSION	AL161661.1 GT:726357

KEYWORDS	HTG; HTGS_PHASE2; HTGS_CANCELLED.
SOURCE	Homo sapiens (human)

ORGANISM

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1
Burton, J.
Direct Submission
Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgehire,
United Kingdom

COMMENT

Center code: SC
Web site: <http://www.banger.ac.uk>

```
----- Project Information
Center project name: dJ984I23
```

Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads

Consensus quality: 93681 bases at least Q4
Consensus quality: 93706 bases at least Q3

Insert size: 93714; sum-of-contigs
Insert size: 109355; 1.0% error; agarose-fp

coverage: 7.07x in Q20 bases; agarose-fp
-----,

- * This sequence will be replaced
- * by the finished sequence as soon as it is available and

FEATURES

1. .93714

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/organism="Homo sapiens"
/mol_type="genomic DNA"

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/chromosome="20"  
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OPTION

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Best Local Similarity	85.0%;	Pred. No. 1.8e+03;		
Matches 17;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;

1 AGUACAGCCAGGATUACGA 20

4 DB

RESULT 32
ACT166715/

LOCUS DEFINITION	111051 bp	DNA	linear	HTG 10-AUG-2005
AC166715				
Bob taurus clone CH240-190K8, *** UNORDERED PIECES.		SEQUENCING IN PROGRESS ***		24

ACCESSION

VERSION	AC166715.2	GI:72095136
KEYWORDS	HTG; HTGS_PHASE1.	
SOURCE	Bos taurus (cow)	

ORGANISM

REFERENCE AUTHORS

Cheng, M.-T., Chu, J., Clerc, C., Cockrell, R., Coyle, M., Cree, A.,
Curry, S., Dai, W., Davis, M. L., Davis, C., Day-Carroll, L., De
Munzy, D., Adams, C., Agaba, I. O., Allen, C., Alsbrooks, S., Archer, P.,
Arredondo, H., Bandaranaike, D., Bangure, L., Beltran, B., Beltran,
Beraducci, A., Biswal, K., Blyth, P., Bonham, K., Bubaz, C., Burch, P.,
Cadore, I., Canada, A., Cardenas, V., Carter, K., Cavazos, I.,
Chacko, J., Chahrouh, M., Chavez, D., Chen, A., Chen, G., Chen, R.,
Cheng, M.-T., Chu, J., Clerc, C., Cockrell, R., Coyle, M., Cree, A.,
Curry, S., Dai, W., Davis, M. L., Davis, C., Day-Carroll, L., De

Anda, C., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H.,
Donlin, J., McCauley, S., Dugan-Rocha, S., Dunn, A., Dublin, K.,
Dunda, D., Egan, A., Escotto, M., Espinosa, V., Eugene, C., Fa, M.,
Fernandez, S., Fernando, P., Flagg, N., Forbes, L., Foster, P.,
Fowler, G., Fu, Q., Fuh, E., Garcia, A., Garcia, R., Garner, T.,
Gaskin, C., Gench, S., Ghose, S., Gill, R., Gonzalez, D.,
Gonzalez-Garay, M., Guevara, W., Holder, M., Haaland, W.,
Hall, B., Hardin, H., Hamilton, K., Harbes, B., Harris, R., Haylak, P.,
Hawes, A., Hawkins, E., Hayes, S., Hemphill, L., Hernandez, J.,
Hines, S., Hitchens, M., Hodgson, A., Hogues, M., Hollins, B.,
Howell, L., T., Hulyk, S., Hume, V., Ito, K., Jackson, A., Jackson, L.,
Jacob, L., Jiang, H., Johnson, B., Johnson, R., Kalathur, K., Kelly, S.,
Kear, T., Khan, Z., King, L., Koyar, C., Kowis, A., Kowis, C., Lara, F.,
Lee, S., Lee, K., Lee, S., Legall, F., I., Lemon, S., Lewis, L., Li, B.,
Li, Y., Li, Z., Linnell, M., Liu, W., Liu, Y., Liu, Y., Liyanage, D.,
London, P., Lopez, J., Lorenz, L., Lozano, R., Luk, T., Madu, R.,
Maheshwari, M., Mahoney, C., Malloy, K., Mansouri, D., Martinez, B.,
McClalland, H., McPherson, J., Mercado, C., Mettler, M.,
Milosavljevic, A., Minja, E., Morgan, M., Morris, S., Muidasa, M.,
Murray, D., Nazareth, L., Ngo, D., Nguyen, N., Norwig-Eastough, E.,
Nott, A., Nwackemele, O., Obregon, M., Ochi-Okorie, C., Odeh, E.,
Okwunonu, G., Okwunonu, K., Parker, D., Pasternak, S., Patel, B.,
Patel, V., Paul, H., Perez, A., Perez, L., Petrosino, J., Pham, T.,
Primus, E., Pu, L., L., Puzo, M., Qiu, X., Quinn, A., Quirroz, J.,
Rabata, D., Rachlin, B., Reigh, R., Ren, Y., Reuter, M., Richards, S.,
Rives, C., Rodriguez, F., Rojas, A., Ruiz, S., Sana, M., Sanders, W.,
Santibanez, J., Santos, R., Savery, G., Scherer, S., Shen, H., Shen, Y.,
Slason, I., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R.,
Svatek, A., Taylor, E., Taylor, T., Thomas, N., Thorn, R., Thornton, R.,
Treylos, Z., Umanal, K., Varigo, C., Verdusco, D., Villaseana, D., Virk, D.,
Volkov, A., Waldron, L., Walker, B., Wang, Q., Wang, S., Warren, J.,
Wei, X., Wheeler, D., Williams, G., Williams, R., Worley, K., Wright, R.,
Zhang, Z., Zhou, J., Weinstock, G., and Gibbs, R.

TITLE
Unpublished
2 (bases 1 to 111051)
Worley, K.C.

JOURNAL
Direct Submission
Submitted (05-AUG-2005) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 111051)
Worley, K.C.

REFERENCE
Direct Submission
Submitted (10-AUG-2005) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Aug 10, 2005 this sequence version replaced gi:71834693.

AUTHORS
Genome Center

TITLE
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help.tmc.edu

JOURNAL
Project Information
Center project name: PKYL
Center clone name: CH240-190K8
Summary Statistics

REFERENCE
Sequencing vector: Plasmid,
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 12309 bases at least Q40
Consensus quality: 12736 bases at least Q30
Consensus quality: 130502 bases at least Q20
Estimated insert size: 134828; sum-of-contigs estimation
Estimated insert size: 143053; agarose-fp estimation
Quality coverage: 2x in Q20 bases; agarose-fp estimation
Quality coverage: 2x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

FEATURES	source
1	4145: contig of 4145 bp in length
4146	4245: gap of unknown length
4246	4573: contig of 2378 bp in length
4574	6673: gap of unknown length
6674	8716: contig of 2043 bp in length
8717	8816: gap of unknown length
8817	13004: contig of 4188 bp in length
13005	13104: gap of unknown length
13105	1657: contig of 3553 bp in length
1658	16757: gap of unknown length
16758	19093: contig of 2336 bp in length
19094	19193: gap of unknown length
19194	26081: contig of 6888 bp in length
26082	26181: gap of unknown length
26182	28768: contig of 2587 bp in length
28769	28868: gap of unknown length
28869	30997: contig of 2123 bp in length
30998	31097: gap of unknown length
31098	33230: contig of 2133 bp in length
33231	33330: gap of unknown length
33331	39577: contig of 6247 bp in length
39578	39677: gap of unknown length
39679	43222: contig of 3545 bp in length
43223	43322: gap of unknown length
43323	46085: contig of 2763 bp in length
46086	46185: gap of unknown length
46186	51780: contig of 5595 bp in length
51781	51880: gap of unknown length
51881	55883: contig of 3903 bp in length
55883	55883: gap of unknown length
55884	58159: contig of 2276 bp in length
58160	58259: gap of unknown length
58260	70331: contig of 12072 bp in length
70332	70431: gap of unknown length
70432	74116: contig of 3685 bp in length
74117	74216: gap of unknown length
74217	76620: contig of 2404 bp in length
76621	76720: gap of unknown length
76721	86525: contig of 9805 bp in length
86526	86625: gap of unknown length
86626	89750: contig of 3125 bp in length
89751	89850: gap of unknown length
89851	93611: contig of 3761 bp in length
93612	93711: gap of unknown length
93712	106994: contig of 13283 bp in length
106995	107094: gap of unknown length
107095	111051: contig of 3957 bp in length.
Location/Qualifiers	
1..111051	
/organism="Bos taurus"	
/mol_type="genomic DNA"	
/db_xref="taxon:9913"	
/clone="CH240-190K8"	
4146..4245	
/estimated_length=unknown	
6574..6673	
/estimated_length=unknown	
8717..8816	
/estimated_length=unknown	
13005..13104	
/estimated_length=unknown	
1658..16757	
/estimated_length=unknown	
19094..19193	
/estimated_length=unknown	
26082..26181	
/estimated_length=unknown	


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gap      28769..28868
          /estimated_length=unknown
gap      30998..31097
          /estimated_length=unknown
gap      33231..33330
          /estimated_length=unknown
gap      39578..39677
          /estimated_length=unknown
gap      43223..43322
          /estimated_length=unknown
gap      46086..46185
          /estimated_length=unknown
gap      51781..51880
          /estimated_length=unknown
gap      55784..55883
          /estimated_length=unknown
gap      58160..58259
          /estimated_length=unknown
gap      70332..70431
          /estimated_length=unknown
gap      74117..74216
          /estimated_length=unknown
gap      76621..76720
          /estimated_length=unknown
gap      86526..86625
          /estimated_length=unknown
gap      89751..89850
          /estimated_length=unknown
gap      93612..93711
          /estimated_length=unknown
gap      106995..107094
          /estimated_length=unknown
ORIGIN
Query Match      84.0%; Score 16.8; DB 14; Length 111051;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

Cy      1 AGGUAACGCCGACUACGA 20
      |||:|||||:|||||
Db      66176 AGGTATAGCCGACATATGA 66157

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RESULT 33
LOCUS      AC073138
DEFINITION Homo sapiens BAC clone RP11-708P17 from 7, complete sequence.
ACCESSION  AC073138
VERSION     AC073138.3 GI:14010936
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 118396)
Hillier,L.W., Fulton,R.S., Fulton,L.A., Graves,T.A., Pepin,K.H.,
Wagner-McPherson,C., Layman,D., Maas,J., Jaeger,S., Walker,R.,
Wyllie,K., Sekhon,M., Becker,M.C., O'Laughlin,M.D., Schaller,M.B.,
Fowell,G.A., Delehaunty,K.D., Miner,T.L., Nash,W.E., Cordes,M.,
Du,H., Sun,H., Edwards,J., Bradshaw-Cordum,H., Ali,J., Andrews,S.,
Isak,A., Vashnunt,A., Nguyen,C., Du,P., Lamar,B., Courtney,L.,
Kalicki,T., Ozerisky,P., Biellik,L., Scott,K., Holmes,A.,
Harkins,R., Harris,A., Strong,C.M., Hou,S., Tomlinson,C.,
Dauphin-Kohlberg,S., Kozlowski-Reilly,A., Leonard,S., Rohlfing,T.,
Rock,S.M., Tin-Wollam,A.M., Abbott,A., Minx,P., Maupin,R.,
Stromwater,C., Latreille,P., Miller,N., Johnson,D., Murray,J.,
Wessner,J.P., Wendt,M.C., Yang,S.P., Schultz,B.R., Wallis,J.W.,
Spieth,J., Bieri,T.A., Nelson,J.O., Berkowicz,N., Wohlmann,P.B.,
Cook,L.L., Hickenbotham,M.T., Eldred,J., Williams,D., Bedell,D.A.,
Mards,E.R., Clifton,S.W., Chisoe,S.L., Marra,M.A., Raymond,C.,
Haugen,E., Gillett,W., Zhou,Y., James,R., Phelps,K., Iadonato,S.,
Bubb,K., Simms,E., Levy,R., Clendenning,J., Kaul,R., Kent,W.J.,

```

```

Furey,T.S., Baertsch,R.A., Brent,M.R., Kehler,E., Plick,P.,
Bork,P., Suyama,M., Bailey,U.A., Portnoy,M.E., Torrents,D.,
Chinwalla,A.T., Gish,W.R., Eddy,S.R., McPherson,U.D., Olson,M.V.,
Bichler,E.E., Green,E.D., Waterston,R.H. and Wilson,R.K.
The DNA sequence of human chromosome 7
Nature 424 (6945), 157-164 (2003)
12853948
2 (bases 1 to 118396)
Du,P., Gibson,A. and Maupin,R.
The sequence of Homo sapiens BAC clone RP11-708P17
Unpublished (2001)
3 (bases 1 to 118396)
Waterston,R.H.
Direct Submission
Submitted (08-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 118396)
Waterston,R.
Direct Submission
Submitted (09-MAY-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
5 (bases 1 to 118396)
Wilson,R.
Direct Submission
Submitted (31-JAN-2004) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On May 9, 2001 this sequence version replaced gi:9838323.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: saplens@wuston.wustl.edu
----- Summary Statistics
Center project name: H_NH0708P17
-----

```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGR Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/CTB/CH7>, send <mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu>

SOURCE INFORMATION:
The RP11-708P17 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,B., Tateo,M., Cateneese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

NEIGHBORING SEQUENCE INFORMATION:
The clone RP11-708P17 shows evidence of possibly several transposons in the growth of the clone, which is not part of the

The clone sequenced to the left is RP4-778K6, 200 bp overlap the clone sequenced to the right is CTD-2305F9. Actual start of this clone is at base position 102929 of RP4-778K6 actual end is at base position 118396 of Rp11-708Bp17.

Bouice

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repeat_region	103. .157	/rptc_family="MALR"	/db_xref="taxon:9606"	/mol_type="genomic DNA"	
repeat_region	201. .247	/rptc_family="MALR"			
repeat_region	352. .413	/rptc_family="MIR"			
repeat_region	428. .873	/rptc_family="MALR"			
repeat_region	880. .1178	/rptc_family="ALu"			
repeat_region	1331. .1414	/rptc_family="MIR"			
repeat_region	1440. .1571	/rptc_family="MIR"			
repeat_region	1598. .1765	/rptc_family="ALu"			
repeat_region	1766. .1806	/rptc_family="TTG)n"			
repeat_region	1807. .1907	/rptc_family="ALu"			
repeat_region	2580. .3448	/rptc_family="L1"			
repeat_region	3477. .3507	/rptc_family="ALu"			
repeat_region	3630. .3921	/rptc_family="ALu"			
repeat_region	4028. .4303	/rptc_family="ALu"			
repeat_region	4306. .4336	/rptc_family="TAA)n"			
repeat_region	4715. .4810	/rptc_family="MIR"			
repeat_region	5300. .5600	/rptc_family="ALu"			
repeat_region	5769. .6046	/rptc_family="ALu"			
repeat_region	6133. .6204	/rptc_family="MER2_type"			
repeat_region	6205. .6507	/rptc_family="ALu"			
repeat_region	6508. .6665	/rptc_family="MER2_type"			
repeat_region	6666. .6971	/rptc_family="ALu"			
repeat_region	6972. .7001	/rptc_family="MER2_type"			
repeat_region	7002. .7189	/rptc_family="MALR"			
repeat_region	7190. .7213	/rptc_family="(GA)n"			
repeat_region	7214. .7401	/rptc_family="MALR"			
repeat_region	7402. .7412	/rptc_family="MER2_type"			
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Query Match	84.0%	Score 16.8	DB 8	Length 118396
Best Local Similarity	80.0%	Pred. No. 1.8e+03		
Matches 16	Conservative	2	Mismatches	2
			Indels	0
			Gaps	0
QY	1 AGTACAGCCAGGACACGCA	20		
db	103784 AGGTACAGACAGGACACTA	103803		

111073 b2 DNA 74 near PBT 03-OCT-2001

LOCUS	AC008794	131572 bp	DATA	Unac-	Full-
DEFINITION	Human sapiens chromosome 19 clone	CTD-2050118			complete sequence.
ACCESSION	AC008794				
VERSION	AC008794.8	GI:15887256			
KEYWORDS	HTG.				

Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;
Homnidae; Homo.

HOLLIDAY, MIMO:
1 (baves 1 to 131972)

AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 DOE Joint Genome Institute.
 Direct Submission
 Unpublished
 2 (bases 1 to 131972)
 Direct Submission

Direct Submission

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 131972)
DOE Joint Genome Institute and Stanford Human Genome Center.

DOE Joint Genome Institute and Stanford Human Genome Center.

JOURNAL Submitted (28-JUL-2000) DOI JOINT GENOME INSTITUTE, 2000
Drive, Walnut Creek, CA 94598, USA
REFERENCE 4 (bases 1 to 131972)
Hudson Genome Center

4 (DABBS 1 CO 1315/2)
DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE
 DIRECT SUBMISSION
 Submitted (03-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell
 Drive, Walnut Creek, CA 94598, USA
 On Oct 3 2001 this sentence version replaced q1:9558576.

www.jg1.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.5% of Sequence!

COMMENT

Cambridgehire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
 Clone requests: clonerequests@sanger.ac.uk
 On Mar 16, 2001 this sequence version replaced gi:10198608.
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
 Bm, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/Map/Chr20>
 RP5-998H6 is from the library RPCT-5 constructed by the group of Pater de Jong. For further details see
<http://www.choil.org/bacpac/home.htm>
 VECTOR: pCYPAC2

----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: vegas@sanger.ac.uk

 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

FEATURES

SOURCE

1. 147815
 /organism="Homo sapiens"
 /mol_type="Genomic DNA"
 /db_xref="RZPD:RPCIP04H06998"
 /db_xref="taxon:9606"
 /chromosome="20"
 /map="q13.1"
 /clone="RP5-998H6"
 /clone_1fb="RPC1-5"
 /clone_2fb="RPC1-5"
 /note="Clone left end: RP5-998H6"
 complement(join(8546..10617,11115..11779))
 /locus_tag="RP5-998H6.2-001"
 complement(join(8946..10617,11115..11779))
 /locus_tag="RP5-998H6.2-001"
 /note="match: cDNAs: AK057411.1"
 complement(join(14275..15619,18488..18739,27130..27247,27368..27489,39965..40101,50849..51102,53537..53730,57368..57535,68050..68169,81505..81799,91582..92237))
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 /locus_tag="RP5-998H6.3-001"
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 /locus_tag="RP5-998H6.3-001"
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 /locus_tag="RP5-998H6.3-001"
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 /gene="CDH22"
 /locus_tag="RP5-998H6.3-001"
 complement(join(15048..15619,18488..18739,27130..27247,27368..27489,39965..40101,50849..51102,53537..53730,57368..57535,68050..68169,81505..81799,91582..91863))
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 /locus_tag="RP5-998H6.3-001"

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 /note="match: proteins: Q63315 Q63561 Q9U99 Q9WTP5"
 /codon_start=1
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 /db_xref="GeneW:13251"
 /db_xref="GOA:Q9U99"
 /db_xref="HSP:INCU"
 /db_xref="InterPro:IPR00233"
 /db_xref="InterPro:IPR002126"
 /db_xref="UniProt/Swiss-Prot:Q9U99"
 /translation="MRPRGRLKAGVAVASPLLLLLPPPTLLGRLMAAGTPSP
 SAPGADQDGLGAGVRKGVWVQFVVEYETSEPLVYKHSDDSDGAKRTYIS
 GAGAGTFLIDELTGDIHMERLDRQKFTYTLRAQARATRLLEPSEFTIKQD
 INSEGRFLHGPYIGSAVLEPSTGVMQADADPTGSSARLYVSLDDEHPT
 VDKRTGVRIRAVPDDLRSEGRKRVYIQTADMGOLGSGSTTVIIVTVNDNPPR
 FPKWTFSTIOESAPRTGTAVGRVAKSDVSGENTMTYHLKSSSGGVFKYTDSD
 TQRAIVVQKRLDSESPVHTVLEALKRVDRPADLGTFRDQAIYRVAVTVVDESP
 EFRPPSGLEVOBDAOVGLVGVTAADPDAARPVYATIDRESDDQITDIDATG
 IYVKGGLDRETAGHNIYVAMEADNMAOLSRASLRIRLIDVNDPELATPYBAVC
 EDKPPQGLIOTIIVVDSGSPPTLSNGTFLIRICGDSGTTIOSCTTAIVMAASLP
 PNRQBDVFLPIVVDGSPPTLSNGTFLIRICGDSGTTIOSCTTAIVMAASLP
 GALLALIVCLIVLVTLITLIRRHHSKLSLSDSDMDMDVYKYNBGGGBODTA
 YDMSALSLYDFEELKGGDGGSHGCGAGGSGGAGSPPOAHLPSRHLPGPSP
 EPPFSVRDPTSRKVALADGLSPVPDAQTVAFGADSPASLSLSHSGSGSBD
 PAYLSWGPRFRPLAALYAGRGDDEAQA"
 29571
 /note="Clone right end: RP4-599F21"
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 60340..60455,60970..61391))
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 /locus_tag="RP5-998H6.3-002"
 complement(join(50363..51102,53537..53730,57368..57535,
 60340..60455,60970..61391))
 /gene="CDH22"
 /locus_tag="RP5-998H6.3-002"
 /note="match: ESTs: BG717973.1
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 polyA_site
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 Best Local Similarity 85.0%; Pred. No. 1.7e+03;
 Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AGUACAGCCAGACUACGA 20
 Db 133134 AGGCACGCCAGACTAAGA 133115
 AC164137 149208 bp DNA linear HTG 01-JUL-2005
 LOCUS AC164137.2 GI:68299844
 DEFINITION Bos taurus clone CH240-14909, WORKING DRAFT SEQUENCE, 8 unordered
 pieces.
 ACCESSION AC164137
 VERSION HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 KEYWORDS Bos taurus (cow)
 SOURCE Bos taurus
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 149208)
 Muzny,D.,Mathe, Metzker,M.,Lee, Abramson,S., Adams,C., Alder,J.,
 Allen,C., Allen,H., Alibrooks,S., Amin,A., Anguiano,D.,
 Anyalebechi,V., Ayodeji,A., Ayodeji,M., Baca,E., Baden,H.,
 Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
 Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,

DEFINITION Gaesterosteus aculeatus clone ch213-199b3, WORKING DRAFT SEQUENCE, 6 ordered pieces.

ACCESSION AC148601 GI:65812358

VERSION AC148601.21

KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.

SOURCE Gaesterosteus aculeatus (three spined stickleback)

ORGANISM Gaesterosteus aculeatus

REFERENCE 1 (bases 1 to 160241)

AUTHORS Qin,B., Lin,S., Postlethwait,J. and Roe,B.A.

TITLE Gaesterosteus aculeatus BAC Clone ch213-199b3

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 160241)

AUTHORS Qin,B., Lin,S., Postlethwait,J. and Roe,B.A.

TITLE Direct Submission

JOURNAL Submitted (20-MAR-2004) Department of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA

REFERENCE 3 (bases 1 to 160241)

AUTHORS Qin,B., Lin,S., Postlethwait,J. and Roe,B.A.

TITLE Direct Submission

JOURNAL Submitted (17-MAY-2005) Department of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA

COMMENT On May 17, 2005 this sequence version replaced gi:62734771.

----- Genome Center

Center: Department of Chemistry And Biochemistry

The University of Oklahoma

Center code:UOKNOR

* NOTE: This is a 'working draft' sequence. It currently

* consists of 6 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 14138: contig of 14138 bp in length

1 14139 14238: gap of unknown length

1 14239 30871: contig of 16533 bp in length

1 30872 30871: gap of unknown length

1 30872 105980: contig of 75109 bp in length

1 105981 106080: gap of unknown length

1 106081 119781: contig of 13701 bp in length

1 119782 119881: gap of unknown length

1 119882 132445: contig of 12564 bp in length

1 132446 132545: gap of unknown length

1 132546 160241: contig of 27696 bp in length.

Location/Qualifiers

1. 160241

/organism="Gaesterosteus aculeatus"

/mol_type="genomic DNA"

/db_xref="taxon:69293"

/clone="ch213-199b3"

/clone_1lb="Gaesterosteus aculeatus BAC library chori-213"

14139. 14238

/estimated_length=unknown

30872. 30871

/estimated_length=unknown

105981. 106080

/estimated_length=unknown

119782. 119881

/estimated_length=unknown

132446. 132545

/estimated_length=unknown

ORIGIN

Query Match 84.0%; Score 16.8; DB 14; Length 160241;

Best Local Similarity 80.0%; Pred. No. 1.7e+03;

Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGTACAGCCAGCACTACGA 20

Db 37690 AAGTACAGCCAGCACTACGA 37671

RESULT 39

AC104460/c 162514 bp DNA linear PRI 29-APR-2002

LOCUS Homo sapiens chromosome 1 clone RP11-438011, complete sequence.

DEFINITION AC104460 AL358195

ACCESSION AC104460

VERSION AC104460.2 GI:20336796

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 162514)

AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Phelps,K.A., Buckley,D., Raymond,C. and Haugen,E.D.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 162514)

AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.

TITLE Direct Submission

JOURNAL Submitted (11-DEC-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA

REFERENCE 3 (bases 1 to 162514)

AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Phelps,K.A., Buckley,D., Raymond,C. and Haugen,E.D.

TITLE Direct Submission

JOURNAL Submitted (29-APR-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA

COMMENT On Apr 29, 2002 this sequence version replaced gi:17488642.

----- Genome Center

Center: University of Washington Genome Center

Center Code: UWGC

Web site: <http://www.genome.washington.edu>

Contact: uwgchgs@u.washington.edu

Drafting Center: SC

----- Project Information

Center project name: chr-1

Center clone name: RP11-438011 (sc0707)

----- Summary Statistics

Sequencing vector: plasmid; 44% of reads

Chemistry: Dye-terminator ET; 50% of reads

Chemistry: Dye-terminator Big Dye; 50% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 162405 bases at least Q40

Consensus quality: 162506 bases at least Q30

Consensus quality: 162514 bases at least Q20

Insert size: 162514; sum-of-contigs

Quality coverage: 8.5x in Q20 bases; sum-of-contigs

Overlapping Sequences:

5': RP11-351A7 AL356361

3': RP11-343J24 AL513543, 2079-bp overlap

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and vector. In order to accurately represent the entire circular BAC, Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

BgIII

EcoRI

HindIII

SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
2811	2818	8696	8816	967	955
2067	2060	6	<800	6382	6531
10775	10477	456	<800	512	<800
864	884	2955	3041	449	<800
10527	10477	6776	6719	7594	7139
4298	4307	1050	1042	171	<800
876	884	4919	4888	9249	9409
3631	3680	8826	8816	1906	1868
5607	5595	459	<800	3557	3589
1603	1598	3805	3756	2100	2112
908	884	1177	1149	598	<800
2061	2060	2345	2423	171	<800
2028	2060	4349	4315	271	<800
12481	12069	6436	6366	316	<800
7722	7866	359	<800	1767	1737
276	<800	3825	3756	1678	1637
1589	1598	3272	3231	1050	1045
9	<800	14452	14645	5693	5729
1522	1514	4834	4745	5093	5197
293	<800	5125	5078	1598	1637
536	<800	1155	1149	1641	1637
670	<800	3024	3231	2496	2442
8285	8270	8795	8816	10018	9903
6365	6524	12695	12466	5345	5419

6461	6524	1044	1042	7113	7139
847	884	4023	4005	1933	1921
425	<800	1711	1670	11	<800
952	884	2590	2778	20	<800
618	<800	4646	4520	3601	3589
2619	2687	230	<800	571	<800
694	<800	5753	5664	4094	4100
2214	2177	2291	2296	5455	5419
4041	4079	8782	8816	45	<800
133	<800	3845	3756	779	872
6223	6218	1307	1286	708	<800
2165	2177	3192	3231	444	<800
2025	2060	1322	1286	1119	1116
1266	1243	1891	1886	5552	5419
1616	1598	2475	2561	9020	8977
582	<800	7176	7237	12783	12802
4518	4449	24	<800	939	955
2913	2978	5953	5946	7007	7139
21935	22201	3167	3231	869	955
1423	1386			2226	2178
2493	2524			4131	4100
10535	10477			649	<800
5957	6035			996	1045
754	<800			91	<800
				3165	3222
				331	<800
				650	<800
				200	<800
				2153	2178
				5726	5729
				5293	5419
				1107	1116

Query Match 84.0%; Score 16.8; DB 8; Length 162514;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGTACAGCCAGACUACGA 20
DB 92664 AGGTACAGCCAGGCTAGGA 92645

RESULT 40
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 LOCUS
 DEFINITION Homo sapiens chromosome UNK clone RP11-195N21, WORKING DRAFT
 ACCESSION AC073317
 VERSION AC073317.5 GI:11079593
 KEYWORDS HTGS, HTGS_PHASE1, HTGS_DRAFT.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 162701)
 Waterston, R.H.
 The sequence of Homo sapiens clone
 Unpublished
 2 (bases 1 to 162701)
 Waterston, R.H.
 Direct Submissions
 Submitted (14-JUN-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 On Nov 3, 2000 this sequence version replaced gi:10337669.

COMMENT
 ----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 Project Information -----
 Center project name: H_NH0195N21
 Summary Statistics -----
 Sequencing vector: pL13, 60%
 Chemistry: Dye-terminator Big Dye, 36% of reads
 Assembly program: Phrap, version 0.990319
 Consensus quality: 149699 bases at least Q40
 Consensus quality: 153330 bases at least Q30
 Consensus quality: 155040 bases at least Q20
 Insert size: 168, agarose-fp
 Insert size: 161702, sum-of-contigs
 Quality coverage: 4.94 in Q20 bases; sum-of-contigs
 Quality coverage: 5.26 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 23 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 1167: contig of 1167 bp in length
 * 1168 1267: gap of unknown length
 * 1268 3212: contig of 1945 bp in length
 * 3212 3313: gap of unknown length
 * 3313 5058: contig of 1746 bp in length
 * 5058 5159: gap of unknown length
 * 5159 7422: contig of 2264 bp in length
 * 7422 7523: gap of unknown length
 * 7523 9791: contig of 2268 bp in length
 * 9791 9891: gap of unknown length
 * 9891 13294: contig of 3404 bp in length
 * 13294 13395: gap of unknown length
 * 13395 16584: gap of 3190 bp in length
 * 16584 20753: contig of 4069 bp in length
 * 20753 20854: gap of unknown length
 * 20854 24327: contig of 3473 bp in length
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 * 24427 28594: contig of 4168 bp in length

FEATURES
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 /db_xref="taxon:9606"
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Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy      1 AGGUAAGCCAGACGACGCA 20
Db      131778 AGGTACAGACGACGACTACTA 131759

RESULT 41
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DEFINITION Homo sapiens chromosome , clone RP11-168G16, complete sequence.
ACCESSION AC015723
VERSION AC015723.8 GI:13357369
KEYWORDS HTG.
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS Birtten,B., Linton,L., Nusbaum,C. and Lander,B.
TITLE 1 (bases 1 to 163386)
JOURNAL Homo sapiens chromosome, clone RP11-168G16
REFERENCE
AUTHORS 2 (bases 1 to 163386)
Birtten,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barina,N., Beckertly,R., Boguslavsky,L., Boukhalter,B.,
Brown,A., Caele,A., Collange,M., Collins,S., Collamore,A.,
Cooke,P., Dearellano,K., Dewar,K., Domingo,M., Donelan,L., Doyle,M.,
Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Haggos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kamm,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Margulis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Seaver,P.,
Strange-Thomann,N., Stojanovic,N., Sudramanjan,A., Talamas,J.,
Teefaye,S., Tittel,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
TITLE Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome
JOURNAL Research, 320 Charles Street, Cambridge, MA 02141, USA
AUTHORS 3 (bases 1 to 163386)
Birtten,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Barina,N., Bastien,V., Boguslavsky,L., Boukhalter,B., Brown,A.,
Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M.,
Collins,S., Collamore,A., Cooke,P., Dearellano,K., Dewar,K.,
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Maclean,C., Macdonald,P., Margulis,N., Mathews,C., McCarthy,M.,
McEwan,P., McKernan,K., McPheters,R., Meldrum,J., Menes,L.,
Milova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Nord,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
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Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rossetti,M., Roy,A., Santos,R., Schauer,S., Schnupack,R., Seaman,S.,
Severy,P., Sougnez,C., Spencer,B., Strange-Thomann,N.,
Stojanovic,N., Straube,N., Sudramanjan,A., Talamas,J., Teefaye,S.,
Theodore,J., Travers,M., Travis,N., Triggillo,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
COMMENT Submitted (01-APR-2001) Whitehead Institute/MIT Center for Genome
JOURNAL Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Mar 16, 2001 this sequence version replaced gi:13194369.
COMMENT All repeats were identified using RepeatMasker:
COMMENT Smit, A.F.A. & Green, P. (1996-1997)
COMMENT http://ftp.genome.washington.edu/RM/RepeatMasker.html

FEATURES
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/mo_type="genomic DNA"
/db_xref="taxon:9606"
/clone_lib="RP11-168G16"
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Query Match 84.0%; Score 16.8; DB 8; Length 163386;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AGGUAAGCCAGACUACGA 20
Db 127341 AGGTACAGCAGACACTGAGA 127322

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RESULT 42
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LOCUS
DEFINITION Human DNA sequence from clone RP11-271B5 on chromosome 13 contains
the RGP9 gene for fibroblast growth factor 9 (glia-activating
factor (GAF, HBFG-9)), a ribosomal protein S7 (40S ribosomal
protein S7) (RPS7) pseudogene and two Cpg islands, complete
sequence.
ACCESSION AL139378
VERSION AL139378.15 GI:8247510
KEYWORDS HMG, Cpg island; RGP9; GAF; HBFG-9; RPS7.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

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misc_feature 166703
/note="Clone_right_end: RP11-271B5"

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 166703;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACAGCCGAGCAGCAGCA 20
|||||
Db 30829 AGGTACAGCCAGAGTACGA 30848

RESULT 43
AC157818 168087 bp DNA linear HTG 01-JUN-2005
LOCUS Mus musculus chromosome 3 clone RP24-268H11 map 3, *** SEQUENCING
DEFINITION IN PROGRESS ***, 5 unordered pieces.

AC157818
AC157818.4 GI:66841572
HTG; HTGS_PHASE1; HTGS_FUULTOP; HTGS_ACTIVEPIN.
Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 168087)
Birren, B., Nussbaum, C., Lander, B., Abouelleil, A., Allen, N.,
Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V.,
Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J.,
Chapel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B.,
Deatellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L.,
Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D.,
Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N.,
Hagopian, D., Hagoos, B., Hall, J., Horton, L., Hulme, W., Iliev, I.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T.,
Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R.,
Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C.,
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mienga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunhthang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,
Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schnapack, R.,
Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Stubbs, M., Talamas, J., Testafaye, S., Theodore, J.,
Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R.,
Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L.,
Zimmer, A. and Zody, M.
Direct Submission
Submitted (01-MAR-2005) Broad Institute of MIT and Harvard, 320
Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 168087)
Birren, B., Nussbaum, C., Lander, B., Abouelleil, A., Allen, N.,
Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V.,
Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J.,
Chapel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B.,
Deatellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L.,
Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D.,
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Hagopian, D., Hagoos, B., Hall, J., Horton, L., Hulme, W., Iliev, I.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T.,
Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R.,
Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C.,
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mienga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunhthang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,
Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schnapack, R.,
Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,

TITLE
JOURNAL
COMMENT

Stojanovic, N., Stubbs, M., Talamas, J., Testafaye, S., Theodore, J.,
Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R.,
Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L.,
Zimmer, A. and Zody, M.
Direct Submission
Submitted (01-JUN-2005) Broad Institute of MIT and Harvard, 320
Charles Street, Cambridge, MA 02141, USA
On Jun 1, 2005 this sequence version replaced g1:62629962.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Smit, A.F.A. & Green, P. (1996-1997)
----- Genome Center
Center: Broad Institute of MIT and Harvard
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@broad.mit.edu
----- Project Information
Center project name: L31870
Center clone name: 268_H_11

***** NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 18596: contig of 18596 bp in length
* 18597 18696: gap of unknown length
* 18697 22311: contig of 3615 bp in length
* 22312 22411: gap of unknown length
* 22412 58665: contig of 36254 bp in length
* 58665 58765: gap of unknown length
* 58765 74058: contig of 15293 bp in length
* 74058 74158: gap of unknown length
* 74158 168087: contig of 93929 bp in length.

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/clone_11b="RPCT-24 Male Mouse BAC"
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ORIGIN

Query Match 84.0%; Score 16.8; DB 14; Length 168087;
Best Local Similarity 85.0%; Pred. No. 1.7e+03;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACAGCCGAGCAGCAGCA 20
|||||
Db 42939 AGGACAGCCGAGCAGCAGCA 42958

RESULT 44
AC131061 187700 bp DNA linear HTG 11-MAR-2003
LOCUS Mus musculus clone RP24-115M17, WORKING DRAFT SEQUENCE, 8 unordered
DEFINITION pieces.
AC131061
AC131061.3 GI:28913177
HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 187700)
Birren, B., Nuebaum, C. and Lander, B.
Mus musculus, clone RP24-115M17
Unpublished
2 (bases 1 to 187700)

AUTHORS
Birren, B., Nuebaum, C., Lander, B., Ali, A., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B.,
Cammarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J. S., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Gaiagna, J.,
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Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrum, J., Menus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Notbu, C., Norman, C. H.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
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Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
Teafaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.

TITLE
Direct Submission

JOURNAL
Submitted (16-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 187700)

REFERENCE
3 (bases 1 to 187700)
Submitted (11-MAR-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 11, 2003 this sequence version replaced gi:28394870.
All repeats were identified using RepeatMasker:
Smt, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

TITLE
JOURNAL
COMMENT

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WITR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L27077
Center clone name: 115 M.17
----- Summary Statistics
Sequencing vector: Plasmid, n/a, 100% of reads
Chemistry: Dye-terminator Big Dye, 100% of reads
Assembly program: Phrap, version 0.960731
Consensus quality: 185316 bases at least Q40
Consensus quality: 186310 bases at least Q30

Consensus quality: 186759 bases at least Q20
Insert size: 184000; agarose-fp
Insert size: 187000; sum-of-contigs
Quality coverage: 9.4 in Q20 bases; agarose-fp
Quality coverage: 9.3 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 65220: contig of 65220 bp in length
* 65320: gap of 100 bp
* 65321 66009: contig of 689 bp in length
* 66010 66109: gap of 100 bp
* 66110 73823: contig of 7714 bp in length
* 73824 73923: gap of 100 bp
* 73924 85287: contig of 1164 bp in length
* 85288 85387: gap of 100 bp
* 85388 99141: contig of 13754 bp in length
* 99142 99241: gap of 100 bp
* 99242 134109: contig of 3486 bp in length
* 134110 134209: gap of 100 bp
* 134210 165462: contig of 31253 bp in length
* 165463 165562: gap of 100 bp
* 165563 187700: contig of 22138 bp in length.

FEATURES
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ORIGIN
Query Match 84.0%; Score 16.8; DB 14; Length 187700;


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LOCUS	AC135809	195041 bp	DNA	linear	ROD 29-MAY-2004
DEFINITION	Mus musculus BAC clone RP23-353F16 from chromosome 7, complete sequence.				
ACCESSION	AC135809				
VERSION	AC135809.4	GI:47777610			
KEYWORDS	HTG.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eumaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 195041)				
AUTHORS	Vanbrunt, A., Van Brunt, A., Kozlowicz, A., Bielicki, L., Haglund, K. and Meyer, R.				
TITLE	The sequence of Mus musculus BAC clone RP23-353F16				
JOURNAL	Unpublished (2001)				
REFERENCE	2 (bases 1 to 195041)				
AUTHORS	McPherson, J. D. and Waterston, R.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (22-OCT-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA				
REFERENCE	3 (bases 1 to 195041)				
AUTHORS	Wilson, R.K.				
TITLE	Direct Submission				
JOURNAL	Submitted (08-MAY-2004) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA				
REFERENCE	4 (bases 1 to 195041)				
AUTHORS	Wilson, R.K.				
TITLE	Direct Submission				
JOURNAL	Submitted (28-MAY-2004) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA				
REFERENCE	5 (bases 1 to 195041)				
AUTHORS	Wilson, R.K.				
TITLE	Direct Submission				
JOURNAL	Submitted (29-MAY-2004) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA				
COMMENT	On May 28, 2004 this sequence version replaced gi:47084674.				

NOTICE:

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

SOURCE INFORMATION:
The RPCR-23 BAC Library has been constructed by Kazuhiro Oseegawa and Minko Tawano in the laboratory of Pieter de Jong (<http://www.chori.org>) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (<http://www.reagen.com>) or Pieter de Jong and coworkers at <http://www.chori.org> or

NEIGHBORING SEQUENCE INFORMATION: This sequence is the entire insert of the clone.

FEATURES
SOURCE

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Query Match 84.0%; Score 16.8; DB 9; Length 195041;
Best Local Similarity 85.0%; Pred. No. 1.7e+03;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGGUAACGCCAGACTACGA 20
DB 63581 AGGTACTGCGACGACCA 63600

RESULT 47
AC127377/c 195767 bp DNA linear ROD 01-JAN-2004
LOCUS Mus musculus BAC clone RP23-51N3 from chromosome 3, complete
DEFINITION sequence.
AC127377


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VERSION
KEYWORDS
AC127377.4 GI:4036333
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurornathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
Courtney,U., Kozlowicz,A., Bielicki,L. and Haakenson,W.
TITLE
The sequence of Mus musculus BAC clone RP23-51N3
REFERENCE
AUTHORS
2 (bases 1 to 195767)
TITLE
Wilson,R.
JOURNAL
Sequencing of Mus musculus
REFERENCE
AUTHORS
Unpublished (2001)
TITLE
3 (bases 1 to 195767)
REFERENCE
AUTHORS
McPherson,J.D. and Waterston,R.H.
TITLE
Direct Submission
JOURNAL
Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE
AUTHORS
4 (bases 1 to 195767)
TITLE
Wilson,R.K.
JOURNAL
Direct Submission
REFERENCE
AUTHORS
Submitted (07-NOV-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE
AUTHORS
5 (bases 1 to 195767)
TITLE
Wilson,R.K.
JOURNAL
Direct Submission
REFERENCE
AUTHORS
Submitted (25-DEC-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE
AUTHORS
6 (bases 1 to 195767)
TITLE
Wilson,R.
JOURNAL
Direct Submission
REFERENCE
AUTHORS
Submitted (01-JAN-2004) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT
On Dec 25, 2003 this sequence version replaced gi:38198744.
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Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
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Summary Statistics
Center project name: M_BA0051N03
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NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.
This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.
MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
http://genome.wustl.edu
SOURCE INFORMATION:
The RGC1-23 BAC Library has been constructed by Kazutoyo Osegawa
and Minako Iateno in the laboratory of Pieter de Jong
(http://www.chori.org) from female C57BL/6J mouse kidney and/or
brain genomic DNA. The clone and detailed information can be
obtained from Research Genetics, Inc. (http://www.reagen.com) or
Pieter de Jong and coworkers at http://www.chori.org
NEIGHBORING SEQUENCE INFORMATION:

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FEATURES
SOURCE

This sequence is the entire insert of the clone.

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/organism="Mus musculus"
/mol_type="genomic DNA"
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/clone_11b="RP21-23"
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Sc=-9.72) "
66101..66174
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Sc=-11.71) "
111223..111295
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complement(132956..133028)
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/note="likely pseudogene (HMM Sc=45.36 / Sec struct
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167203..168307
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ORIGIN

Query Match	84.0%	Score 16.8	DB 9	Length 195767
Best Local Similarity	85.0%	Pred. No. 1.7e+03		
Matches 17; Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0;

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QY      1 AGGUAAGCCAGGACTUACGA 20
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Db      56269 AGGAACAGGCAAGACTACGA 56250

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RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE
48	AC104205/c					
	AC104205	201745 bp	DNA	linear	ROD 15-JUL-2005	
	Mus musculus	chromosome 3, clone	RP23-250M22,	complete	sequence.	
	AC104205					
	AC104205.15	GI:70887890				
	HTG.					
	Mus musculus	(house mouse)				

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS	
1 (bases 1 to 201745)	
Birren, B., Nusbaum, C. and Lander, E.	
Mus musculus chromosome 3, clone RP23-250M22	
Unpublished	
2 (bases 1 to 201745)	
Birren, B., Linton, J., Nusbaum, C., Lander, E.,	

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontae; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 201745)
 Birren, B., Nusbaum, C. and Lander, E.
 Mus musculus chromosome 3, clone RP23-250M22
 Unpublished
 2 (bases 1 to 201745)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N.,
 Anderson, S., Barna, N., Bastien, V., Boguski, L., Bouckgele, B.,
 Brown, A., Camarata, J., Campiagno, A., Chang, J., Chazaro, B.,
 Choquet, Y., Colangelo, M., Collins, S., Collingmore, A., Cook, A.,
 Cooke, P., Deatellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
 Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
 Hinde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,

TITLE
JOURNAL
REFERENCE
AUTHORS

Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lacroque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C., MacDonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Meldrum, J., Menus, L., Mhova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhkanh, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strause, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigg, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (06-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 201745)

TITLE
JOURNAL
REFERENCE
AUTHORS

Birren, B., Nusbaum, C., Lander, E., Abouelella, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., MacDonald, P., Major, J., Manning, J., Mlenga, V., McCarthy, M., Meldrum, J., Menus, L., Mhova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Notbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhkanh, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schnupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (26-MAY-2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 201745)

Birren, B., Nusbaum, C., Lander, E., Abouelella, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., MacDonald, P., Major, J., Manning, J., Mlenga, V., McCarthy, M., Meldrum, J., Menus, L., Mhova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Notbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhkanh, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schnupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (15-JUL-2005) Broad Institute of MIT and Harvard, 320

Charles Street, Cambridge, MA 02141, USA

On Jul 15, 2005 this sequence version replaced gi:66730823.

All repeats were identified using RepeatMasker:

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center

Center: Broad Institute of MIT and Harvard
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@broad.mit.edu
Project Information
Center project name: L19628
Center clone name: 250_M_22

FEATURES
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/rpt_family="L1_MM"
3550..3828
/rpt_family="L2"
complement(3945..4088)
/rpt_family="Lx2"
4345..4422
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4521..4666
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15028..15047
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18189..18405
/rpt_family="UBR1B"
complement(19145..19197)
/rpt_family="MIR3"
complement(19401..19536)
/rpt_family="MLTIG3"
19780..19888
/rpt_family="RMR15"
20315..20714
/rpt_family="MTC"
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/rpt_family="B4"
22753..22824
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23995..24048
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Beat Local Similarity	85.0%;	Pred. No. 1.7e+03;		
Matches 17;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0

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QY      1 AGGUAACAGCCAGGACTUACGA 20
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Db      78233 AGGAACAGCCAGGACTAGGA 78214

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LOCUS	AC145989					
DEFINITION	Pan troglodytes chromosome UNK clone RPa3-16604, *** SEQUENCING IN					
ACCESSION	AC145989					
VERSION	AC145989.1	GI:3386940				
KEYWORDS	HTG; HTGS; PHASE1.					
SOURCE	Pan troglodytes (chimpanzee)					
ORGANISM	Pan troglodytes					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;					
	Homnidae; Pan.					
REFERENCE	1 (bases 1 to 204393)					
AUTHORS	Wilson,R.K.					
TITLE	The sequence of Pan troglodytes clone					
JOURNAL	Unpublished					
REFERENCE	2 (bases 1 to 204393)					
AUTHORS	Wilson,R.K.					
TITLE	Direct Submission					
JOURNAL	Submitted (01-AUG-2003) Genetics, Genome Sequencing Center, 4444					
COMMENT	Forest Park Parkway, St. Louis, MO 63108, USA					

```

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Center: Washington Genome Center
Center code: W0GSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information
Center project name: C_PTL66004
-----
Summary Statistics
-----

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```

Sequencing vector: M13: 0%
Sequencing vector: Pasmid: 100%
Chemistry: Dye-primed ET: 0% of reads
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 169315 bases at least Q40
Consensus quality: 192131 bases at least Q30
Consensus quality: 194979 bases at least Q20
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 27 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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FEATURES
source
Location/Qualifiers
1. .204393
/organism="Pan troglodytes"

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1	1302: contig of 1302 bp in length
1303	1402: gap of unknown length
1403	2811: contig of 1409 bp in length
2812	2911: gap of unknown length
2912	4488: contig of 1577 bp in length
4489	4588: gap of unknown length
4589	5802: contig of 1214 bp in length
5803	5902: gap of unknown length
5903	7452: contig of 1557 bp in length
7460	7552: gap of unknown length
7560	9074: contig of 1515 bp in length
9075	9174: gap of unknown length
9175	10338: contig of 1164 bp in length
10339	11928: contig of 1490 bp in length
11929	12082: gap of unknown length
12029	13086: contig of 1058 bp in length
13087	13186: gap of unknown length
13187	14390: contig of 1404 bp in length
14391	14690: gap of unknown length
14691	15988: contig of 1298 bp in length
15889	16088: gap of unknown length
16089	17273: contig of 1185 bp in length
17274	17373: gap of unknown length
17374	18705: contig of 1332 bp in length
18706	18805: gap of unknown length
18806	20080: contig of 1275 bp in length
20081	20180: gap of unknown length
20181	21588: contig of 1408 bp in length
21589	21688: gap of unknown length
21689	23906: contig of 2218 bp in length
23907	24006: gap of unknown length
24007	27685: contig of 3679 bp in length
27686	27785: gap of unknown length
27786	31139: contig of 3414 bp in length
31200	31239: gap of unknown length
31300	37408: contig of 6109 bp in length
37409	37508: gap of unknown length
37509	43246: contig of 5738 bp in length
43247	43346: gap of unknown length
43347	53109: contig of 9763 bp in length
53110	53209: gap of unknown length
53209	62904: contig of 9695 bp in length
62905	63004: gap of unknown length
63005	74475: contig of 11471 bp in length
74476	74575: gap of unknown length
74576	89303: contig of 14728 bp in length
89304	89403: gap of unknown length
89404	108282: contig of 18889 bp in length
108293	108392: gap of unknown length
108393	147659: contig of 39267 bp in length
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147760	204393: contig of 56634 bp in length

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Query Match 84.0%; Score 16.8; DB 14; Length 204393;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGUNACGCCAGACUACGA 20
Db 167917 AGGTACAGACGAGACTACCA 167936

RESULT 50
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LOCUS 206775 bp DNA linear ROD 21-JUL-2005
DEFINITION Mus musculus chromosome 3, clone RP23-187N22, complete sequence.
ACCESSION AC158309
VERSION AC158309.6 GI:71044080
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 206775)
Birren, B., Nuebaum, C. and Lander, E.
Mus musculus chromosome 3, clone RP23-187N22
Unpublished
2 (bases 1 to 206775)
Birren, B., Nuebaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, M., Anderson, S., Arachchi, H.M., Barina, N., Baetle, V.,
Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J.,
Chapel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B.,
DeBellef, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L.,
Ericsson, J., Fato, S., Ferreira, P., FitzGerald, M., Gage, D.,
Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N.,
Hagopian, D., Hages, B., Hall, J., Horton, L., Hulme, W., Iliev, I.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kelle, C., Landers, T.,
Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R.,
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McCarthy, M., Meldrum, J., Menus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norby, C.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunhthang, P., Pierre, N., Rachupka, A., Ramasamy, D., Raymond, C.,
Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupbach, R.,
Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Stubbs, M., Talansky, H., Testaye, S., Theodore, J.,
Topham, K., Travers, M., Vassiliev, H., Venkatasubramanian, V.S., Viel, R.,
Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zaitoun, J., Zembek, L.,
Zimmer, A. and Zody, M.

```


GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:35:00 ; Search time 914.538 Seconds
(without alignments)
1118.796 Million cell updates/sec

Title: US-10-800-926-1

Perfect score: 18

Sequence: 1 agaggugcagcgsgua 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database :

GenBank1:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_str:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hyg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	18	100.0	18	6	AR154731 Sequence
C 3	18	100.0	18	6	BD069939 Use of nu
C 4	18	100.0	18	6	BD205570 Method of
C 5	18	100.0	18	6	BD261112 Methods a
C 6	18	100.0	18	6	BD267877 Methods f
C 7	18	100.0	18	6	AR222220 Sequence
C 8	18	100.0	18	6	AR432481 Sequence
C 9	18	100.0	18	6	AX103812 Sequence
C 10	18	100.0	18	6	AX103864 Sequence
C 11	18	100.0	18	6	AX355457 Sequence
C 12	18	100.0	18	6	AX555590 Sequence
C 13	18	100.0	18	6	AX546865 Sequence
C 14	18	100.0	18	6	AX546917 Sequence
C 15	18	100.0	18	6	BD009122 Immunost
C 16	17	94.4	17	6	AR052611 Sequence
C 17	17	94.4	17	6	BD187524 REGULATIO
C 18	17	94.4	17	6	AR630675 Sequence

19	16.4	91.1	289	1	AY207027	AY207027 Acinetoba
20	16	88.9	32	6	AX513690	AX513690 Sequence
21	16	88.9	32	6	AX513691	AX513691 Sequence
22	16	88.9	101451	14	AC138105	AC138105 Mus muscu
23	16	88.9	110000	14	CT005253_2	Continuation (3 of
24	16	88.9	191504	14	AC021215	AC021215 Homo sapi
25	15.4	85.6	544	3	AF432629	AF432629 Unculture
26	15.4	85.6	625	3	AY988985	AY988985 Unculture
27	15.4	85.6	849	3	DO123679	DO123679 Unculture
28	15.4	85.6	855	3	DS025692	DS025692 Unculture
29	15.4	85.6	1029	3	R5052692	R5052692 Rhizospor
30	15.4	85.6	1330	3	AY102340	AY102340 Unculture
31	15.4	85.6	1331	3	AY102345	AY102345 Unculture
32	15.4	85.6	1871	5	BC082645	BC082645 Xenopus 1
33	15.4	85.6	2394	5	BC073203	BC073203 Xenopus 1
34	15.4	85.6	132418	2	AC159431	AC159431 Trypanoso
35	15.4	85.6	142479	2	AC159420	AC159420 Trypanoso
36	15.4	85.6	144820	14	AC099556	AC099556 Trypanoso
37	15.4	85.6	150671	2	AC007862	AC007862 Trypanoso
38	15.4	85.6	286178	14	AC091290	AC091290 Mus muscu
39	15.4	85.6	344249	1	BX842654	BX842654 Bdellovib
40	15.4	85.6	347625	1	BX248356	BX248356 Coryneb
41	15	83.3	17	6	AR052610	AR052610 Sequence
42	15	83.3	17	6	BD187523	BD187523 REGULATIO
43	15	83.3	17	6	BD192460	BD192460 Compositi
44	15	83.3	17	6	AR630674	AR630674 Sequence
45	15	83.3	17	6	AR653968	AR653968 Sequence
46	15	83.3	426	10	G22341	G22341 human STS W
47	15	83.3	779	6	BD186637	BD186637 Nucleic a
48	15	83.3	1936	6	CQ729047	CQ729047 Sequence
49	15	83.3	1936	6	AX333656	AX333656 Sequence
50	15	83.3	1936	6	AX780022	AX780022 Sequence
51	15	83.3	1936	8	HMMTIRE1	M62810 Human mitoc
52	15	83.3	2774	8	HSMTFDNA	X64269 H.sapiens g
53	15	83.3	43440	7	AY954968	AY954968 Bacteriop
54	15	83.3	84158	15	AC067754	Continuation (26 o
55	15	83.3	98874	15	AC067754	AC067754 Arabidops
56	15	83.3	194282	14	AC068897	AC068897 Homo sapi
57	15	83.3	195448	8	AC023170	AC023170 Homo sapi
58	14.8	82.2	447	1	MSR516039	AJ516039 Micrococc
59	14.8	82.2	534	3	AY712503	AY712503 Unculture
60	14.8	82.2	551	10	BV379519	BV379519 S245P6190
61	14.8	82.2	553	10	BV278497	BV278497 S232P6271
62	14.8	82.2	654	10	BV256945	BV256945 S235P6167
63	14.8	82.2	916	1	PSRGT	D00342 Pseudomonas
64	14.8	82.2	1381	3	AY222091	AY222091 Unculture
65	14.8	82.2	2938	5	BC072817	BC072817 Xenopus 1
66	14.8	82.2	12248	1	AB001929	AB001929 Deinococc
67	14.8	82.2	14340	1	AB010345	AB010345 Methanopy
68	14.8	82.2	14878	15	AF440398	AF440398 Mycosphae
69	14.8	82.2	29255	5	AL627162	AL627162 Zebrafish
70	14.8	82.2	35159	1	AY943952	AY943952 Streptomy
71	14.8	82.2	98945	8	AC016961	AC016961 Homo sapi
72	14.8	82.2	110000	1	CP000075_14	Continuation (15 o
73	14.8	82.2	110000	1	CP000075_15	Continuation (16 o
74	14.8	82.2	110000	14	AP006491_2	Continuation (3 of
75	14.8	82.2	110000	14	AP006491_3	Continuation (4 of
76	14.8	82.2	110000	15	AP008218_120	Continuation (121
77	14.8	82.2	121515	14	AC155380	AC155380 Zee maye
78	14.8	82.2	122493	14	AL161737	AL161737 Homo sapi
79	14.8	82.2	125750	14	AC092011	AC092011 Fells cat
80	14.8	82.2	129841	14	AC140102	AC140102 Fells cat
81	14.8	82.2	133073	14	AC154475	AC154475 Daerypus n
82	14.8	82.2	146845	14	CR847989	CR847989 Danto rer
83	14.8	82.2	149982	14	AC148745	AC148745 Bos tauru
84	14.8	82.2	150221	14	AC144676	AC144676 Rattus no
85	14.8	82.2	162820	8	AL138765	AL138765 Human muscu
86	14.8	82.2	167712	14	AC023809	AC023809 Mus muscu
87	14.8	82.2	173244	5	AL929252	AL929252 Zebrafish
88	14.8	82.2	178009	7	AC119549	AC119549 Rattus no
89	14.8	82.2	180500	14	AY967407	AY967407 Enterobac
90	14.8	82.2	183056	5	BX927369	BX927369 Zebrafish
91	14.8	82.2	187325	14	AC142432	AC142432 Rattus no

92	14.8	82.2	1944222	9	AC154368	Mus muscu	C 165	14.4	80.0	110000	14	CT005265_05	Continuation (6 of
C 93	14.8	82.2	194316	9	AC108844	Mus muscu	166	14.4	80.0	110000	14	LMFLCHR26_4	Continuation (5 of
C 94	14.8	82.2	204106	9	AL591113	Mouse DNA	167	14.4	80.0	110000	14	LMFLCHR26_5	Continuation (6 of
C 95	14.8	82.2	2084723	14	AC134942	Homo sapi	168	14.4	80.0	123255	3	AC006003	Continuation (5 of
C 96	14.8	82.2	210476	14	AC164045	Bos tauru	C 169	14.4	80.0	130733	8	AF210726	Mus sapi
C 97	14.8	82.2	218320	14	AC128945	Rattus no	C 170	14.4	80.0	130910	14	AC141688	Mus sapi
C 98	14.8	82.2	223076	14	AC133262	Rattus no	C 171	14.4	80.0	131217	13	AY528864	Mus sapi
C 99	14.8	82.2	243210	14	AC136831	Rattus no	C 172	14.4	80.0	133719	13	AF083501	Mus sapi
C 100	14.8	82.2	244843	14	AC110712	Rattus no	173	14.4	80.0	134226	13	IC1101G	Mus sapi
C 101	14.8	82.2	246890	14	AC117302	Rattus no	174	14.4	80.0	160855	14	AC011579	Homo sapi
C 102	14.8	82.2	246971	14	AC094480	Rattus no	C 175	14.4	80.0	161090	8	AC117415	Homo sapi
C 103	14.8	82.2	254671	14	AC103573	Rattus no	C 176	14.4	80.0	164270	13	AB049735	Gallid he
C 104	14.8	82.2	261992	14	AC119481	Rattus no	C 177	14.4	80.0	164270	13	AB049735	Gallid he
C 105	14.8	82.2	283519	14	CR753823	Danio rer	178	14.4	80.0	164681	9	AC101196	Mus muscu
C 106	14.8	82.2	295712	14	AC120456	Rattus no	C 179	14.4	80.0	167610	14	CR974453	Mus muscu
C 107	14.8	82.2	309050	1	SC0939119	Strepotom	C 180	14.4	80.0	168201	8	AC087675	Homo sapi
C 108	14.8	82.2	326663	8	BX321858	Nitrosomo	C 181	14.4	80.0	169824	14	AP001854	Homo sapi
C 109	14.8	82.2	326663	8	AP011889	Human Xq2	C 182	14.4	80.0	170880	14	AC145870	Homo sapi
C 110	14.4	80.0	378	6	AX070757	Sequence	C 183	14.4	80.0	170943	14	AC166551	Pen trogl
C 111	14.4	80.0	386	10	BV394357	S243P6109	C 184	14.4	80.0	184026	1	AP006619	Nocardia
C 112	14.4	80.0	655	15	AF162080	Harporhyc	C 185	14.4	80.0	190669	9	AL5590429	Mouse DNA
C 113	14.4	80.0	1748	5	BC090363	Xenopus t	C 186	14.4	80.0	194319	9	AL561082	Bos tauru
C 114	14.4	80.0	2000	6	AX509069	Sequence	C 187	14.4	80.0	194520	14	AC148837	Pen trogl
C 115	14.4	80.0	2000	8	HXY0280RF	X99270 H. sapient	C 188	14.4	80.0	204209	14	AC160523	Pen trogl
C 116	14.4	80.0	2193	6	C0868596	Sequence	C 189	14.4	80.0	204658	14	AC106579	Rattus no
C 117	14.4	80.0	2193	6	AX65681	Sequence	C 190	14.4	80.0	205732	9	AC108439	Mus muscu
C 118	14.4	80.0	2193	6	MM06140	Mus muscu	C 191	14.4	80.0	206543	14	AC164931	Oryctolag
C 119	14.4	80.0	2238	4	RABNANUCOT	M84020 Oryctolag	C 192	14.4	80.0	208503	9	AC116730	Mus muscu
C 120	14.4	80.0	2259	6	111726	Sequence 1	C 193	14.4	80.0	211493	14	CR956635	Sus scrofa
C 121	14.4	80.0	2580	2	OCBTBTTUB	BC036558 Mus muscu	C 194	14.4	80.0	211611	14	AC163008	Mus muscu
C 122	14.4	80.0	4028	4	OCATG1	Li0111 Octopus dof	C 195	14.4	80.0	219065	14	AC137014	Rattus

C 238	14	77.8	110000	1	CP000030_10	Continuation (11 o	311	13.8	76.7	259	2	AY572592	AY572592 Toxoplaem
239	14	77.8	110000	1	CP000075_02	Continuation (3 of	312	13.8	76.7	259	2	AY572593	AY572593 Toxoplaem
240	14	77.8	110000	1	CP000075_70	Continuation (21 o	313	13.8	76.7	259	2	AY572597	AY572597 Toxoplaem
241	14	77.8	110000	15	AP008209_230	Continuation (231	314	13.8	76.7	259	2	AY572599	AY572599 Toxoplaem
C 242	14	77.8	113685	15	AC135557	AC135557 Oryza sat	315	13.8	76.7	259	2	AY572600	AY572600 Toxoplaem
C 243	14	77.8	119773	14	AC155464	AC155464 Zea mays	316	13.8	76.7	259	2	AY572601	AY572601 Toxoplaem
C 244	14	77.8	129014	8	AC004916	AC004916 Homo sapi	317	13.8	76.7	259	2	AY572602	AY572602 Toxoplaem
C 245	14	77.8	131995	13	OPU75930	U75930 Oryza sat	318	13.8	76.7	259	2	AY572602	AY572602 Toxoplaem
246	14	77.8	137304	8	AC005627	AC005627 Homo sapi	319	13.8	76.7	335	6	AB518080	AB518080 Sequence
247	14	77.8	141703	8	ALJ360269	ALJ360269 Homo sapi	320	13.8	76.7	335	6	AB518385	AB518385 Sequence
248	14	77.8	142538	15	AC135227	AC135227 Oryza sat	321	13.8	76.7	364	6	BD026494	BD026494 Sequence
C 249	14	77.8	156251	14	AC107325	AC107325 Drosophila	322	13.8	76.7	364	6	AB686884	AB686884 Sequence
C 250	14	77.8	161371	14	AC096972	AC096972 Homo sapi	323	13.8	76.7	417	1	KX049162	KX049162 Sequence
251	14	77.8	168103	14	AC149435	AC149435 Pan trogl	324	13.8	76.7	425	1	AF214552	AF214552 Bacillus
252	14	77.8	168959	14	AC141841	AC141841 Apis mell	325	13.8	76.7	435	15	AF349712	AF349712 Rubeula
253	14	77.8	169818	14	AC155502	AC155502 Zea mays	326	13.8	76.7	466	3	AF432646	AF432646 Unculture
C 254	14	77.8	170523	8	AP002387	AP002387 Homo sapi	327	13.8	76.7	491	3	AY144435	AY144435 Unculture
C 255	14	77.8	171415	14	AP002771	AP002771 Homo sapi	328	13.8	76.7	491	3	AY144451	AY144451 Unculture
C 256	14	77.8	171976	8	AC150278	AC150278 Pan trogl	329	13.8	76.7	491	3	AY144457	AY144457 Unculture
257	14	77.8	174133	8	AC093183	AC093183 Homo sapi	330	13.8	76.7	491	3	AY144459	AY144459 Unculture
C 258	14	77.8	176875	8	AC018638	AC018638 Homo sapi	331	13.8	76.7	491	3	AY144463	AY144463 Unculture
C 259	14	77.8	183541	8	AL606534	AL606534 Human DNA	332	13.8	76.7	494	3	AY144464	AY144464 Unculture
C 260	14	77.8	183948	8	AC009376	AC009376 Drosophila	333	13.8	76.7	494	3	DO080950	DO080950 Unculture
261	14	77.8	188138	8	AC147478	AC147478 Pan trogl	334	13.8	76.7	505	3	AF432645	AF432645 Unculture
262	14	77.8	203635	8	AC148310	AC148310 Pan trogl	335	13.8	76.7	506	3	AY145578	AY145578 Unculture
C 263	14	77.8	235814	14	AC106156	AC106156 Rattus no	336	13.8	76.7	523	6	AB520752	AB520752 Sequence
C 264	14	77.8	240438	14	AC152285	AC152285 Bos tauru	337	13.8	76.7	540	15	AF629423	AF629423 Monascus
265	14	77.8	244139	14	AC162214	AC162214 Bos tauru	338	13.8	76.7	555	6	CQ731328	CQ731328 Sequence
266	14	77.8	305312	1	AB003516	AB003516 Drosophila	339	13.8	76.7	574	15	AF230899	AF230899 Rubeula m
267	14	77.8	349370	1	BX571659	BX571659 Wolinella	340	13.8	76.7	576	15	RCR277911	RCR277911 Rubeula c
C 268	13.8	76.7	24	6	BD093109	BD093109 Novel pol	341	13.8	76.7	590	3	AY596155	AY596155 Unculture
C 269	13.8	76.7	24	6	AB584503	AB584503 Sequence	342	13.8	76.7	597	3	AY187599	AY187599 Unculture
C 270	13.8	76.7	24	6	BD010808	BD010808 Novel pol	343	13.8	76.7	600	6	AB505374	AB505374 Sequence
271	13.8	76.7	100	9	AX992565	AX992565 Sequence	344	13.8	76.7	633	10	BV341081	BV341081 Unculture
272	13.8	76.7	147	9	MUSIGHOP	M30556 Mouse Ig re	345	13.8	76.7	636	3	AY988876	AY988876 Unculture
C 273	13.8	76.7	184	10	AB165303	AB165303 Bos tauru	346	13.8	76.7	637	10	BV079092	BV079092 Unculture
274	13.8	76.7	255	2	AY572579	AY572579 Toxoplaem	347	13.8	76.7	654	10	BV043921	BV043921 Unculture
275	13.8	76.7	255	2	AY572594	AY572594 Toxoplaem	348	13.8	76.7	672	3	AY534199	AY534199 Unculture
276	13.8	76.7	257	2	AY572562	AY572562 Toxoplaem	349	13.8	76.7	684	15	AY061657	AY061657 Rubeula a
277	13.8	76.7	257	2	AY572565	AY572565 Toxoplaem	350	13.8	76.7	686	3	AY988952	AY988952 Unculture
278	13.8	76.7	257	2	AY572566	AY572566 Toxoplaem	351	13.8	76.7	688	15	AY750161	AY750161 Rubeula b
279	13.8	76.7	257	2	AY572567	AY572567 Toxoplaem	352	13.8	76.7	696	8	HSN323652	HSN323652 Homo sapi
280	13.8	76.7	257	2	AY572568	AY572568 Toxoplaem	353	13.8	76.7	698	3	AY988969	AY988969 Unculture
281	13.8	76.7	257	2	AY572569	AY572569 Toxoplaem	354	13.8	76.7	699	15	AP418620	AP418620 Rubeula m
282	13.8	76.7	257	2	AY572571	AY572571 Toxoplaem	355	13.8	76.7	701	15	AP418619	AP418619 Rubeula e
283	13.8	76.7	257	2	AY572572	AY572572 Toxoplaem	356	13.8	76.7	708	15	AY061712	AY061712 Rubeula r
284	13.8	76.7	257	2	AY572573	AY572573 Toxoplaem	357	13.8	76.7	721	15	AY061673	AY061673 Rubeula e
285	13.8	76.7	257	2	AY572574	AY572574 Toxoplaem	358	13.8	76.7	726	6	AX100248	AX100248 Sequence
286	13.8	76.7	257	2	AY572575	AY572575 Toxoplaem	359	13.8	76.7	730	8	HSN329655	HSN329655 Homo sapi
287	13.8	76.7	257	2	AY572576	AY572576 Toxoplaem	360	13.8	76.7	733	10	BV603787	BV603787 Rubeula c
288	13.8	76.7	257	2	AY572577	AY572577 Toxoplaem	361	13.8	76.7	733	15	RCR277910	RCR277910 Unculture
289	13.8	76.7	257	2	AY572578	AY572578 Toxoplaem	362	13.8	76.7	742	3	AY989140	AY989140 Unculture
290	13.8	76.7	257	2	AY572580	AY572580 Toxoplaem	363	13.8	76.7	743	3	BC002873	BC002873 Homo sapi
291	13.8	76.7	257	2	AY572581	AY572581 Toxoplaem	364	13.8	76.7	744	15	AY061717	AY061717 Rubeula r
292	13.8	76.7	257	2	AY572582	AY572582 Toxoplaem	365	13.8	76.7	762	3	AY917642	AY917642 Unculture
293	13.8	76.7	257	2	AY572583	AY572583 Toxoplaem	366	13.8	76.7	827	10	BV018264	BV018264 Unculture
294	13.8	76.7	257	2	AY572585	AY572585 Toxoplaem	367	13.8	76.7	832	3	AT795718	AT795718 Unculture
295	13.8	76.7	257	2	AY572588	AY572588 Toxoplaem	368	13.8	76.7	875	4	SHPLZM3A	SHPLZM3A Sheep lysoz
296	13.8	76.7	257	2	AY572590	AY572590 Toxoplaem	369	13.8	76.7	875	4	SHPLZM4A	SHPLZM4A Sheep lysoz
297	13.8	76.7	257	2	AY572591	AY572591 Toxoplaem	370	13.8	76.7	875	4	SHPLZM4B	SHPLZM4B Sheep lysoz
298	13.8	76.7	257	2	AY572595	AY572595 Toxoplaem	371	13.8	76.7	881	4	SHPLZM2A	SHPLZM2A Sheep lysoz
299	13.8	76.7	257	2	AY572596	AY572596 Toxoplaem	372	13.8	76.7	891	4	BOVLSZ1B	BOVLSZ1B Bovine lysoz
300	13.8	76.7	257	2	AY572598	AY572598 Toxoplaem	373	13.8	76.7	906	4	BOVLSZ1A	BOVLSZ1A Bovine lysoz
301	13.8	76.7	257	2	AY572603	AY572603 Toxoplaem	374	13.8	76.7	981	5	AF616032	AF616032 Gallus ga
302	13.8	76.7	257	2	AY572604	AY572604 Toxoplaem	375	13.8	76.7	991	8	AF263921	AF263921 Homo sapi
303	13.8	76.7	257	2	DO009075	DO009075 Toxoplaem	376	13.8	76.7	1006	1	BPSODB	BPSODB Bordetella
304	13.8	76.7	259	2	AY572563	AY572563 Toxoplaem	377	13.8	76.7	1006	1	BPSODB	BPSODB Bordetella
305	13.8	76.7	259	2	AY572564	AY572564 Toxoplaem	378	13.8	76.7	1030	11	AP339037	AP339037 Cloning v
306	13.8	76.7	259	2	AY572570	AY572570 Toxoplaem	379	13.8	76.7	1066	15	AP348915	AP348915 Nitella o
307	13.8	76.7	259	2	AY572574	AY572574 Toxoplaem	380	13.8	76.7	1087	5	BX933774	BX933774 Gallus ga
308	13.8	76.7	259	2	AY572586	AY572586 Toxoplaem	381	13.8	76.7	1090	15	AY228360	AY228360 Rubeula c
309	13.8	76.7	259	2	AY572587	AY572587 Toxoplaem	382	13.8	76.7	1115	2	FM0252962	FM0252962 Flabellif
310	13.8	76.7	259	2	AY572589	AY572589 Toxoplaem	383	13.8	76.7	1118	6	BD252095	BD252095 47 secret

C 384	13.8	76.7	1236	6	AR628236	Sequence	C 457	13.8	76.7	14384	1	D90705	D90705	Bactericidal
C 385	13.8	76.7	1242	4	OPa4672	Ochotona	C 458	13.8	76.7	15116	14	AC009579_4	Continuation (5 of	
C 386	13.8	76.7	1248	1	AF127006	Bacterich	C 459	13.8	76.7	15782	6	AR619699	Sequence	
C 387	13.8	76.7	1248	1	AF127007	Bacterich	C 460	13.8	76.7	16325	14	AC015144	AC015144	
C 388	13.8	76.7	1259	15	AR335443	Russula	C 461	13.8	76.7	17062	6	C0590729	C0590729	
C 389	13.8	76.7	1278	3	AM072427	Uncultured	C 462	13.8	76.7	18657	1	D90704	D90704	
C 390	13.8	76.7	1283	3	MABRRM	Marine Buba	C 463	13.8	76.7	20334	8	AB001764	AB001764	
C 391	13.8	76.7	1289	6	AX040114	Sequence	C 464	13.8	76.7	20704	1	CR383702	CR383702	
C 392	13.8	76.7	1291	3	PS125260	Polysiph	C 465	13.8	76.7	21846	1	AT095165	AT095165	
C 393	13.8	76.7	1298	15	AY228350	Sequence	C 466	13.8	76.7	24045	1	AB070941	AB070941	
C 394	13.8	76.7	1322	1	AY515123	Bartonella	C 467	13.8	76.7	25517	1	AP170880	AP170880	
C 395	13.8	76.7	1338	6	C0614079	Sequence	C 468	13.8	76.7	25617	6	AX707121	AX707121	
C 396	13.8	76.7	1370	2	AY973624	Caudospor	C 469	13.8	76.7	29000	8	AY02789386	AY02789386	
C 397	13.8	76.7	1374	2	AF132544	Wetia	C 470	13.8	76.7	33443	14	AC014332	AC014332	
C 398	13.8	76.7	1375	2	AY090069	Polysiph	C 471	13.8	76.7	35984	14	AC153806	AC153806	
C 399	13.8	76.7	1414	6	AR520687	Sequence	C 472	13.8	76.7	36123	2	AC093553	AC093553	
C 400	13.8	76.7	1455	1	AF328417	Seccarot	C 473	13.8	76.7	37941	1	ADPC92361	ADPC92361	
C 401	13.8	76.7	1457	1	AF328417	Seccarot	C 474	13.8	76.7	39261	14	AC020271	AC020271	
C 402	13.8	76.7	1450	3	AY555803	Unculture	C 475	13.8	76.7	41924	14	AC087403	AC087403	
C 403	13.8	76.7	1505	3	AY955088	Unculture	C 476	13.8	76.7	42569	14	HS305C8	HS305C8	
C 404	13.8	76.7	1521	5	BX935504	Gallus ga	C 477	13.8	76.7	50000	6	AX081173	AX081173	
C 405	13.8	76.7	1705	5	CR942584	Xenopus t	C 478	13.8	76.7	53178	6	C0363755	C0363755	
C 406	13.8	76.7	1753	6	CO412938	Sequence	C 479	13.8	76.7	60298	8	AL359508	AL359508	
C 407	13.8	76.7	1808	5	BC063354	Xenopus t	C 480	13.8	76.7	63934	8	AC010699	AC010699	
C 408	13.8	76.7	1937	6	C0595464	Sequence	C 481	13.8	76.7	65978	8	AL596184	AL596184	
C 409	13.8	76.7	1949	2	AF322044	Malawimon	C 482	13.8	76.7	66669	14	AME16952	AME16952	
C 410	13.8	76.7	2001	5	AF322044	Gallus ga	C 483	13.8	76.7	68842	14	AC026915	AC026915	
C 411	13.8	76.7	2019	6	AR627784	Sequence	C 484	13.8	76.7	71496	14	AC090722	AC090722	
C 412	13.8	76.7	2098	6	AR183233	Sequence	C 485	13.8	76.7	71639	14	AC162785	AC162785	
C 413	13.8	76.7	2170	8	AB185652	Macaca fa	C 486	13.8	76.7	71907	14	AC014585	AC014585	
C 414	13.8	76.7	2283	4	DQ119288	Bos tauru	C 487	13.8	76.7	76297	14	CR954201_10	CR954201_10	
C 415	13.8	76.7	2323	1	AF329831	Haemophil	C 488	13.8	76.7	79575	15	AP006357	AP006357	
C 416	13.8	76.7	2395	1	AF025768	Brinla c	C 489	13.8	76.7	80530	14	AC165498	AC165498	
C 417	13.8	76.7	2534	2	TOXTUBBA	Sequence	C 490	13.8	76.7	82383	8	AL591623	AL591623	
C 418	13.8	76.7	3295	6	C0590720	Sequence	C 491	13.8	76.7	84392	14	AC013393	AC013393	
C 419	13.8	76.7	3295	2	AF125444	Cenothad	C 492	13.8	76.7	87286	14	AC014436	AC014436	
C 420	13.8	76.7	3297	2	AY210836	Peripatus	C 493	13.8	76.7	87790	14	AL359498	AL359498	
C 421	13.8	76.7	3506	2	AY310313	Brichoelr	C 494	13.8	76.7	91840	8	AC112254	AC112254	
C 422	13.8	76.7	4140	6	AR505320	Sequence	C 495	13.8	76.7	92375	15	AP003905	AP003905	
C 423	13.8	76.7	4347	15	AF015276	Volvox ca	C 496	13.8	76.7	92509	8	AL646086	AL646086	
C 424	13.8	76.7	4625	2	AY278365	Giardia i	C 497	13.8	76.7	94212	8	AP000246	AP000246	
C 425	13.8	76.7	5973	6	C0595463	Sequence	C 498	13.8	76.7	97477	15	AC148965	AC148965	
C 426	13.8	76.7	6497	6	CQ614078	Sequence	C 499	13.8	76.7	100000	8	AP000207	AP000207	
C 427	13.8	76.7	6816	6	AR175747	Sequence	C 500	13.8	76.7	101027	8	AC023160	AC023160	
C 428	13.8	76.7	6816	6	AR352550	Sequence	C 501	13.8	76.7	101509	14	AC027353	AC027353	
C 429	13.8	76.7	6816	6	AR656259	Sequence	C 502	13.8	76.7	101586	14	AP007489	AP007489	
C 430	13.8	76.7	6855	6	AR175748	Sequence	C 503	13.8	76.7	105956	8	AC074136	AC074136	
C 431	13.8	76.7	6855	6	AR352551	Sequence	C 504	13.8	76.7	106707	14	AC113606	AC113606	
C 432	13.8	76.7	6855	6	AR656260	Sequence	C 505	13.8	76.7	107356	8	AC113606	AC113606	
C 433	13.8	76.7	6866	6	AR453043	Sequence	C 506	13.8	76.7	109766	14	AC117712	AC117712	
C 434	13.8	76.7	6866	6	AX281155	Sequence	C 507	13.8	76.7	110000	1	AB005174_07	AB005174_07	
C 435	13.8	76.7	6866	6	AX345569	Sequence	C 508	13.8	76.7	110000	1	AB005674_06	AB005674_06	
C 436	13.8	76.7	7382	9	MUSACGRCA	Mus muscu	C 509	13.8	76.7	110000	1	CR555306_19	CR555306_19	
C 437	13.8	76.7	7562	15	AF176575	Emerticell	C 510	13.8	76.7	110000	1	CR555306_20	CR555306_20	
C 438	13.8	76.7	7919	13	HPV10	Human papil	C 511	13.8	76.7	110000	1	U00096_06	U00096_06	
C 439	13.8	76.7	8346	6	AX323713	Sequence	C 512	13.8	76.7	110000	1	AB013598_29	AB013598_29	
C 440	13.8	76.7	9336	15	AF178850	Aspergill	C 513	13.8	76.7	110000	1	AB013598_30	AB013598_30	
C 441	13.8	76.7	9331	1	AF54614481	Streptomy	C 514	13.8	76.7	110000	1	AB016822_21	AB016822_21	
C 442	13.8	76.7	9556	6	AR619587	Sequence	C 515	13.8	76.7	110000	1	AB016853_16	AB016853_16	
C 443	13.8	76.7	9626	6	AB007991	Agrodacte	C 516	13.8	76.7	110000	1	AB016853_17	AB016853_17	
C 444	13.8	76.7	10016	6	C0595466	Sequence	C 517	13.8	76.7	110000	1	AB017283_16	AB017283_16	
C 445	13.8	76.7	10464	8	AE004634	Pseudomon	C 518	13.8	76.7	110000	1	AP008231_16	AP008231_16	
C 446	13.8	76.7	10557	8	HUMIMP	Sequence	C 519	13.8	76.7	110000	1	BA000007_07	BA000007_07	
C 447	13.8	76.7	11033	1	AE007311	Sinorhizo	C 520	13.8	76.7	110000	1	BA000012_08	BA000012_08	
C 448	13.8	76.7	11853	1	AF110737	Sinorhizo	C 521	13.8	76.7	110000	1	BA000030_26	BA000030_26	
C 449	13.8	76.7	11897	1	AE009025	Agrodacte	C 522	13.8	76.7	110000	1	BA000030_52	BA000030_52	
C 450	13.8	76.7	11953	8	AL646019	Human DNA	C 523	13.8	76.7	110000	1	BA000030_72	BA000030_72	
C 451	13.8	76.7	12092	4	BOVLYSOZMA	Bos tauru	C 524	13.8	76.7	110000	1	BA000030_87	BA000030_87	
C 452	13.8	76.7	12222	4	BOVLYSOZMA	Bos tauru	C 525	13.8	76.7	110000	1	BA000045_30	BA000045_30	
C 453	13.8	76.7	13319	1	AE010317	Methanopy	C 526	13.8	76.7	110000	1	BX571965_01	BX571965_01	
C 454	13.8	76.7	13428	1	AE010315	Methanopy	C 527	13.8	76.7	110000	1	BX580851_22	BX580851_22	
C 455	13.8	76.7	14180	6	C0595469	Sequence	C 528	13.8	76.7	110000	1	CP000026_11	CP000026_11	
C 456	13.8	76.7	14359	1	AE001221	Treponema	C 529	13.8	76.7	110000	1	CP000031_00	CP000031_00	

530	13.8	76.7	110000	1	CP000050	00	CP000050 Xanthomon	603	13.8	76.7	130226	9	AC162229	AC162229 Mus muscu
531	13.8	76.7	110000	2	CP000058	15	Continuation (16 o	604	13.8	76.7	134161	8	AC104336	AC104336 Homo sapi
532	13.8	76.7	110000	1	AB003536	1	Continuation (12 of	605	13.8	76.7	134431	13	AY386265	AY386265 Bovine pa
533	13.8	76.7	110000	2	CP000079	00	CP000079 Leishmani	606	13.8	76.7	136742	1	EC082598	U82598 Escherichia
534	13.8	76.7	110000	2	CP000080	03	Continuation (4 of	607	13.8	76.7	137029	15	AC099040	AC099040 Oryza sat
535	13.8	76.7	110000	2	CP000080	03	Continuation (4 of	608	13.8	76.7	138533	8	AC011357	AC011357 Homo sapi
536	13.8	76.7	110000	6	BD430733	15	Continuation (16 o	609	13.8	76.7	138716	15	AC091234	AC091234 Oryza sat
537	13.8	76.7	110000	14	AC009579	3	Continuation (4 of	610	13.8	76.7	140561	15	AC137822	AC137822 Medicago
538	13.8	76.7	110000	14	AC110929	3	Continuation (4 of	611	13.8	76.7	141925	14	AC098702	AC098702 Felis cat
539	13.8	76.7	110000	14	AC110967	1	Continuation (2 of	612	13.8	76.7	142248	15	AC107315	AC107315 Genomic B
540	13.8	76.7	110000	14	AC115642	1	Continuation (2 of	613	13.8	76.7	142696	14	AC143051	AL329472 Human DNA
541	13.8	76.7	110000	14	AC020850	07	AC020850 Mus muscu	614	13.8	76.7	143060	15	OS092947	AL329472 Human DNA
542	13.8	76.7	110000	14	AL133712	6	Continuation (2 of	615	13.8	76.7	143093	15	AP006155	AL329472 Human DNA
543	13.8	76.7	110000	14	AL133712	6	Continuation (2 of	616	13.8	76.7	144644	8	AP006155	AL329472 Human DNA
544	13.8	76.7	110000	14	AP006499	00	AP006499 Cyanidios	617	13.8	76.7	145709	15	AC069288	AC069288 Homo sapi
545	13.8	76.7	110000	14	CR954199	08	Continuation (9 of	618	13.8	76.7	146548	14	AC023858	AC023858 Homo sapi
546	13.8	76.7	110000	14	CR954200	07	Continuation (8 of	619	13.8	76.7	147075	14	AC139166	AC139166 Rattus no
547	13.8	76.7	110000	14	CR954201	09	Continuation (10 o	620	13.8	76.7	148055	14	AC128178	AC128178 Rattus no
548	13.8	76.7	110000	14	CR954202	06	Continuation (7 of	621	13.8	76.7	148120	14	AC141805	AC141805 Apis mell
549	13.8	76.7	110000	14	CR954204	07	Continuation (8 of	622	13.8	76.7	148373	15	AC134348	AC134348 Oryza sat
550	13.8	76.7	110000	14	CR954210	00	Continuation (3 of	623	13.8	76.7	148845	8	HS1114A1	AL035664 Human DNA
551	13.8	76.7	110000	14	CR954212	02	Continuation (3 of	624	13.8	76.7	149118	9	AC116520	AC116520 Mus muscu
552	13.8	76.7	110000	14	CR954216	02	Continuation (3 of	625	13.8	76.7	149430	13	AY464052	AY464052 Equine he
553	13.8	76.7	110000	14	CT005244	0	CT005244 Leishmani	626	13.8	76.7	149854	9	AC117225	AC117225 Mus muscu
554	13.8	76.7	110000	14	CT005252	0	CT005252 Leishmani	627	13.8	76.7	150224	13	AY665713	AY665713 Equine he
555	13.8	76.7	110000	14	CT005253	0	CT005253 Leishmani	628	13.8	76.7	150228	14	AC091994	AC091994 Homo sapi
556	13.8	76.7	110000	14	CT005253	0	Continuation (3 of	629	13.8	76.7	150299	14	AC157251	AC157251 Daeypus n
557	13.8	76.7	110000	14	CT005255	12	Continuation (2 of	630	13.8	76.7	150317	15	AP005739	AP005739 Oryza sat
558	13.8	76.7	110000	14	CT005262	06	Continuation (7 of	631	13.8	76.7	150849	14	AC141935	AC141935 Rattus no
559	13.8	76.7	110000	14	CT005266	05	Continuation (6 of	632	13.8	76.7	151182	8	AL611942	AL611942 Human DNA
560	13.8	76.7	110000	14	CT005270	01	Continuation (2 of	633	13.8	76.7	151262	9	AL928698	AL928698 Mouse DNA
561	13.8	76.7	110000	14	CT005272	10	Continuation (11 o	634	13.8	76.7	151584	14	AC146305	AC146305 Homo sapi
562	13.8	76.7	110000	14	LMPLCR32	17	Continuation (18 o	635	13.8	76.7	151796	14	AC096995	AC096995 Homo sapi
563	13.8	76.7	110000	15	AP008214	032	Continuation (33 o	636	13.8	76.7	151806	15	AP002093	AP002093 Oryza sat
564	13.8	76.7	110000	15	AP008215	052	Continuation (53 o	637	13.8	76.7	151933	14	AP002093	AP002093 Oryza sat
565	13.8	76.7	110000	15	AP008216	069	Continuation (70 o	638	13.8	76.7	154681	14	AC099008	AC099008 Drosophi
566	13.8	76.7	110000	15	AP008216	239	Continuation (72 o	639	13.8	76.7	154986	2	AC141766	AC141766 Apis mell
567	13.8	76.7	110000	15	CR382129	19	Continuation (20 o	640	13.8	76.7	155030	14	AC141807	AC141807 Apis mell
568	13.8	76.7	110000	15	AB017341	05	Continuation (6 of	641	13.8	76.7	155942	14	AC136691	AC136691 Homo sapi
569	13.8	76.7	110000	15	AB017345	03	Continuation (4 of	642	13.8	76.7	156411	14	AC141335	AC141335 Rattus no
570	13.8	76.7	110000	15	AP008207	060	Continuation (61 o	643	13.8	76.7	157686	14	BS000110	BS000110 Pan trogl
571	13.8	76.7	110000	15	AP008208	061	Continuation (62 o	644	13.8	76.7	157974	14	AC121070	AC121070 Sus scrof
572	13.8	76.7	110000	15	AP008209	092	Continuation (93 o	645	13.8	76.7	158033	8	AC018926	AC018926 Homo sapi
573	13.8	76.7	110000	15	AP008209	195	Continuation (196 o	646	13.8	76.7	158508	14	AC063934	AC063934 Homo sapi
574	13.8	76.7	110000	15	AP008209	246	Continuation (247 o	647	13.8	76.7	158740	2	AC159452	AC159452 Trypanoso
575	13.8	76.7	110000	15	AP008210	066	Continuation (67 o	648	13.8	76.7	159122	14	AC025556	AC025556 Homo sapi
576	13.8	76.7	110000	15	AP008210	188	Continuation (189 o	649	13.8	76.7	159857	14	AC018767	AC018767 Homo sapi
577	13.8	76.7	110000	15	AP008210	239	Continuation (240 o	650	13.8	76.7	159893	8	AC116903	AC116903 Homo sapi
578	13.8	76.7	110000	15	AP008211	157	Continuation (158 o	651	13.8	76.7	160129	15	OS090082	AL160667 Oryza sat
579	13.8	76.7	110000	15	AP008211	170	Continuation (171 o	652	13.8	76.7	160298	14	AC067818	AC067818 Homo sapi
580	13.8	76.7	111590	8	HS104815		Continuation (171 o	653	13.8	76.7	160718	14	AC067839	AC067839 Homo sapi
581	13.8	76.7	112460	8	HS104815		Continuation (171 o	654	13.8	76.7	160718	14	AC067839	AC067839 Homo sapi
582	13.8	76.7	115043	8	AL663070		Continuation (171 o	655	13.8	76.7	160813	14	AC155412	AC155412 Zee maye
583	13.8	76.7	115767	8	AC012310		Continuation (171 o	656	13.8	76.7	160817	2	AC008316	AC008316 Drosophi
584	13.8	76.7	116326	5	EX323467		Continuation (171 o	657	13.8	76.7	161139	8	AC132812	AC132812 Homo sapi
585	13.8	76.7	116326	5	EX323467		Continuation (171 o	658	13.8	76.7	161139	9	AC133503	AC133503 Mus muscu
586	13.8	76.7	117951	8	AL391803		Continuation (171 o	659	13.8	76.7	161598	14	AC127513	AC127513 Homo sapi
587	13.8	76.7	118227	14	AC148516		Continuation (171 o	660	13.8	76.7	164396	14	AC024961	AC024961 Homo sapi
588	13.8	76.7	118741	8	AC005319		Continuation (171 o	661	13.8	76.7	164971	2	AC016792	AC016792 Mus muscu
589	13.8	76.7	118995	8	AC005319		Continuation (171 o	662	13.8	76.7	165510	14	AC023677	AC023677 Homo sapi
590	13.8	76.7	119523	15	AC104706		Continuation (171 o	663	13.8	76.7	165768	14	AC023517	AC023517 Homo sapi
591	13.8	76.7	119523	15	AC104706		Continuation (171 o	664	13.8	76.7	165878	14	AC133153	AC133153 Mus muscu
592	13.8	76.7	120173	14	AC137630		Continuation (171 o	665	13.8	76.7	167886	14	AC166031	AC166031 Sus scrof
593	13.8	76.7	121515	8	AC155380		Continuation (171 o	666	13.8	76.7	168153	14	AC131519	AC131519 Rattus no
594	13.8	76.7	121774	14	AC084059		Continuation (171 o	667	13.8	76.7	168208	8	AC091133	AC091133 Mus muscu
595	13.8	76.7	122288	8	AL359384		Continuation (171 o	668	13.8	76.7	168613	14	AL359883	AL359883 Zee maye
596	13.8	76.7	123795	14	AP007824		Continuation (171 o	669	13.8	76.7	168658	14	AC152918	AC152918 Homo sapi
597	13.8	76.7	124025	8	AL160169		Continuation (171 o	670	13.8	76.7	168658	14	AC152918	AC152918 Homo sapi
598	13.8	76.7	124571	8	AL450384		Continuation (171 o	671	13.8	76.7	168731	8	AC007012	AC007012 Homo sapi
599	13.8	76.7	124666	14	AC155390		Continuation (171 o	672	13.8	76.7	169770	14	AC141843	AC141843 Apis mell
600	13.8	76.7	125032	8	AC1515286		Continuation (171 o	673	13.8	76.7	169985	8	CNS05780	AL359283 Human chr
601	13.8	76.7	126945	14	AC162433		Continuation (171 o	674	13.8	76.7	170914	2	AC010843	AC010843 Drosophi
602	13.8	76.7	127374	9	AC107675		Continuation (171 o	675	13.8	76.7	171062	14	AC022066	AC022066 Homo sapi

676	13.8	76.7	171289	8	AC096887	Homo sapi	c 749	13.8	76.7	201229	9	AC114578	AC114578	Mus muscu
677	13.8	76.7	172474	14	AC146950	Zea mays	c 750	13.8	76.7	201309	14	AC159518	AC159518	Bos tauru
678	13.8	76.7	172481	1	AC102240	Mus muscu	c 751	13.8	76.7	201673	14	AL591544	AL591544	Mus muscu
c 679	13.8	76.7	173071	14	AC166012	Oryctolag	752	13.8	76.7	203450	14	AP002009	AP002009	Homo sapi
680	13.8	76.7	173509	2	AC010031	AC010031	c 753	13.8	76.7	204855	9	AC133100	AC133100	Mus muscu
681	13.8	76.7	173608	8	AC107993	AC107993	c 754	13.8	76.7	204915	14	AC163150	AC163150	Mus muscu
c 682	13.8	76.7	173708	15	AC022251	Homo sapi	c 755	13.8	76.7	205516	8	AC008781	AC008781	Homo sapi
c 683	13.8	76.7	175153	15	AP003977	Oryza sat	c 756	13.8	76.7	205601	14	AC166865	AC166865	Oryctolag
684	13.8	76.7	175630	14	AC150234	AC150234	c 757	13.8	76.7	205642	14	AC007898	AC007898	Homo sapi
685	13.8	76.7	175896	2	AC150407	AC150407	c 758	13.8	76.7	206182	9	AC107720	AC107720	Mus muscu
c 686	13.8	76.7	175946	8	AC150407	AC150407	c 759	13.8	76.7	206524	14	AC109838	AC109838	Rattus no
687	13.8	76.7	175946	8	AC150407	AC150407	c 760	13.8	76.7	207439	13	AT509253	AT509253	Ostreifid h
c 688	13.8	76.7	176349	15	AP002092	AP002092	c 761	13.8	76.7	210972	14	AC090288	AC090288	Mus muscu
c 689	13.8	76.7	176479	14	AC135631	AC135631	c 762	13.8	76.7	211115	9	AC147568	AC147568	Mus muscu
690	13.8	76.7	176526	14	AP001192	AP001192	c 763	13.8	76.7	211335	8	AC112640	AC112640	Homo sapi
c 691	13.8	76.7	176615	15	OS0700035	AL606595	c 764	13.8	76.7	211680	9	AL603682	AL603682	Mus muscu
c 692	13.8	76.7	177028	2	AC008315	AC008315	c 765	13.8	76.7	212973	9	AL683847	AL683847	Mus muscu
c 693	13.8	76.7	177364	9	AC156274	AC156274	c 766	13.8	76.7	214031	14	AC134141	AC134141	Mus muscu
694	13.8	76.7	177883	14	AC046159	AC046159	c 767	13.8	76.7	214343	14	AC151563	AC151563	Mus muscu
695	13.8	76.7	178292	14	AC120830	AC120830	c 768	13.8	76.7	214445	9	AC110556	AC110556	Mus muscu
696	13.8	76.7	178315	8	AC122688	AC122688	c 769	13.8	76.7	214893	14	AC151972	AC151972	Mus muscu
697	13.8	76.7	178488	14	AC151856	AC151856	c 770	13.8	76.7	215050	1	AL646057	AL646057	Rattus no
698	13.8	76.7	180426	15	AC134342	AC134342	c 771	13.8	76.7	215441	8	AP002800	AP002800	Homo sapi
c 699	13.8	76.7	180888	8	AC007491	AC007491	c 772	13.8	76.7	215647	14	AC068591	AC068591	Homo sapi
c 700	13.8	76.7	182213	14	AC136685	AC136685	c 773	13.8	76.7	215955	14	AC133815	AC133815	Rattus no
c 701	13.8	76.7	182432	14	AC120832	AC120832	c 774	13.8	76.7	216041	14	AC112524	AC112524	Drosophill
702	13.8	76.7	182650	2	AC159404	AC159404	c 775	13.8	76.7	216266	9	AC073797	AC073797	Mus muscu
c 703	13.8	76.7	182847	14	AC126229	AC126229	c 776	13.8	76.7	216807	9	AC079681	AC079681	Mus muscu
c 704	13.8	76.7	183039	14	AC025288	AC025288	c 777	13.8	76.7	217265	9	AC145294	AC145294	Mus muscu
c 705	13.8	76.7	183161	2	AC007851	AC007851	c 778	13.8	76.7	218631	14	AC109532	AC109532	Rattus no
706	13.8	76.7	183347	15	CN8077P7	AL713930	c 779	13.8	76.7	218747	9	AC093339	AC093339	Mus muscu
707	13.8	76.7	183607	14	AC121176	AC121176	c 780	13.8	76.7	218880	14	AC150974	AC150974	Bos tauru
708	13.8	76.7	184010	14	AC150025	AC150025	c 781	13.8	76.7	220193	2	AC135719	AC135719	Homo sapi
709	13.8	76.7	184140	8	AC090630	AC090630	c 782	13.8	76.7	220679	14	AE003704	AE003704	Drosophill
710	13.8	76.7	184855	9	AC124713	AC124713	c 783	13.8	76.7	221217	14	CR388081	CR388081	Danio rer
c 711	13.8	76.7	185655	9	MM0296304	AJ296304	c 784	13.8	76.7	221668	14	AC160265	AC160265	Bos tauru
c 712	13.8	76.7	185810	2	AC010995	AC010995	c 785	13.8	76.7	221873	14	AC128173	AC128173	Rattus no
713	13.8	76.7	186000	8	AC023892	AC023892	c 786	13.8	76.7	222853	14	AC160699	AC160699	Bos tauru
714	13.8	76.7	186000	14	AC153265	AC153265	c 787	13.8	76.7	223528	14	CR769780	CR769780	Danio rer
715	13.8	76.7	186217	9	AC122310	AC122310	c 788	13.8	76.7	223726	9	AL626807	AL626807	Mus muscu
c 716	13.8	76.7	186350	14	AC022688	AC022688	c 789	13.8	76.7	223726	9	AC147221	AC147221	Mus muscu
c 717	13.8	76.7	186848	14	AC145556	AC145556	c 790	13.8	76.7	223854	9	AL606562	AL606562	Mus muscu
c 718	13.8	76.7	187347	14	AC025880	AC025880	c 791	13.8	76.7	223987	14	AC147800	AC147800	Mus muscu
c 719	13.8	76.7	187707	15	AC077693	AC077693	c 792	13.8	76.7	224445	14	AC098492	AC098492	Rattus no
720	13.8	76.7	187958	14	AC135578	AC135578	c 793	13.8	76.7	225234	14	AC127530	AC127530	Homo sapi
721	13.8	76.7	188679	14	AC023121	AC023121	c 794	13.8	76.7	225537	14	AC114529	AC114529	Rattus no
c 722	13.8	76.7	188834	9	AC098642	AC098642	c 795	13.8	76.7	227313	14	AC161389	AC161389	Bos tauru
c 723	13.8	76.7	189055	14	AC073716	AC073716	c 796	13.8	76.7	228458	9	AC158782	AC158782	Mus muscu
c 724	13.8	76.7	190000	14	AC004479	AC004479	c 797	13.8	76.7	228718	14	AC103423	AC103423	Rattus no
725	13.8	76.7	190310	14	AC023225	AC023225	c 798	13.8	76.7	229092	14	AC160332	AC160332	Bos tauru
c 726	13.8	76.7	190330	2	AC005720	AC005720	c 799	13.8	76.7	229231	14	AC115211	AC115211	Rattus no
c 727	13.8	76.7	191557	8	AC008506	AC008506	c 800	13.8	76.7	229899	14	AC141728	AC141728	Al646057
c 728	13.8	76.7	192735	14	AC150719	AC150719	c 801	13.8	76.7	230138	13	AR232689	AR232689	Rat cyrom
c 729	13.8	76.7	193083	9	AC124584	AC124584	c 802	13.8	76.7	230854	14	AC165155	AC165155	Mus muscu
730	13.8	76.7	193953	14	AC149623	AC149623	c 803	13.8	76.7	231435	14	AC130519	AC130519	Rattus no
c 731	13.8	76.7	194024	14	AC166992	AC166992	c 804	13.8	76.7	231716	9	AC135409	AC135409	Rattus no
c 732	13.8	76.7	194474	14	AC137536	AC137536	c 805	13.8	76.7	236685	14	AC084744	AC084744	Mus muscu
c 733	13.8	76.7	194810	14	AC150924	AC150924	c 806	13.8	76.7	236838	9	AC125451	AC125451	Mus muscu
734	13.8	76.7	194905	8	AC068896	AC068896	c 807	13.8	76.7	237343	14	AC094780	AC094780	Rattus no
735	13.8	76.7	194986	14	AC152015	AC152015	c 808	13.8	76.7	237877	14	AC095587	AC095587	Rattus no
736	13.8	76.7	195204	9	AC132956	AC132956	c 809	13.8	76.7	238323	2	AB003684	AB003684	Drosophill
c 737	13.8	76.7	195904	9	AC125525	AC125525	c 810	13.8	76.7	238608	14	AC095637	AC095637	Rattus no
c 738	13.8	76.7	196315	5	AC149502	AC149502	c 811	13.8	76.7	239057	14	AC116637	AC116637	Rattus no
c 739	13.8	76.7	198050	1	AL646061	AL646061	c 812	13.8	76.7	239467	9	AC113395	AC113395	Mus muscu
740	13.8	76.7	198224	14	AC161090	AC161090	c 813	13.8	76.7	239467	14	AC111384	AC111384	Rattus no
741	13.8	76.7	198254	14	AC016049	AC016049	c 814	13.8	76.7	240325	14	AC120246	AC120246	Rattus no
c 742	13.8	76.7	199182	8	AC005562	AC005562	c 815	13.8	76.7	242112	9	AC122923	AC122923	Mus muscu
c 743	13.8	76.7	199182	8	AC005562	AC005562	c 816	13.8	76.7	242159	14	AC091567	AC091567	Homo sapi
744	13.8	76.7	199893	14	AC110206	AC110206	c 817	13.8	76.7	242322	8	AC095668	AC095668	Homo sapi
c 745	13.8	76.7	200452	8	AC025529	AC025529	c 818	13.8	76.7	243369	14	AC115514	AC115514	Rattus no
c 746	13.8	76.7	200503	9	AC015804	AC015804	c 819	13.8	76.7	244008	14	AC136692	AC136692	Homo sapi
747	13.8	76.7	200791	14	AC123724	AC123724	c 820	13.8	76.7	245651	14	AC126537	AC126537	Rattus no
c 748	13.8	76.7	200875	9	AC144942	AC144942	c 821	13.8	76.7	246779	14	AC095254	AC095254	Rattus no

822	13.8	76.7	250010	14	AC074027	AC074027 Mus muscu	C 895	13.4	74.4	525	2	AF509342	AF509342 Anopheles
823	13.8	76.7	250029	2	AE003559	AE003559 Drosophill	C 896	13.4	74.4	526	2	AF509349	AF509349 Anopheles
824	13.8	76.7	252427	14	AC111287	AC111287 Rattus no	C 897	13.4	74.4	527	2	AY172564	AY172564 Anopheles
825	13.8	76.7	253887	14	AC135126	AC135126 Rattus no	C 898	13.4	74.4	528	2	AF509350	AF509350 Anopheles
826	13.8	76.7	255678	14	AC099432	AC099432 Rattus no	C 899	13.4	74.4	529	2	AY365051	AY365051 Anopheles
827	13.8	76.7	255952	14	AL513473	AL513473 Homo sapi	C 900	13.4	74.4	530	2	AF509348	AF509348 Anopheles
828	13.8	76.7	256393	14	AC020870	AC020870 Mus muscu	C 901	13.4	74.4	531	2	AY172565	AY172565 Anopheles
829	13.8	76.7	256938	14	AC097368	AC097368 Rattus no	C 902	13.4	74.4	534	10	G44735	G44735 unc1079 CA
830	13.8	76.7	259210	14	AC073368	AC073368 Homo sapi	C 903	13.4	74.4	540	2	AY172566	AY172566 Anopheles
831	13.8	76.7	261024	14	AE017256	AE017256 Wolbachia	C 904	13.4	74.4	540	2	AY172567	AY172567 Anopheles
832	13.8	76.7	264964	14	AC152738	AC152738 Bos tauru	C 905	13.4	74.4	544	8	HSB342035	HSB342035 Homo sapi
833	13.8	76.7	265118	6	CNSPAX06	AXI48288 Pyrococcu	C 906	13.4	74.4	563	6	AE617360	AE617360 Sequence
834	13.8	76.7	265118	6	AX041922	AX041922 Sequence	C 907	13.4	74.4	578	2	AY768540	AY768540 Anopheles
835	13.8	76.7	266114	14	AC103150	AC103150 Rattus no	C 908	13.4	74.4	578	2	AY768542	AY768542 Anopheles
836	13.8	76.7	268984	2	AE001274	AE001274 Leishmani	C 909	13.4	74.4	589	9	MMU23100	MMU23100 Mus muscu
837	13.8	76.7	279011	8	AE006467	AE006467 Homo sapi	C 910	13.4	74.4	597	2	AY691517	AY691517 Anopheles
838	13.8	76.7	282207	14	AC163583	AC163583 Bos tauru	C 911	13.4	74.4	597	2	AY691518	AY691518 Anopheles
839	13.8	76.7	286712	14	AC157079	AC157079 Bos tauru	C 912	13.4	74.4	597	2	AY691519	AY691519 Anopheles
840	13.8	76.7	287287	2	AE003816	AE003816 Drosophill	C 913	13.4	74.4	597	2	AY691520	AY691520 Anopheles
841	13.8	76.7	290029	14	AE016980	AE016980 Shigella	C 914	13.4	74.4	597	2	AY691521	AY691521 Anopheles
842	13.8	76.7	291262	14	AC156198	AC156198 Bos tauru	C 915	13.4	74.4	608	15	HCO492626	HCO492626 Haldina c
843	13.8	76.7	292409	5	BXS30407	BXS30407 Zebrafish	C 916	13.4	74.4	608	15	HCO492631	HCO492631 Haldina c
844	13.8	76.7	296756	2	AE003492	AE003492 Drosophill	C 917	13.4	74.4	618	2	AY049004	AY049004 Anopheles
845	13.8	76.7	300029	15	AE017121	AE017121 Oryza sat	C 918	13.4	74.4	652	10	BV353697	BV353697 S230P6263
846	13.8	76.7	300540	1	AE017154	AE017154 Haemophil	C 919	13.4	74.4	662	2	AF406615	AF406615 Anopheles
847	13.8	76.7	300883	14	AE016809	AE016809 Vibrio vu	C 920	13.4	74.4	663	2	AF469855	AF469855 Anopheles
848	13.8	76.7	302214	14	AC117305	AC117305 Rattus no	C 921	13.4	74.4	663	2	AF469856	AF469856 Anopheles
849	13.8	76.7	302228	15	AE017070	AE017070 Oryza sat	C 922	13.4	74.4	663	2	AF469857	AF469857 Anopheles
850	13.8	76.7	305584	1	AE016920	AE016920 Chromobac	C 923	13.4	74.4	663	2	AF469858	AF469858 Anopheles
851	13.8	76.7	306050	14	AC123202	AC123202 Rattus no	C 924	13.4	74.4	663	2	AF469859	AF469859 Anopheles
852	13.8	76.7	310059	14	AC152075	AC152075 Mus muscu	C 925	13.4	74.4	663	2	AF469860	AF469860 Anopheles
853	13.8	76.7	310580	9	SC0939113	AL939113 Streptomy	C 926	13.4	74.4	663	2	AF469861	AF469861 Anopheles
854	13.8	76.7	312488	9	AC139934	AC139934 Mus muscu	C 927	13.4	74.4	663	2	AF469862	AF469862 Anopheles
855	13.8	76.7	324050	1	BX251410	BX251410 Tropherym	C 928	13.4	74.4	663	2	AF469863	AF469863 Anopheles
856	13.8	76.7	324227	1	AE016852	AE016852 Tropherym	C 929	13.4	74.4	663	2	AF469864	AF469864 Anopheles
857	13.8	76.7	330026	14	AC160694	AC160694 Bos tauru	C 930	13.4	74.4	663	2	AF469865	AF469865 Anopheles
858	13.8	76.7	332252	14	AC130121	AC130121 Rattus no	C 931	13.4	74.4	663	2	AF469866	AF469866 Anopheles
859	13.8	76.7	337344	6	CQ869859	CQ869859 Sequence	C 932	13.4	74.4	663	2	AF469867	AF469867 Anopheles
860	13.8	76.7	340000	8	AP001710	AP001710 Homo sapi	C 933	13.4	74.4	663	2	AF469868	AF469868 Anopheles
861	13.8	76.7	340968	14	AC115312	AC115312 Rattus no	C 934	13.4	74.4	663	2	AF469869	AF469869 Anopheles
862	13.8	76.7	342833	14	AC142817	AC142817 Macaca mu	C 935	13.4	74.4	663	2	AF469870	AF469870 Anopheles
863	13.8	76.7	346274	1	BX640443	BX640443 Bordetell	C 936	13.4	74.4	663	2	AF469871	AF469871 Anopheles
864	13.8	76.7	348014	1	BX640430	BX640430 Bordetell	C 937	13.4	74.4	663	2	AF469872	AF469872 Anopheles
865	13.8	76.7	349672	1	BX640419	BX640419 Bordetell	C 938	13.4	74.4	663	2	AF469873	AF469873 Anopheles
866	13.6	75.6	817	2	AF394534	AF394534 Babesia c	C 939	13.4	74.4	663	2	AF469874	AF469874 Anopheles
867	13.4	74.4	179	6	AR263919	AR263919 Sequence	C 940	13.4	74.4	663	2	AF469875	AF469875 Anopheles
868	13.4	74.4	252	5	AY453207	AY453207 Coregonus	C 941	13.4	74.4	663	2	AF469876	AF469876 Anopheles
869	13.4	74.4	329	8	CPA532606	AJ532606 Clereium	C 942	13.4	74.4	663	2	AF469877	AF469877 Anopheles
870	13.4	74.4	329	8	HSB342043	AJ342043 Homo sapi	C 943	13.4	74.4	663	2	AF469878	AF469878 Anopheles
871	13.4	74.4	375	2	AF333384	AF333384 Anopheles	C 944	13.4	74.4	663	2	AF469879	AF469879 Anopheles
872	13.4	74.4	375	2	AY049003	AY049003 Anopheles	C 945	13.4	74.4	663	2	AF469880	AF469880 Anopheles
873	13.4	74.4	382	6	AR618448	AR618448 Sequence	C 946	13.4	74.4	663	2	AF469881	AF469881 Anopheles
874	13.4	74.4	390	2	AF509353	AF509353 Anopheles	C 947	13.4	74.4	663	2	AF469882	AF469882 Anopheles
875	13.4	74.4	448	2	AB088384	AB088384 Anopheles	C 948	13.4	74.4	663	2	AF469883	AF469883 Anopheles
876	13.4	74.4	451	2	AB088383	AB088383 Anopheles	C 949	13.4	74.4	663	2	AF469884	AF469884 Anopheles
877	13.4	74.4	455	2	AY049001	AY049001 Anopheles	C 950	13.4	74.4	663	2	AF469885	AF469885 Anopheles
878	13.4	74.4	455	2	AY049005	AY049005 Anopheles	C 951	13.4	74.4	663	2	AF469886	AF469886 Anopheles
879	13.4	74.4	463	2	AF440768	AF440768 Anopheles	C 952	13.4	74.4	663	2	AF469887	AF469887 Anopheles
880	13.4	74.4	471	6	BD165509	BD165509 Novel pol	C 953	13.4	74.4	663	2	AF469888	AF469888 Anopheles
881	13.4	74.4	471	6	AX123392	AX123392 Sequence	C 954	13.4	74.4	663	2	AF469889	AF469889 Anopheles
882	13.4	74.4	475	2	AY953514	AY953514 Anopheles	C 955	13.4	74.4	663	2	AF469890	AF469890 Anopheles
883	13.4	74.4	475	2	AY953515	AY953515 Anopheles	C 956	13.4	74.4	663	2	AF469891	AF469891 Anopheles
884	13.4	74.4	486	15	AY544551	AY544551 Anopheles	C 957	13.4	74.4	663	2	AF469892	AF469892 Anopheles
885	13.4	74.4	495	2	AF509351	AF509351 Hordium p	C 958	13.4	74.4	663	2	AF469893	AF469893 Anopheles
886	13.4	74.4	508	2	AF509352	AF509352 Anopheles	C 959	13.4	74.4	663	2	AF469894	AF469894 Anopheles
887	13.4	74.4	512	2	AF509344	AF509344 Anopheles	C 960	13.4	74.4	663	2	AF469895	AF469895 Anopheles
888	13.4	74.4	512	2	AF509346	AF509346 Anopheles	C 961	13.4	74.4	663	2	AF469896	AF469896 Anopheles
889	13.4	74.4	513	2	AF167298	AF167298 Anopheles	C 962	13.4	74.4	663	2	AF469897	AF469897 Anopheles
890	13.4	74.4	513	2	AF509343	AF509343 Anopheles	C 963	13.4	74.4	663	2	AF469898	AF469898 Anopheles
891	13.4	74.4	515	2	AF167299	AF167299 Anopheles	C 964	13.4	74.4	663	2	AF469899	AF469899 Anopheles
892	13.4	74.4	517	2	AF167299	AF167299 Anopheles	C 965	13.4	74.4	663	2	AF469900	AF469900 Anopheles
893	13.4	74.4	518	2	AF509347	AF509347 Anopheles	C 966	13.4	74.4	663	2	AF469901	AF469901 Anopheles
894	13.4	74.4	520	2	AF509345	AF509345 Anopheles	C 967	13.4	74.4	663	2	AF469902	AF469902 Anopheles

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c 968 13.4 74.4 663 2 AY662412
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ALIGNMENTS

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RESULT 1
LOCUS AR146348/c 18 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 60 from patent US 6218371.
ACCESSION AR146348
VERSION AR146348.1 GI:15109537
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kriegl,A.M. and Weiner,G.
TITLES Methods and products for stimulating the immune system using
JOURNAL immunotherapeutic oligonucleotides and cytokines
FEATURES
PATENT: US 6218371-A 60 17-APR-2001;
LOCATION/Qualifiers
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ORIGIN
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QY 1 AGAGGGGCGCAGCGGUA 18
Db 18 AGAGGGGCGCAGCGGUA 1

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RESULT 2
LOCUS AR154731/c 18 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 60 from patent US 6239116.
ACCESSION AR154731

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VERSION AR154731.1 GI:15122784
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kriegl,A.M. and Kline,J.N.
TITLES Immunostimulatory nucleic acid molecules
JOURNAL Patent: US 6239116-A 60 29-MAY-2001;
FEATURES
LOCATION/Qualifiers
source 1..18
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QY 1 AGAGGGGCGCAGCGGUA 18
Db 18 AGAGGGGCGCAGCGGUA 1

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RESULT 3
LOCUS BD069939/c 18 bp DNA linear PAT 27-AUG-2002
DEFINITION Use of nucleic acids containing unmethylated CpG dinucleotide in
ACCESSION BD069939
VERSION BD069939.1 GI:22615542
KEYWORDS JP 2001513776-A/28.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schwartz,D.A. and Kriegl,A.M.
TITLES Use of nucleic acids containing unmethylated CpG dinucleotide in
JOURNAL the treatment of LPS-associated disorders
PATENT: JP 2001513776-A 28 04-SEP-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION
OS Artificial Sequence
PN JP 2001513776-A/28
PD 04-SEP-2001
PR 25-FEB-1998 JP 1998537810
PR 28-FEB-1997 US 60/039405
PI DAVID A SCHWARTZ,ARTHUR M KRIEG
PC A61K49/00,C07H21/02,C07H21/04,A01N43/04
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FH Key
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Db 18 AGAGGGGCGCAGCGGUA 1

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RESULT 4
LOCUS BD205570/c 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Method of controlling hematopoiesis by using CpG oligonucleotide.
ACCESSION BD205570

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VERSION BD205570.1 GI:33015340
KEYWORDS JP 2002514397-A/60.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Wagner, H. and Lipford, G.
TITLE Method of controlling hematopoiesis by using CpG oligonucleotide
JOURNAL Patent: JP 2002514397-A 60 21-MAY-2002,
CORY PHARMACEUTICALS GMBH, CORY PHARMACEUTICALS GROUP INC
COMMENT OS Artificial Sequence
PN JP 2002514397-A/60
PD 21-MAY-2002
PR 14-MAY-1999 JP 2000547969
PC 14-MAY-1998 US 60/085516, 02-FEB-1999 US 09/241653 PI
HERMANN WAGNER, GRAVSON LIPFORD
C12N15/09, A61K31/70, A61K39/39, C07H21/04//A61K45/00, C12N15/00
CC Synthetic Sequence
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Location/Qualifiers
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Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.8e+02;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
BD261112/c 18 bp DNA linear PAT 17-JUL-2003
LOCUS Methods and products for stimulating the immune system using
DEFINITION immunotherapeutic oligonucleotides and cytokines.
ACCESSION BD261112.1 GI:33070882
VERSION BD261112.1
KEYWORDS JP 2002510644-A/60.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kriegl, A.M. and Weiner, G.
TITLE Methods and products for stimulating the immune system using
JOURNAL immunotherapeutic oligonucleotides and cytokines
PATENT: JP 2002510644-A 60 09-APR-2002;
UNIVERSITY OF IOWA RESEARCH FOUNDATION
COMMENT OS Artificial Sequence
PN JP 2002510644-A/60
PD 09-APR-2002
PR 02-APR-1999 JP 2000542030
PC 03-APR-1998 US 60/080729
PI ARTHUR M KRIEG, GEORGE WEINER
PC A61K38/00, A61K31/7088, A61K39/00, A61P15/00, A61P35/00, A61P37/04,
A61K37/02
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FEATURES
source
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Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGGGUCCGACGCGGUA 18
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18 AGAGGGTCCGACGCGGTA 1

RESULT 6
BD267877/c 18 bp DNA linear PAT 17-JUL-2003
LOCUS Method for the prevention and treatment of parasitic infections
DEFINITION and related diseases using CPG oligonucleotides.
ACCESSION BD267877.1 GI:33077645
VERSION BD267877.1
KEYWORDS JP 2002513763-A/50.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Gramzinski, R.A., Kriegl, A.M., Davis, H.L. and Hoffman, S.L.
TITLE Method for the prevention and treatment of parasitic infections
JOURNAL and related diseases using CPG oligonucleotides
PATENT: JP 2002513763-A 50 14-MAY-2002;
UNIVERSITY OF IOWA RESEARCH FOUNDATION, OTTAWA CIVIC LOEB RESEARCH
INSTITUTE, UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY
OF THE NAVY
COMMENT OS Artificial Sequence
PN JP 2002513763-A/50
PD 14-MAY-2002
PR 06-MAY-1999 JP 2000546780
PC 06-MAY-1998 US 60/084512
PI ROBERT A GRAMZINSKI, ARTHUR M KRIEG, HEATHER L DAVIS, STEPHEN L
PI HOFFMAN
PC A61K31/711, A61K9/127, A61K38/00, A61K38/22, A61K45/00, A61P31/00,
A61P33/00//
PC C12N15/09, A61K37/02, A61K37/24, C12N15/00
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FH Key Location/Qualifiers
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Location/Qualifiers
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Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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AR222220/c 18 bp DNA linear PAT 26-SEP-2002
LOCUS Sequence 54 from patent US 6429199.
DEFINITION AR222220
ACCESSION AR222220.1 GI:23329685
VERSION AR222220.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kriegl, A.M. and Hartmann, G.
TITLE Immunostimulatory nucleic acid molecules for activating dendritic
JOURNAL cells
PATENT: US 6429199-A 54 06-AUG-2002;

FEATURES University of Iowa Research Foundation; Iowa City, IA
 source 1.18
 /organism="unknown"
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Query Match 100.0%; Score 18; DB 6; Length 18;
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 18 AGAGGUGCGACGCGGTA 1

RESULT 8
 AR432481/c 18 bp DNA linear PAT 18-DEC-2003
 LOCUS Sequence 60 from patent US 6653292.
 DEFINITION AR432481
 ACCESSION AR432481.1 GI:40194816
 VERSION
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Kriegl,A.M. and Weither,G.
 TITLE Method of treating cancer using immunostimulatory oligonucleotides
 JOURNAL Patent: US 6653292-A 60 25-NOV-2003;
 University of Iowa Research Foundation; Iowa City, IA
 FEATURES source 1.18
 /organism="unknown"
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Query Match 100.0%; Score 18; DB 6; Length 18;
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RESULT 9
 AX103812/c 18 bp DNA linear PAT 30-APR-2001
 LOCUS Sequence 4 from Patent WO0122972.
 DEFINITION AX103812
 ACCESSION AX103812
 VERSION AX103812.1 GI:13920009
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Kriegl,A.M., Schetter,C. and Vollmer,J.C.
 TITLE Immunostimulatory nucleic acids
 JOURNAL Patent: WO 0122972-A 4 05-APR-2001;
 UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
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 FEATURES source 1.18
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 AX103864/c 18 bp DNA linear PAT 30-APR-2001
 LOCUS Sequence 56 from Patent WO0122972.
 DEFINITION AX103864
 ACCESSION AX103864
 VERSION AX103864.1 GI:13920061
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Kriegl,A.M., Schetter,C. and Vollmer,J.C.
 TITLE Immunostimulatory nucleic acids
 JOURNAL Patent: WO 0122972-A 56 05-APR-2001;
 UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
 GmbH (DE)
 FEATURES source 1.18
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 QY 1 AGAGGUGCGACGCGGUA 18
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 18 AGAGGUGCGACGCGGTA 1

RESULT 11
 AX355457/c 18 bp DNA linear PAT 06-FEB-2002
 LOCUS Sequence 485 from Patent WO0197843.
 DEFINITION AX355457
 ACCESSION AX355457
 VERSION AX355457.1 GI:18620125
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Welner,G. and Hartmann,G.
 TITLE Methods for enhancing antibody-induced cell lysis and treating
 JOURNAL Patent: WO 0197843-A 485 27-DEC-2001;
 UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
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 18 AGAGGUGCGACGCGGTA 1

RESULT 12
 AX455590/c 18 bp DNA linear PAT 06-FEB-2002
 LOCUS Sequence 485 from Patent WO0197843.
 DEFINITION AX455590
 ACCESSION AX455590
 VERSION AX455590.1 GI:18620125
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Welner,G. and Hartmann,G.
 TITLE Methods for enhancing antibody-induced cell lysis and treating
 JOURNAL Patent: WO 0197843-A 485 27-DEC-2001;
 UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
 FEATURES source 1.18
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RESULT 13
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 ACCESSION AX455590
 VERSION AX455590.1 GI:18620125
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Welner,G. and Hartmann,G.
 TITLE Methods for enhancing antibody-induced cell lysis and treating
 JOURNAL Patent: WO 0197843-A 485 27-DEC-2001;
 UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
 FEATURES source 1.18
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 /db_xref="taxon:32630"

LOCUS AX455590 18 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 67 from Patent WO0222809.
ACCESSION AX455590
VERSION AX455590.1 GI:21714658
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bauer, S., Lipford, G. and Wagner, H.
TITLE Process for high throughput screening of cps-based
immuno-agonist/antagonist
JOURNAL Patent: WO 0222809-A 67 21-MAR-2002;
Coley Pharmaceutical GmbH (DE)
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source Location/Qualifiers
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Best Local Similarity 88.9%; Pred. No. 4.8e+02;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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RESULT 13
AX546865/c 18 bp DNA linear PAT 01-MAR-2003
LOCUS AX546865
DEFINITION Sequence 4 from Patent WO02053141.
ACCESSION AX546865
VERSION AX546865.1 GI:25812009
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bratzler, R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 4 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
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Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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AX546917/c 18 bp DNA linear PAT 01-MAR-2003
LOCUS AX546917
DEFINITION Sequence 56 from Patent WO02053141.
ACCESSION AX546917
VERSION AX546917.1 GI:25812061
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Bratzler, R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 56 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
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RESULT 15
BD009122/c 18 bp DNA linear PAT 31-JAN-2002
LOCUS BD009122
DEFINITION Immunostimulatory nucleic acid molecules.
ACCESSION BD009122
VERSION BD009122.1 GI:18637495
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg, A.M. and Kline, J.N.
TITLE Immunostimulatory nucleic acid molecules
JOURNAL Patent: JP 2001503267-A 74 13-MAR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION
COMMENT OS Artificial Sequence
PN JP 2001503267-A/74
PD 13-MAR-2001
PF 30-OCT-1997 JP 1998520784
PR 30-OCT-1996 US 08/738652
PI ARTHUR M KRIEG, JOEL N KLINE
PC C07H21/00, C07H21/02, C07H21/04, A61K31/175, A61K31/335, A61K31/47,
PC A61K31/70
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RESULT 16
AR052611/c 17 bp DNA linear PAT 29-SEP-1999
LOCUS AR052611
DEFINITION Sequence 9 from patent US 5831066.
ACCESSION AR052611
VERSION AR052611.1 GI:5975975
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Reed,J.C.
TITLES Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 9 03-NOV-1998;
FEATURES Location/Qualifiers
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Db 17 GAGGGTCGACGCGGTA 1

RESULT 17
BD187524/c 17 bp DNA linear PAT 17-JUL-2003
LOCUS REGULATION OF bcl-2 GENE EXPRESSION.
BD187524
VERSION BD187524.1 GI:32397263
KEYWORDS JP 2003026609-A/9.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Reed,J.C.
TITLES REGULATION OF bcl-2 GENE EXPRESSION
JOURNAL Patent: JP 2003026609-A 9 29-JAN-2003;
John C REED
OS Artificial Sequence
PN JP 2003026609-A/9
PD 29-JAN-2003
PF 19-JUN-2002 JP 2002178753
PR 20-SEP-1993 US 08/124256
PI John C reed
CC Description of Artificial Sequence: Designed DNA based on bcl-
CC 2 gene Location/Qualifiers.
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Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GAGGGUCCGACGCGGUA 18
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Db 17 GAGGGTCGACGCGGTA 1

RESULT 18
AR630675/c 17 bp DNA linear PAT 14-FEB-2005
LOCUS AR630675
DEFINITION Sequence 9 from patent US 6641541.
ACCESSION AR630675
VERSION AR630675.1 GI:59766403
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Reed,J.C.

TITLE Regulation of BCL-2 gene expression
JOURNAL Patent: US 6841541-A 9 11-JAN-2005;
FEATURES The Trustees of the University of Pennsylvania; Philadelphia, PA
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

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Best Local Similarity 88.2%; Pred. No. 1.5e+03;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GAGGGUCCGACGCGGUA 18
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Db 17 GAGGGTCGACGCGGTA 1

RESULT 19
AY207027 289 bp DNA linear BCT 17-MAR-2003
LOCUS Acinetobacter sp. S429_2 16S ribosomal RNA gene, partial sequence.
DEFINITION AY207027
ACCESSION AY207027.1 GI:29027585
VERSION
KEYWORDS
SOURCE
ORGANISM Acinetobacter sp. S429_2
Acinetobacter sp. S429_2
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Acinetobacter.
REFERENCE 1 (bases 1 to 289)
AUTHORS Vandroekhoven,K., Wattiau,P., De mot,R. and Springael,D.
TITLES Acinetobacter sp. diversity in environmental samples assessed by an
Acinetobacter 16S rDNA specific PCR-DGGE system
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 289)
AUTHORS Vandroekhoven,K., Wattiau,P., De mot,R. and Springael,D.
TITLES Direct Submission
JOURNAL Submitted (24-DEC-2002) Environmental Technology, Vito (Flemisch
Institute for Technological Research), Boeretang 200, Mol 2400,
Belgium
FEATURES Location/Qualifiers
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/clone="6_2"
/product="16S ribosomal RNA"

ORIGIN
Query Match 91.1%; Score 16.4; DB 1; Length 289;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGAGGGUCCGACGCGGUA 18
|||||:|||||:|
Db 110 AGAGGGTCGACGCGGTA 127

RESULT 20
AX513690/c 32 bp DNA linear PAT 06-OCT-2002
LOCUS AX513690
DEFINITION Sequence 79 from Patent W00226757.
ACCESSION AX513690
VERSION AX513690.1 GI:23559810
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Kandimala,R.R., Zhao,Q., Yu,D. and Agrawal,S.
TITLES Modulation of Immunostimulatory activity of Immunostimulatory

oligonucleotide analogs by positional chemical changes

JOURNAL Patent: WO 0226757-A 79 04-APR-2002;

FEATURES

source

1. .32
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="modified linkage of oligodeoxynucleotide phosphorothioate"

modified_base
16
/note="5' 5' linkage"
/mod_base=OTHER

ORIGIN

Query Match 88.9%; Score 16; DB 6; Length 32;
Best Local Similarity 87.5%; Pred. No. 4.3e+03;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGGTGCACGCGGUA 18
|||||
16 AGGGTGCACGCGGTA 1

RESULT 21
AX513691/c 32 bp DNA linear PAT 05-OCT-2002
LOCUS AX513691 Sequence 80 from Patent WO0226757.
DEFINITION AX513691
ACCESSION AX513691
VERSION AX513691.1 GI:23559811
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Kandimalla, B.R., Zhao, Q., Yu, D. and Agrawal, S.
TITLE Modulation of immunostimulatory activity of immunostimulatory
JOURNAL oligonucleotide analogs by positional chemical changes
Patent: WO 0226757-A 80 04-APR-2002;
HYBRIDON, INC. (US)
FEATURES
source
1. .32
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="modified linkage of oligodeoxynucleotide phosphorothioate"

modified_base
16
/note="3' 3' linkage"
/mod_base=OTHER

ORIGIN

Query Match 88.9%; Score 16; DB 6; Length 32;
Best Local Similarity 87.5%; Pred. No. 4.3e+03;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGGTGCACGCGGUA 18
|||||
32 AGGGTGCACGCGGTA 17

RESULT 22
AC138105/c 101451 bp DNA linear HTG 13-DEC-2002
LOCUS AC138105 Mus musculus clone RP23-114F22, LOW-PASS SEQUENCE SAMPLING.
DEFINITION AC138105
ACCESSION AC138105
VERSION AC138105.1 GI:26665790
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 101451)
AUTHORS Birren, B., Nusbaum, C. and Lander, E.
JOURNAL Mus musculus, clone RP23-114F22
REFERENCE 2 (bases 1 to 101451)
AUTHORS Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barnett, N., Bartley, V., Bloom, T., Boudgavsky, L., Boukhalter, B.,
Cammarata, T., Chang, J., Charato, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., DeRellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
Fato, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kelle, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J.,
Matthews, C., McCarthy, M., Meldrum, J., Meneses, L., Mihova, T.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R.,
Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schnpack, R.,
Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Talamas, J., Testaye, S., Theodore, J., Topham, K.,
Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (13-DEC-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIRB
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: 114_F_22

* NOTE: This record contains 78 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1 1187: contig of 1187 bp in length
* 1188 1287: gap of 100 bp
* 1288 2490: contig of 1203 bp in length
* 2491 2590: gap of 100 bp
* 2591 3756: contig of 1166 bp in length
* 3757 3856: gap of 100 bp
* 3857 4942: contig of 1086 bp in length
* 4943 5042: gap of 100 bp
* 5043 6213: contig of 1171 bp in length
* 6214 6314: gap of 100 bp
* 6314 7531: contig of 1218 bp in length
* 7532 7632: gap of 100 bp
* 7632 8845: contig of 1214 bp in length
* 8846 8945: gap of 100 bp
* 8946 10075: contig of 1130 bp in length
* 10076 10175: gap of 100 bp
* 10176 11316: contig of 1141 bp in length
* 11317 11416: gap of 100 bp
* 11417 12599: contig of 1183 bp in length
* 12600 12699: gap of 100 bp
* 12700 13909: contig of 1210 bp in length
* 13910 14009: gap of 100 bp
* 14010 15320: contig of 1211 bp in length
* 15321 15320: gap of 100 bp

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* 15321 16571: contig of 1251 bp in length
* 16572 16671: gap of 100 bp
* 16739 17839: contig of 1168 bp in length
* 17840 17939: gap of 100 bp
* 17940 19118: contig of 1179 bp in length
* 19119 19218: gap of 100 bp
* 19219 20438: contig of 1220 bp in length
* 20439 20538: gap of 100 bp
* 20539 21768: contig of 1230 bp in length
* 21769 21868: gap of 100 bp
* 21869 23075: contig of 1207 bp in length
* 23076 23176: gap of 100 bp
* 23176 24381: contig of 1206 bp in length
* 24382 24481: gap of 100 bp
* 24482 25689: contig of 1208 bp in length
* 25690 25790: gap of 100 bp
* 25790 26988: contig of 1199 bp in length
* 26989 27088: gap of 100 bp
* 27089 28249: contig of 1161 bp in length
* 28250 28349: gap of 100 bp
* 28350 29546: contig of 1197 bp in length
* 29547 29647: gap of 100 bp
* 29647 30892: contig of 1246 bp in length
* 30893 30992: gap of 100 bp
* 30993 32185: contig of 1193 bp in length
* 32186 32285: gap of 100 bp
* 32286 33507: contig of 1222 bp in length
* 33508 33607: gap of 100 bp
* 33608 34851: contig of 1244 bp in length
* 34852 34951: gap of 100 bp
* 34952 36177: contig of 1226 bp in length
* 36178 36277: gap of 100 bp
* 36278 37514: contig of 1237 bp in length
* 37515 37614: gap of 100 bp
* 37615 38778: contig of 1164 bp in length
* 38779 38878: gap of 100 bp
* 38879 40134: contig of 1256 bp in length
* 40135 40234: gap of 100 bp
* 40235 41412: contig of 1178 bp in length
* 41413 41512: gap of 100 bp
* 41513 42727: contig of 1215 bp in length
* 42728 42827: gap of 100 bp
* 42828 44042: contig of 1215 bp in length
* 44043 44142: gap of 100 bp
* 44143 45399: contig of 1257 bp in length
* 45400 45499: gap of 100 bp
* 45500 46708: contig of 1209 bp in length
* 46709 46808: gap of 100 bp
* 46809 48057: contig of 1249 bp in length
* 48058 48157: gap of 100 bp
* 48158 49407: contig of 1250 bp in length
* 49408 49507: gap of 100 bp
* 49508 50743: contig of 1236 bp in length
* 50744 50843: gap of 100 bp
* 50844 52031: contig of 1188 bp in length
* 52032 52131: gap of 100 bp
* 52132 53326: contig of 1195 bp in length
* 53327 53426: gap of 100 bp
* 53427 54639: contig of 1213 bp in length
* 54640 54739: gap of 100 bp
* 54740 55975: contig of 1236 bp in length
* 55976 56075: gap of 100 bp
* 56076 57343: contig of 1268 bp in length
* 57344 57443: gap of 100 bp
* 57444 58637: contig of 1194 bp in length
* 58638 58737: gap of 100 bp
* 58738 59995: contig of 1258 bp in length
* 59996 60095: gap of 100 bp
* 60096 61348: contig of 1253 bp in length
* 61349 61448: gap of 100 bp
* 61449 62684: contig of 1236 bp in length
* 62685 62784: gap of 100 bp
* 62785 64008: contig of 1224 bp in length

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* 64009 64108: gap of 100 bp
* 64109 65248: contig of 1140 bp in length
* 65249 65348: gap of 100 bp
* 65349 66409: contig of 1061 bp in length
* 66410 66509: gap of 100 bp
* 66510 67698: contig of 1189 bp in length
* 67699 67798: gap of 100 bp
* 67799 68964: contig of 1166 bp in length
* 68965 69064: gap of 100 bp
* 69065 70330: contig of 1266 bp in length
* 70331 70430: gap of 100 bp
* 70431 71614: contig of 1184 bp in length
* 71615 71714: gap of 100 bp
* 71715 72995: contig of 1281 bp in length
* 72996 73095: gap of 100 bp
* 73096 74345: contig of 1250 bp in length
* 74346 74445: gap of 100 bp
* 74446 75658: contig of 1213 bp in length
* 75659 75758: gap of 100 bp
* 75759 76993: contig of 1235 bp in length
* 76994 77093: gap of 100 bp
* 77094 78291: contig of 1198 bp in length
* 78292 78391: gap of 100 bp
* 78392 79561: contig of 1170 bp in length
* 79562 79661: gap of 100 bp
* 79662 80855: contig of 1194 bp in length
* 80856 80955: gap of 100 bp
* 80956 82128: contig of 1173 bp in length
* 82129 82228: gap of 100 bp
* 82229 83441: contig of 1213 bp in length
* 83442 83541: gap of 100 bp
* 83542 84760: contig of 1219 bp in length
* 84761 84860: gap of 100 bp
* 84861 86083: contig of 1223 bp in length
* 86084 86183: gap of 100 bp
* 86184 87401: contig of 1218 bp in length
* 87402 87501: gap of 100 bp
* 87502 88707: contig of 1206 bp in length
* 88708 88807: gap of 100 bp
* 88808 90003: contig of 1196 bp in length
* 90004 90103: gap of 100 bp
* 90104 91253: contig of 1150 bp in length
* 91254 91353: gap of 100 bp
* 91354 92484: contig of 1131 bp in length

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Query Match 88.9% Score 16; DB 14; Length 101451;
 Best Local Similarity 87.5% Pred. No. 1,1e+03;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACCGCGU 17
 DB 29716 GAGGUGCGACCGCGU 29701

RESULT 23
 CT005253_2
 WPCOMMENT
 Sequence split into 7 fragments LOCUS CT005253 Accession CT005253

Fragment Name	Begin	End
CT005253_0	1	110000
CT005253_1	100001	210000
CT005253_2	200001	310000
CT005253_3	300001	410000
CT005253_4	400001	510000
CT005253_5	500001	610000
CT005253_6	600001	622648

Continuation (3 of 7) of CT005253 from base 200001 (CT005253 *Leishmania major* strain Frlé

Query Match 88.9% Score 16; DB 14; Length 110000;
 Best Local Similarity 93.8% Pred. No. 1,1e+03;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACCGCG 16

```

|||||:|||||
Db      29363 AGAGGCTCCGACCGG 29378

RESULT 24
LOCUS   AC021215/c
DEFINITION Homo sapiens chromosome 17 clone RP11-497H17, WORKING DRAFT
ACCESSION AC021215
VERSION   AC021215.4 GI:8570248
KEYWORDS  HTG; HTGS PHAS81; HTGS_DRAFT.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homiidae; Homo.
          1 (bases 1 to 191504)
          Waterston,R.H.
          The sequence of Homo sapiens clone
          Unpublished
          2 (bases 1 to 191504)
          Waterston,R.H.
          Project Information
          Center project name: H NH0497H17
          ----- Summary Statistics -----
          Sequencing vector: pUC19, 88%
          Chemistry: Dye-terminator Big Dye; 12% of reads
          Assembly program: Phrap; version 0.990319
          Consensus quality: 168128 bases at least Q40
          Consensus quality: 175861 bases at least Q30
          Consensus quality: 181010 bases at least Q20
          Insert size: 193000; agarose-fp
          Insert size: 188604; sum-of-contigs
          Quality coverage: 3.80 in Q20 bases; agarose-fp
          Quality coverage: 3.98 in Q20 bases; sum-of-contigs
          -----
          * NOTE: This is a 'working draft' sequence. It currently
          * consists of 30 contigs. The true order of the pieces
          * is not known and their order in this sequence record is
          * arbitrary. Gaps between the contigs are represented as
          * runs of N, but the exact sizes of the gaps are unknown.
          * This record will be updated with the finished sequence
          * as soon as it is available and the accession number will
          * be preserved.
          1
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          2047 2146: gap of unknown length
          2147 3411: contig of 1265 bp in length
          3412 3511: gap of unknown length
          3512 4820: contig of 1309 bp in length
          4821 4920: gap of unknown length
          4921 7643: contig of 2723 bp in length
          7644 7743: gap of unknown length
          7744 10452: contig of 2709 bp in length
          10453 10552: gap of unknown length
          10553 12922: contig of 2370 bp in length
          12923 13022: gap of unknown length
          13023 15483: contig of 2461 bp in length
          15484 15583: gap of unknown length
          15584 18198: contig of 2615 bp in length
          18199 18298: gap of unknown length

```

```

18299 21370: contig of 3072 bp in length
21371 21470: gap of unknown length
21471 27499: contig of 6029 bp in length
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27600 31447: contig of 3848 bp in length
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34778 37543: contig of 2766 bp in length
37544 37643: gap of unknown length
37644 42653: contig of 5010 bp in length
42654 42753: gap of unknown length
42754 46336: contig of 3683 bp in length
46337 46536: gap of unknown length
46537 50069: contig of 3533 bp in length
50070 50169: gap of unknown length
50170 55438: contig of 5269 bp in length
55439 55538: gap of unknown length
55539 60458: contig of 4920 bp in length
60459 60558: gap of unknown length
60559 66583: contig of 6025 bp in length
66584 66683: gap of unknown length
66684 74323: contig of 7640 bp in length
74324 74423: gap of unknown length
74424 79047: contig of 4624 bp in length
79048 79147: gap of unknown length
79148 86014: contig of 6867 bp in length
86015 86114: gap of unknown length
86115 91308: contig of 5194 bp in length
91309 91408: gap of unknown length
91409 101455: contig of 10047 bp in length
101456 101555: gap of unknown length
101556 109192: contig of 7637 bp in length
109193 109292: gap of unknown length
109293 125435: contig of 16143 bp in length
125436 125535: gap of unknown length
125536 142370: contig of 16735 bp in length
142371 142370: gap of unknown length
142371 156610: contig of 14240 bp in length
156611 156710: gap of unknown length
156711 172015: contig of 15505 bp in length
172016 172115: gap of unknown length
172116 191504: contig of 19389 bp in length.

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         2147..3411
            /note="assembly_name:Contig6"
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         3512..4820
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         4921..7643
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         7644..7743
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         7744..10452
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         18199..18298
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15484..15583
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18199..18298
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18299..21370
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21371..21470
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42754..46436
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46437..46536
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46537..50069
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50070..50169
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50170..55438
/notes="assembly_name:Contig21"
55439..55538
/estimated_length=unknown
55539..60458
/notes="assembly_name:Contig22"
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/estimated_length=unknown
60559..66583
/notes="assembly_name:Contig23"
66584..66683
/estimated_length=unknown
66684..74323
/notes="assembly_name:Contig24"
74324..74423
/estimated_length=unknown
74424..79047
/notes="assembly_name:Contig25"
79048..79147
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Query Match      88.9%; Score 16; DB 14; Length 191504;
Best Local Similarity 87.5%; Pred. No. 9.8e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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RESULT 25
AF432629/c
LOCUS          AF432629          544 bp      DNA      linear      ENV 03-MAY-2004

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DEFINITION      Uncultured bacterium clone S52.30PG 16S ribosomal RNA gene, partial
sequence.
ACCESSION      AF432629
VERSION        AF432629.1 GI:27363039
KEYWORDS
SOURCE
ORGANISM
REFERENCES
AUTHORS
Chow,M.L., Radomaki,C.C., McDermott,J.M., Davies,J. and
Axelrood,P.E.
1 (bases 1 to 544)
Bacteria; environmental samples.
TITLE
Molecular characterization of bacterial diversity in lodgepole pine
(Pinus contorta) rhizosphere soils from British Columbia forest
soils differing in disturbance and geographic source
PENG Microbiol. Ecol. 42, 347-357 (2002)
2 (bases 1 to 544)
Harris,J.K., Chow,M.L., Chittaranjan,S., Radomaki,C.C.,
McDermott,J.M., Davies,J., Pace,N.R. and Axelrood,P.E.
Expansion of the bacterial phylogenetic tree: significant
survey-points for further mapping of bacterial diversity
Unpublished
3 (bases 1 to 544)
Chow,M.L., Radomaki,C.C., McDermott,J.M., Davies,J. and
Axelrood,P.E.
Direct Submission
Submitted (12-OCT-2001) BC Research Inc., 3650 Westbrook Mall,
Vancouver, BC V6S 2L2, Canada
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:77133"
/clone="S52.30PG"
/environmental sample
/notes="from lodgepole pine rhizosphere soil from the
British Columbia Ministry of Forests Long-Term Soil
Productivity (LTSP) installation near Prince George, BC,
Canada"
<1..>544
/product="16S ribosomal RNA"

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FEATURES
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/organism="uncultured bacterium"
/mol_type="genomic DNA"
/db_xref="taxon:77133"
/clone="S52.30PG"
/environmental sample
/notes="from lodgepole pine rhizosphere soil from the
British Columbia Ministry of Forests Long-Term Soil
Productivity (LTSP) installation near Prince George, BC,
Canada"
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/product="16S ribosomal RNA"

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ORIGIN
Query Match      85.6%; Score 15.4; DB 3; Length 544;
Best Local Similarity 82.4%; Pred. No. 5.3e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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CY          2  GAGGTCGACGCGGUA 18
Db          137 GAGGTCGTCACGCGTA 121
RESULT 26
AY988985/c
LOCUS          AY988985          625 bp      DNA      linear      ENV 02-MAY-2005
DEFINITION      Uncultured soil bacterium clone LJA.6F04 16S ribosomal RNA gene,
partial sequence.
ACCESSION      AY988985
VERSION        AY988985.1 GI:62913134
KEYWORDS
SOURCE
ORGANISM
uncultured soil bacterium
uncultured soil bacterium
Bacteria; environmental samples.
1 (bases 1 to 625)
Schloss,P.D. and Handelsman,J.
The last word: toward a sample based census of bacteria in soil
Unpublished
2 (bases 1 to 625)
Schloss,P.D. and Handelsman,J.
Direct Submission
Submitted (29-MAR-2005) Department of Plant Pathology, University
of Wisconsin-Madison, 1630 Linden Drive, Madison, WI 53705, USA
Location/Qualifiers
1..625

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/organism="uncultured soil bacterium"
/mol_type="genomic DNA"
/isolation_source="soil"
/db_xref="taxon:164851"
/clone="11A.6P04"
/environmental_sample
/country="USA: Alaska"
/product="16S ribosomal RNA"

ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 625;
Best Local Similarity 82.4%; Pred. No. 5.2e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGGUA 18
|||||:|||||:
119 GAGGGTCGTACGCGGTA 103

Db

RESULT 27
DQ123679/c 849 bp DNA linear ENV 02-AUG-2005
LOCUS
DEFINITION Uncultured soil bacterium clone PAH-Bio-08 16S ribosomal RNA gene,
partial sequence.
ACCESSION DQ123679
VERSION DQ123679.1 GI:71384051
KEYWORDS ENV.
SOURCE uncultured soil bacterium
ORGANISM uncultured soil bacterium
REFERENCE 1 (bases 1 to 849)
AUTHORS Singleton,D.R., Sangaiiah,R., Gold,A., Ball,L.M. and Aitken,M.D.
TITLE 'Division of Labor' in the Bacterial Degradation of Polycyclic
Aromatic Hydrocarbons in a Bioreactor Treating Contaminated Soil
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 849)
AUTHORS Singleton,D.R., Sangaiiah,R., Gold,A., Ball,L.M. and Aitken,M.D.
TITLE Direct Submission
JOURNAL Submitted (11-JUN-2005) Environmental Sciences & Engineering,
University of North Carolina, CB#7431, Chapel Hill, NC 27599, USA
FEATURES
source
1..849
/organism="uncultured soil bacterium"
/mol_type="genomic DNA"
/isolation_source="PAH-contaminated soil"
/db_xref="taxon:164851"
/clone="PAH-Bio-08"
/environmental_sample
<1..>849
/product="16S ribosomal RNA"

ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 849;
Best Local Similarity 82.4%; Pred. No. 4.9e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGGUA 18
|||||:|||||:
115 GAGGGTCGTACGCGGTA 99

Db

RESULT 28
DQ123747/c 855 bp DNA linear ENV 02-AUG-2005
LOCUS
DEFINITION Uncultured soil bacterium clone PAH-Bio-87 16S ribosomal RNA gene,
partial sequence.
ACCESSION DQ123747
VERSION DQ123747.1 GI:71384119
KEYWORDS ENV.
SOURCE uncultured soil bacterium
ORGANISM uncultured soil bacterium
Bacteria; environmental samples.

1 (bases 1 to 855)
Singleton,D.R., Sangaiiah,R., Gold,A., Ball,L.M. and Aitken,M.D.
TITLE 'Division of Labor' in the Bacterial Degradation of Polycyclic
Aromatic Hydrocarbons in a Bioreactor Treating Contaminated Soil
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 855)
AUTHORS Singleton,D.R., Sangaiiah,R., Gold,A., Ball,L.M. and Aitken,M.D.
TITLE Direct Submission
JOURNAL Submitted (11-JUN-2005) Environmental Sciences & Engineering,
University of North Carolina, CB#7431, Chapel Hill, NC 27599, USA
FEATURES
source
1..855
/organism="uncultured soil bacterium"
/mol_type="genomic DNA"
/isolation_source="PAH-contaminated soil"
/db_xref="taxon:164851"
/clone="PAH-Bio-87"
/environmental_sample
<1..>855
/product="16S ribosomal RNA"

ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 855;
Best Local Similarity 82.4%; Pred. No. 4.9e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGGUA 18
|||||:|||||:
115 GAGGGTCGTACGCGGTA 99

Db

RESULT 29
RSC0252692/c 1029 bp DNA linear ENV 18-AUG-2000
LOCUS
DEFINITION Rhizosphere soil bacterium clone RSC-II-71, 16S rRNA gene
(partial).
ACCESSION RSC0252692
VERSION RSC0252692.1 GI:9857208
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.
SOURCE rhizosphere soil bacterium RSC-II-71
ORGANISM rhizosphere soil bacterium RSC-II-71
REFERENCE 1
AUTHORS Lukow,T.
TITLE Vergleichende Charakterisierung der bakteriellen
Rhizosphärenengemeinschaften transgener versus nicht-transgener
Kartoffelpflanzen
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1029)
AUTHORS Lukow,T.
TITLE Direct Submission
JOURNAL Submitted (16-AUG-1999) Lukow T., Biogeochemie, Max-Planck-Institut
für terrestrische Mikrobiologie, Karl-von-Frisch-Strasse, 35043
Marburg, GERMANY
FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:102490"
/clone="RSC-II-71"
1..1029
/gene="16S rRNA"
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/gene="16S rRNA"
/product="16S ribosomal RNA"

ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 1029;
Best Local Similarity 82.4%; Pred. No. 4.8e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGGUA 18
|||||:|||||:
115 GAGGGTCGTACGCGGTA 99

Db 172 GAAGTCCGACCGCGTA 156

RESULT 30
LOCUS AY102340/c
DEFINITION uncultured bacterium clone a13154 16S ribosomal RNA gene, partial sequence.
ACCESSION AY102340
VERSION AY102340.1 GI:21322295
KEYWORDS ENV.
SOURCE uncultured bacterium
ORGANISM Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 1330)
AUTHORS Ellis,R.J., Morgan,P., Weightman,A.J. and Fry,J.C.
TITLE Cultivation-Dependent and -Independent Approaches for Determining Bacterial Diversity in Heavy-Metal-Contaminated Soil
JOURNAL Appl. Environ. Microbiol. 69 (6), 3223-3230 (2003)
PUBMED 12788719
REFERENCES 2 (bases 1 to 1330)
AUTHORS Ellis,R.J., Morgan,P., Weightman,A.J. and Fry,J.C.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-2002) Imperial College at Silwood Park, NERC Center for Population Biology, Ascot, Berks SL5 7PY, UK
LOCATION/Qualifiers
1. .1330
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/mol_type="genomic DNA"
/db_xref="taxon:77133"
/clone="a13154"
/environmental_sample
<1. .>1330
/product="16S ribosomal RNA"

ORIGIN

RNA

Query Match 85.6%; Score 15.4; DB 3; Length 1330;
Best Local Similarity 82.4%; Pred. No. 4.6e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACCGCGTA 18
|||||:|||||:|
Db 130 GAGGTCGTAACCGCGTA 114

RESULT 31
LOCUS AY102345/c
DEFINITION uncultured bacterium clone a13101 16S ribosomal RNA gene, partial sequence.
ACCESSION AY102345
VERSION AY102345.1 GI:21322300
KEYWORDS ENV.
SOURCE uncultured bacterium
ORGANISM Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 1331)
AUTHORS Ellis,R.J., Morgan,P., Weightman,A.J. and Fry,J.C.
TITLE Cultivation-Dependent and -Independent Approaches for Determining Bacterial Diversity in Heavy-Metal-Contaminated Soil
JOURNAL Appl. Environ. Microbiol. 69 (6), 3223-3230 (2003)
PUBMED 12788719
REFERENCES 2 (bases 1 to 1331)
AUTHORS Ellis,R.J., Morgan,P., Weightman,A.J. and Fry,J.C.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-2002) Imperial College at Silwood Park, NERC Center for Population Biology, Ascot, Berks SL5 7PY, UK
LOCATION/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:77133"
/clone="a13101"

FEATURES
source

ORIGIN

RNA

Query Match 85.6%; Score 15.4; DB 3; Length 1331;
Best Local Similarity 82.4%; Pred. No. 4.6e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACCGCGTA 18
|||||:|||||:|
Db 131 GAGGTCGTAACCGCGTA 115

RESULT 32
LOCUS BC082645/c
DEFINITION Xenopus laevis hypothetical LOC494668, mRNA (cDNA clone MGC:81662 IMAGE:684519), complete cds.
ACCESSION BC082645
VERSION BC082645.1 GI:52139140
KEYWORDS MGC.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus; Xenopus.
REFERENCE 1 (bases 1 to 1871)
AUTHORS Klein,S.L., Strassberg,R.L., Wagner,L., Pontius,J., Clifton,S.W. and Richardson,P.
TITLE Genetic and genomic tools for Xenopus research: The NIH Xenopus Initiative
JOURNAL Dev. Dyn. 225 (4), 384-391 (2002)
PUBMED 12454917
REFERENCES 2 (bases 1 to 1871)
AUTHORS Strassberg,R.L., Feingold,R.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Sherman,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.U., Usdin,T.B., Tothylki,S., Carninci,P., Prange,C., Kana,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Whlady,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulik,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahy,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmitt,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skelton,U., Smalins,D.E., Scherch,A., Schein,J.B., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCES 3 (bases 1 to 1871)
AUTHORS Klein,S. and Gerhard,D.S.
TITLE Direct Submission
JOURNAL Submitted (15-SEP-2004) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD 20892-7510, USA
NIH-MGC Project
Contact: XGC help desk
Email: gscgbs-remail.nih.gov
Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
Info@bcgsc.bc.ca

REMARK
COMMENT

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Ohi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Telka Olson, Diana Palmquist, Anca Petrescu, Anna Lilia Prabhu, Parvaneh Saeedi, JR Santos, Angelique Scherch, Ursula Skalska, Duane Smalish, Jeff Stott, Miranda Tsai, George Yang, Jacque Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNLT at: <http://image.llnl.gov>
Series: IRK Plate: 159 Row: 1 Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein.

FEATURES

source

1..1871
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/mol_type="mRNA"
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/protein_id="AAH82645.1"
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/translation="MWKLFVGNLPPEATOPELKSLFEORGRVTECDIINKGVFVHMD
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ATLECDIVDYAFVMEISAEALDAIKINDTEPKRKHVQLSTRSLRATVGMERT
RCYRCGEGHWSKECPDQMAKLEDEPGYPPSPDPYGPMSAAVRYAVAKQVYD
BEERSIVYORVRYRPSYPALIERRYNALPQASTISYERKIDSPYERHLLPFP
POLPSYTYRERSPIRSSASSSMETRYTERRLSPILRSPADPRCRSDSYERVO
YF"

CDS

gene

ORIGIN

Query Match 85.6%; Score 15.4; DB 5; Length 1871;
Best Local Similarity 88.2%; Pred. No. 4.3e+03;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY

Db

2 GAGGATCGCAGCGGGA 18
|||||
872 GAGGCGCGCAGCGGTA 856

RESULT 33

BC073203/c

LOCUS BC073203 2394 bp mRNA linear VRT 03-AUG-2004
DEFINITION xenopus laevis MGC80472 protein, mRNA (CDNA clone MGC:80472
IMAGE:5156366), complete cds.
ACCESSION BC073203
VERSION BC073203.1 GI:49255989
KEYWORDS MGC.
SOURCE xenopus laevis (African clawed frog)
ORGANISM xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 2394)
Klein, S.L., Strauberg, R.L., Wagner, L., Pontius, J., Clifton, S.W.
and Richardson, P.
Genetic and genomic tools for Xenopus research: The NIH Xenopus
Initiative
JOURNAL Dev. Dyn. 225 (4), 384-391 (2002)
PUBMED 12454917

REFERENCE

AUTHORS

2 (bases 1 to 2394)
Strauberg, R.L., Feinold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Sherman, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, R., Moore, T., Max, S.I., Wang, J., Hsieh, P.,
Ditchenko, L., Marusik, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Donald, M.F., Casavant, T.L.,
Scheer, T.B., Brownstein, M.J., Udell, T.B., Tothlyki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.V., Bosak, S.A., McSwan, P.J.,
McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Huylk, S.W.,
Villalon, D.K., Mozy, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahney, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Gimwood, J., Schmitz, J., Myers, R.M.,
Butterfield, Y.S., Krzywnicki, M.I., Skalska, U., Smalish, D.E.,
Scherch, A., Schein, J.R., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
3 (bases 1 to 2394)
Klein, S. and Gerhardt, D.S.
Direct Submission
Submitted (14-JUN-2004) National Institutes of Health, Xenopus Gene
Collection (XGC), National Institute of Child Health and Human
Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD
20892-7510, USA
NIH-MGC Project
Contact: XGC help desk
Email: xgcbp-remail.nih.gov
Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLT)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth
Featherstone, Malachi Griffith, Ohi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Telka Olson, Diana Palmquist, Anca Petrescu, Anna Lilia Prabhu,
Parvaneh Saeedi, JR Santos, Angelique Scherch, Ursula Skalska,
Duane Smalish, Jeff Stott, Miranda Tsai, George Yang, Jacque
Schein, Asim Siddiqui, Rob Holt, Marco Marra.

REMARK

COMMENT

FEATURES

source

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/clone_lib="NICHD_XGC_Emb1"
/lab_host="DH10B"
/note="Vector: PCMV-SPORT6"
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/gene="MGC80472"
/db_xref="GeneID:444116"
554..1564
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/codon_start=1
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/protein_id="AAH73203.1"
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LCRCGDKGHWKCEPLDQMAKSGAGYPPSPDYGPMRSAGGYRAVYARVYD
DDERFETIDYQRYRVRPSSYDILLERLTGCLPAAATYSYRERIESPFYEHLLDPP
POLPSSYVAREKPIRRSSASSMETHYTERRLSIFIMNPPADDPKRCRSDSYDRVQ
YL"

ORIGIN
Query Match      85.6%; Score 15.4; DB 5; Length 2394;
Best Local Similarity 88.2%; Pred. No.4.1e+03;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 GAGGAGCGCAGCGCGGUA 18
      ||||| ||||| |||||
Db      1263 GAGGAGCGCAGCGCGGTA 1247

RESULT 34
AC159431      132418 bp DNA linear INV 02-APR-2005
LOCUS      Trypanosoma brucei chromosome 8 clone RPCI93-28F14, complete
DEFINITION      sequence.
ACCESSION      AC159431
VERSION      AC159431.1 GI:62176003
KEYWORDS      HTG.
SOURCE      Trypanosoma brucei
ORGANISM      Trypanosoma brucei
            Burkarya; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE      1 (bases 1 to 132418)
AUTHORS      Ghedin,E., Blandin,G., Bartholomew,D., Caler,E., Haas,B.,
            Hamrick,L., Shalimov,J., Hou,L., Djikeng,A., Feldblyum,T.,
            Hostetler,J., Johnson,J., Jones,K., Koo,H.L., Larkin,C., Pai,G.,
            Peterson,J., Khalak,H.G., Salzberg,S., Simpson,A.U., Tallon,L., Van
            Aken,S., Wansless,D., White,O., Wortman,J., Frazer,C.M. and
            El-Sayed,N.M.A.
COMMENT      Unpublished
            2 (bases 1 to 132418)
            Haas,B., Blandin,G. and El-Sayed,N.
            Direct Submission
            Submitted (02-APR-2005) The Institute for Genomic Research, 9712
            Medical Center Dr., Rockville, MD 20850, USA, nelsayed@igf.org
            BAC clone RPCI93-28F14 from Trypanosoma brucei chromosome 8.
            Putative protein coding regions (>30 codons) were predicted by
            combining the output of the gene finding algorithm GLIMMER with
            similarity data and manual annotation of open reading frames.
            Further refinement of gene models (additions, deletions and
            alterations to boundary coordinates) were done manually based on
            detailed comparisons with the T. cruzi and L. major genomes. Genes
            on BACs were assigned a systematic name based on the chromosome and
            the BAC from which they originated (e.g. Tb03.27F10.410). Gene
            products were assigned a putative function when they shared
            significant similarity with experimentally characterized gene
            products or when they contained functionally known protein domains.
            Gene products were labelled either 'hypothetical protein', or
            'hypothetical protein, conserved' in the case of products showing
            significant similarity with proteins or domains of unknown function
            from other organisms. Gene products of unknown function with
            predicted orthologs in Trypanosoma cruzi and Leishmania major
            genomes were automatically classified as conserved proteins. Short
            predicted coding sequences (less than 150 codons) with no
            additional evidence of coding potential were labelled 'hypothetical
            protein, unlikely'.
FEATURES             location/Qualifiers
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                        /chromosome="8"
                        /clone="RPCI93-28F14"

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                    go_process: RNA processing [gold 0003961]"
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                    SSGSGPLDSIVIGRSMSPSSRDILTGQLATLIRCTGRPAPTLHA.PMDA.PIH
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12978..13016
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13042..13063
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/misc_feature      /note="A-rich"
15526..15574
/note="A-rich"
/misc_feature      /note="T-rich"
15682..15727
/note="T-rich"
/misc_feature      /note="AT-rich"
15757..15785
/note="AT-rich"
repeat_region     16081..16112
/note="microsatellite"
/rpt_type=tandem
/rpt_unl="ca"
gene              /locus_tag="Tb927.8.2790"
16412..16729
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(pseudogene), putative"
/pseudo
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conserved"
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/product="hypothetical protein, conserved"
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/note="go function: calcium ion binding [goId 0005509]"
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/product="hypothetical protein, conserved"
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/db_xref="GI:62176005"
/translation="MGCLPPDDIGPVSIDHVNENAPVLSDEDLILVRSYLLPTD
VREAAVFNHRYVCECLRAQORHYMTGHLPOKSTVSMASAPVPAECGKLTTPV
RAASGDNVAKERKAPVSPDCVNGSECRKREYVAVLGAEGROFEPDGAIP
TEVMSFLRMQOPVEYLLXQALBEKLTGAALAAAPRERSPGVGGKRPQDGS
KAKKQSVRGGRPNNTKSLNLDHDLLEBQSGSGRTVTPPLFLYISNSELG
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<18622..>21228
/locus_tag="Tb927.8.2810"

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Query Match      85.6%; Score 15.4; DB 2; Length 132418;
Best Local Similarity 82.4%; Pred. No. 2.1e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 GAGGUCGACGCGGUA 18
|||||:|||||:|
Db      2690 GAGGTCGACGCGGTA 2706

RESULT 35
AC159420
LOCUS      AC159420      142479 bp      DNA      linear      INV 02-APR-2005
DEFINITION Trypanosoma brucei chromosome 8 clone RPlC193-26A17, complete
sequence.
ACCESSION   AC159420
VERSION     AC159420.1 GI:62175571
KEYWORDS    HTG.
SOURCE      Trypanosoma brucei
ORGANISM    Trypanosoma brucei
            Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1 (bases 1 to 142479)
AUTHORS    Ghedin, B., Blandin, G., Bartholomew, D., Caler, E., Haas, B.,
            Hamick, L., Shalton, J., Hou, L., Djikeng, A., Feldblyum, T.,
            Hostetler, J., Johnson, J., Jones, K., Koo, H.L., Larkin, C., Pai, G.,
            Peterson, J., Khalak, H.G., Salzberg, S., Simpson, A.J., Tallon, L., Van
            Aken, S., Wanless, D., White, O., Wortman, J., Frazer, C.M. and
            El-Sayed, N.M.A.
            Unpublished
            2 (bases 1 to 142479)
            Haas, B., Blandin, G. and El-Sayed, N.
            Direct Submission
            Submitted (02-APR-2005) The Institute for Genomic Research, 9712
            Medical Center Dr. Rockville, MD 20850, USA, nelsayed@tigr.org
            BAC clone RPlC193-26A17 from Trypanosoma brucei chromosome 8.
            Putative protein coding regions (>30 codons) were predicted by
            combining the output of the gene finding algorithm GLIMMER with
            similarity data and manual annotation of open reading frames.
            Further refinement of gene models (additions, deletions and
            alterations to boundary coordinates) were done manually based on
            detailed comparisons with the T. cruzi and L. major genomes. Genes
            on BACs were assigned a systematic name based on the chromosome and
            the BAC from which they originated (e.g. Tb03.27F10.410). Gene
            products were assigned a putative function when they shared
            significant similarity with experimentally characterized gene
            products or when they contained functionally known protein domains.
            Gene products were labelled either 'hypothetical protein' or
            'hypothetical protein, conserved' in the case of products showing
            significant similarity with proteins or domains of unknown function
            from other organisms. Gene products of unknown function with
            predicted orthologs in Trypanosoma cruzi and Leishmania major
            genomes were automatically classified as conserved proteins. Short
            predicted coding sequences (less than 150 codons) with no
            additional evidence of coding potential were labelled 'hypothetical
            protein, unlikely'.
            location/Qualifiers
FEATURES             source
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   /isolate="GUTa10.1"
   /db_xref="taxon:5691"
   /chromosome="8"
   /clone="RPlC193-26A17"
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/note="annotation for this sequence region can be found on
overlapping clone 26A11."
<855..>33398
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/note="synonym: Tb08.26A17.20; hypothetical protein,
conserved"

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misc_feature

gene

[illegible]

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misc_feature	9209..9285
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	/note="synonym: Tb08.26A17.70; hypothetical protein,
	conserved"
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	/product="hypothetical protein, conserved"
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	REVRSDVASFAALAESATRKAGADVGAAMPENIIGASRPDSATAVVYLKLSGVASV
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	/rpt_type=tandem
	/rpt_unit="ta"
gene	<10984..>11649
	/locus_tag="TB927.8.2300"
	/note="synonym: Tb08.26A17.80; hypothetical protein,
	conserved"
mRNA	<10984..>11649
	/locus_tag="TB927.8.2300"
	/product="hypothetical protein, conserved"
CDS	10984..11649
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	/db_xref="GI:62175587"
	/translation="MDDYKRKSAMLMTKGIIELRSPPALVCTIRRFKPMGSKETTL
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	LAEVVDNGKFEGIVERPDLBSRAAYOKMLDGGAPPDPRARRAIERIIGVADATKVY
	CGMWGYHLVMTYRTLTGTYESSEBELLEVGMKRWVILGCFMOITTFMMVVALYRNL
	REF"
repeat_region	12097..12123
	/note="microsatellite"
	/rpt_type=tandem
	/rpt_unit="ca"
gene	<12258..>12587
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mRNA	<12258..>12587
	/locus_tag="TB927.8.2310"
	/product="(H+)-ATPase G subunit, putative"
CDS	12258..12587
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	/BC number="3.6.3.14"
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	[goid 0000219]:"
	go_function: ATPase activity [goid 0016867];
	go_process: vacuolar acidification [goid 0007035]"
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QY 2 GAGGUGCAGCGCGUA 18
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 Db 136646 GAGGTCGACGCGGTA 136662

RESULT 36
 AC099556 144820 bp DNA linear HTG 05-APR-2002
 LOCUS AC099556
 DEFINITION Trypanosoma brucei chromosome VIII clone RPCI93-26A17, ***
 SEQUENCING IN PROGRESS ***

AC099556
 AC099556
 HTG: HTGS PHASE2.
 SOURCE Trypanosoma brucei
 ORGANISM Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE
 AUTHORS 1 (bases 1 to 144820)
 TITLE El-Sayed, N.M., Ghedin, E., Song, J., Larkin, C., Wanless, D., Jones, K., Peterson, J., Hou, L., Zhao, H., Mason, T., Millscher, J., Pai, G., Van Aken, S., Utecht, T., Khalak, H.G., Gerard, C., Leech, V., Ullu, E., Melville, S., White, O., Adams, M.D., Donelson, J.E. and Fraser, C.M.
 JOURNAL Trypanosoma brucei GUTa10.1 RPCI93-26A17 BAC genomic sequence
 TITLE Unpublished
 AUTHORS 2 (bases 1 to 144820)
 TITLE El-Sayed, N.M., Khalak, H. and Adams, M.D.
 JOURNAL Direct Submission
 SUBMITTED (16-NOV-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
 REFERENCE 3 (bases 1 to 144820)
 TITLE El-Sayed, N.M., Khalak, H. and Adams, M.D.
 JOURNAL Direct Submission
 SUBMITTED (05-APR-2002) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA

COMMENT
 On Apr 5, 2002 this sequence version replaced gi:14425288.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 1 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * been provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 144820: contig of 144820 bp in length.
 * Location/Qualifiers
 1. 144820
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /isolate="GUTa10.1"
 /db_xref="taxon:5691"
 /chromosome="VIII"
 /clone="RPCI93-26A17"

ORIGIN
 Query Match 85.6%; Score 15.4; DB 14; Length 144820;
 Best Local Similarity 82.4%; Pred. No. 2e+03;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGUGCAGCGCGUA 18
 |||||:|||||:|||||:
 Db 137827 GAGGTCGACGCGGTA 137843

RESULT 37
 AC007862 150671 bp DNA linear INV 07-APR-2005
 LOCUS AC007862
 DEFINITION Trypanosoma brucei chromosome 2 clone RPCI93-10C8, complete
 SEQUENCING IN PROGRESS ***

AC007862
 AC007862
 HTG: HTGS PHASE2.
 SOURCE Trypanosoma brucei
 ORGANISM Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE
 AUTHORS 1 (bases 1 to 150671)
 TITLE Ghedin, E., Blandin, G., Bartholomew, D., Caler, E., Haas, B., Hannick, L., Shallow, J., Hou, L., Djikeng, A., Feldblyum, T., Hostetler, J., Johnson, J., Jones, K., Koo, H.L., Larkin, C., Pai, G., Peterson, J., Khalak, H.G., Salberg, S., Simpson, A.J., Tallon, L., Van Aken, S., Wanless, D., White, O., Wortman, J., Fraser, C.M. and El-Sayed, N.M.A.
 JOURNAL Unpublished
 AUTHORS 2 (bases 1 to 150671)
 TITLE El-Sayed, N.M., Khalak, H. and Adams, M.D.
 JOURNAL Direct Submission
 SUBMITTED (16-JUN-1999) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
 REFERENCE 3 (bases 1 to 150671)
 TITLE Haas, B., Blandin, G. and El-Sayed, N.
 JOURNAL Direct Submission
 SUBMITTED (07-APR-2005) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, nelsayed@tigr.org
 On Apr 7, 2005 this sequence version replaced gi:14787186.
 BAC clone RPCI93-10C8 from Trypanosoma brucei chromosome 2.
 Putative protein coding regions (>30 codons) were predicted by combining the output of the gene finding algorithm GLIMMER with similarity data and manual annotation of open reading frames.
 Further refinement of gene models (additions, deletions and alterations to boundary coordinates) were done manually based on detailed comparisons with the T. cruzi and L. major genomes. Genes on BACs were assigned a systematic name based on the chromosome and the BAC from which they originated (e.g. TP03.27F10.410). Gene products were assigned a putative function when they shared significant similarity with experimentally characterized gene products or when they contained functionally known protein domains. Gene products were labelled either 'hypothetical protein', or 'hypothetical protein, conserved' in the case of products showing significant similarity with proteins or domains of unknown function from other organisms. Gene products of unknown function with predicted orthologs in Trypanosoma cruzi and Leishmania major genomes were automatically classified as conserved proteins. Short predicted coding sequences (less than 150 codons) with no additional evidence of coding potential were labelled 'hypothetical protein, unlikely'.
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 1. 19399
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 7365..7402
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 13647..13672
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 /note="synonym: 10C8.65; hypothetical protein, conserved"

ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE
 AUTHORS 1 (bases 1 to 150671)
 TITLE Ghedin, E., Blandin, G., Bartholomew, D., Caler, E., Haas, B., Hannick, L., Shallow, J., Hou, L., Djikeng, A., Feldblyum, T., Hostetler, J., Johnson, J., Jones, K., Koo, H.L., Larkin, C., Pai, G., Peterson, J., Khalak, H.G., Salberg, S., Simpson, A.J., Tallon, L., Van Aken, S., Wanless, D., White, O., Wortman, J., Fraser, C.M. and El-Sayed, N.M.A.
 JOURNAL Unpublished
 AUTHORS 2 (bases 1 to 150671)
 TITLE El-Sayed, N.M., Khalak, H. and Adams, M.D.
 JOURNAL Direct Submission
 SUBMITTED (16-JUN-1999) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
 REFERENCE 3 (bases 1 to 150671)
 TITLE Haas, B., Blandin, G. and El-Sayed, N.
 JOURNAL Direct Submission
 SUBMITTED (07-APR-2005) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, nelsayed@tigr.org
 On Apr 7, 2005 this sequence version replaced gi:14787186.
 BAC clone RPCI93-10C8 from Trypanosoma brucei chromosome 2.
 Putative protein coding regions (>30 codons) were predicted by combining the output of the gene finding algorithm GLIMMER with similarity data and manual annotation of open reading frames.
 Further refinement of gene models (additions, deletions and alterations to boundary coordinates) were done manually based on detailed comparisons with the T. cruzi and L. major genomes. Genes on BACs were assigned a systematic name based on the chromosome and the BAC from which they originated (e.g. TP03.27F10.410). Gene products were assigned a putative function when they shared significant similarity with experimentally characterized gene products or when they contained functionally known protein domains. Gene products were labelled either 'hypothetical protein', or 'hypothetical protein, conserved' in the case of products showing significant similarity with proteins or domains of unknown function from other organisms. Gene products of unknown function with predicted orthologs in Trypanosoma cruzi and Leishmania major genomes were automatically classified as conserved proteins. Short predicted coding sequences (less than 150 codons) with no additional evidence of coding potential were labelled 'hypothetical protein, unlikely'.
 Location/Qualifiers
 1. 150671
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 1. 19399
 /note="annotation for this sequence region can be found on overlapping clone 25N14."
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 /note="AT-rich"
 7365..7402
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 13647..13672
 /note="microsatellite"
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 /rpt_unit="caa"
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 /locus_tag="TD927.2.2530"
 /note="synonym: 10C8.65; hypothetical protein, conserved"

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          KNPASREBALAAVRAIGVDSLATLCASSPCVGCNVCNDVADAEVLAICLIISAV
          SVADSQWVLESVHRVAFICLHGVTCTTPNSKKSSTSGCAAPSRNRRTGII
          MNDETLESPTCARDGFBGAKGKDGYPAGPPTNKGLITNI EHSIDATSGLSGR
          IGETGRPLTCGDEMALSKGHDNGVSASETVDNLKVEAASDTOTELVDSPCLD
          VOQCGCKGQREPIHCSEELPADGTTPLSCSTAGEMALHENGKGTDSDDSPKADY
          SNKNVHRVYNGEVPDLOCWVGKORSGEVYNGRLPTDLKASIHSPSNAAED
          TYESLFTEDGVVISTGTPCSEKSESMIDVEAPSHSVSVAATVPYVYKGVSS
          SPYTRGDVLDSESGELKAPSOULIEMVDGCAKSPMLTGQDDEPLRSLMLSKITALP
          TTRQAGALINADAGLKSSTLDPSYAGAAKRS CPLAAVSTIVTDDIGTCGGSTLT
          EATGASGPASVSKQSGESTSHPMFAHTAPISVGSTORGRGSGGAPDADDK
          SNGRGEOPSSCSAAPLPPTVAFRLFPASGELTEHPBGATCAITREVTAAPOPOL
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          /product="hypothetical protein, conserved"
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          TGAARVMDGDFLREFGFRSDKMPHGGIISARNVSNITKRSSEKSNMHP
          MIQHVAVLHITPGLTDPGTETLNDKDFASHIRQCHNGELSCPHLSHQNSAADTFR
          THGQDNFSSGADAEAREPFASSDSVGVMVIRCCSETFPFLAFNTGTHHEWIC
          KPHITLMPOTBEATLIGRTSVADAADAVAPILMAROSLCITLRANFPPOSQAKGM
          GELSTLYVYAGCTALTASRKLVAEOLLETTMORQOSRPHPTNHRPFLSCASQ
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          /product="hypothetical protein, conserved"
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          LNSQSVTVDGVNTEPLTODTGLTVQVSAASNSTSPRLSPVALGALVSAATPLVNR
          AASCRASQSVSVVSLSPRLSLALTEPSTCISVRGSSSTRSSAPPOHLSMSNSPT
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          THARVGSERDIFPHPSMSMDIRVERGRDPSLKGNTASLNRSSPRTOPLDHYKA
          PSAPVQIMERPVTYVNRITLKNITDVALSGGSSDDPTEDFNDFADGSGSDDFG
          BEDSRFGHSHMORQLFAPLMSKWRISRCASSYKRSRLKRAAGSAAAGDNLA
          ERLQLEOIRVTFEALEREKHOQOQSAATGADAAEKPRRAAPHAASGSGST
          NNDCAVSPASMSPVKSKRSRTAAEVDLITTPVGNQGTSLSLSTPSSSRTLDN
          NIVKSGVSSDGERAACBPTEGLNDVREYIVSYCDSSNGTTEASPDODRVDH
          KMLPDAISIDPEHLPSNGSCSRSSMSKGTBAAPHVILKPTPRSTTISYHRTVS
          VASLIQKLMVDOSGKISIKLNQSHSTGLADSKELTSPSKONQOQKRRRPPANWD
          RTKNLATVSRVNSNGAAPPVACVKTAGVPVAPVPLAPTTIVSPGAPVYAA
          TPHYKSTKHYPRNTPVHERGKDRRGRCHSPERGSGTSPQSGLTFALVGAQTKV
          GIRLAVSGCNGNVTTQSATPMTARPVCGRRYRTTCSNPOSSATAGVATANKR
          SSGCQTTTPRNVAAGNAVGPSPSSGGAAPFQSNATNGSRTCGSMQSLVLSGM
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Query Match      85.6%; Score 15.4; DB 2; Length 150671;
Best Local Similarity 82.4%; Pred. No. 2e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 AAGGGUGGACGCGGU 17
Db      26280 AAGGGGTCGCCCGCGT 26296

RESULT 38
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LOCUS
DEFINITION
MUS musculus strain C57BL/6J chromosome 7 clone R223-27G15, WORKING
DRAFT SEQUENCE, 28 unordered pieces.
ACCESSION
AC091290
VERSION
AC091290.9 GI:20127973
KEYWORDS
HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE
MUS musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 286178)
Li,J., Montgomery,K.T., Grille,G., Chiu,D., Decker,J., Pusina,M.,
Golitz,J., Halder,A., Hall,L., Han,J., Ioshikhes,I.P., Lee,E.,

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REFERENCE	Perera,A., Shim,C., Thomas,B. and Kucherlapati,R.
JOURNAL	High Throughput Mouse Sequencing
AUTHORS	Unpublished
TITLE	2 (bases 1 to 286178)
JOURNAL	Li,L., Montgomery,K.T., Grills,G., Chiu,D., Decker,J., Fusina,M.,
REFERENCE	Goltz,J., Haider,A., Hall,L., Han,J., Ioshikhes,I.P., Lee,E.,
AUTHORS	Perera,A., Shim,C., Thomas,B. and Kucherlapati,R.
TITLE	Direct Submission
JOURNAL	Submitted (13-APR-2001) Department of Molecular Genetics, Albert
REFERENCE	Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,
AUTHORS	Bronx, NY 10461, USA
TITLE	3 (bases 1 to 286178)
JOURNAL	Li,L., Montgomery,K.T., Grills,G., Chiu,D., Decker,J., Fusina,M.,
REFERENCE	Goltz,J., Haider,A., Hall,L., Han,J., Ioshikhes,I.P., Lee,E.,
AUTHORS	Perera,A., Shim,C., Thomas,B. and Kucherlapati,R.
TITLE	Direct Submission
JOURNAL	Submitted (10-APR-2002) Harvard Partners Center for Genetics and
REFERENCE	Genomics, Harvard Medical School, 65 Landsdowne St, Cambridge, MA
AUTHORS	02139, USA
TITLE	On Apr 10, 2002 this sequence version replaced gi:199039369.
JOURNAL	-----Genome Center
REFERENCE	Center: Harvard Partners Genome Center
AUTHORS	Center Code: HPGC
TITLE	Web site: http://www.hpgcg.org/Sequence/mouse.html
JOURNAL	Contact: hpgcmenudel.mgh.harvard.edu
REFERENCE	-----Summary Statistics
AUTHORS	Center project name: ALV
TITLE	Sequencing vector: pUC18; L08752
JOURNAL	Chemistry: Dye-terminator Big Dye; 100%
REFERENCE	*Consensus quality: 276132 at least Q20
AUTHORS	*Consensus quality: 273505 at least Q30
TITLE	*Consensus quality: 270014 at least Q40
JOURNAL	*Estimated insert size: agarose-pp - N/A
REFERENCE	*Estimated insert size: 285638 - sum-of-ctnigs
AUTHORS	Quality coverage: agarose-pp - N/A
TITLE	Quality coverage: 8.3 x in Q20 bases; sum-of-ctnigs estimation
JOURNAL	-----
REFERENCE	* NOTE: This is a 'working draft' sequence. It currently
AUTHORS	* consists of 28 ctnigs. The true order of the pieces
TITLE	* is not known and their order in this sequence record is
JOURNAL	* arbitrary. Gaps between the ctnigs are represented as
REFERENCE	* runs of N, but the exact sizes of the gaps are unknown.
AUTHORS	* This record will be updated with the finished sequence
TITLE	* as soon as it is available and the accession number will
JOURNAL	* be preserved.
REFERENCE	1 75134: ctnig of 75134 bp in length
AUTHORS	* 75135 75154: gap of unknown length
TITLE	* 75155 110704: ctnig of 35550 bp in length
JOURNAL	* 110705 110724: gap of unknown length
REFERENCE	* 110725 144861: ctnig of 34137 bp in length
AUTHORS	* 144862 144881: gap of unknown length
TITLE	* 144882 168480: ctnig of 23599 bp in length
JOURNAL	* 168481 168500: gap of unknown length
REFERENCE	* 168501 190093: ctnig of 21593 bp in length
AUTHORS	* 190094 190113: gap of unknown length
TITLE	* 190114 212059: ctnig of 21946 bp in length
JOURNAL	* 212060 212079: gap of unknown length
REFERENCE	* 212080 221367: ctnig of 9288 bp in length
AUTHORS	* 221368 221387: gap of unknown length
TITLE	* 221388 222587: ctnig of 11200 bp in length
JOURNAL	* 222588 232607: gap of unknown length
REFERENCE	* 232608 241890: ctnig of 9283 bp in length
AUTHORS	* 241891 250226: ctnig of 8316 bp in length
TITLE	* 250227 250246: gap of unknown length
JOURNAL	* 250247 256300: ctnig of 6054 bp in length
REFERENCE	* 256301 256320: gap of unknown length
AUTHORS	* 256321 259653: ctnig of 3333 bp in length
TITLE	* 259654 259673: gap of unknown length
JOURNAL	* 259674 263360: ctnig of 3687 bp in length
REFERENCE	* 263361 263380: gap of unknown length
AUTHORS	* 263381 265711: ctnig of 2331 bp in length
TITLE	* 265712 265731: gap of unknown length

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	*	270607	270909: contig of 303 bp in length
	*	270910	270929: gap of unknown length
	*	270930	271949: contig of 1020 bp in length
	*	271950	271969: gap of unknown length
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	*	281924	281944: contig of 1329 bp in length
	*	281925	281944: gap of unknown length
	*	283510	283530: contig of 1566 bp in length
	*	283511	283530: gap of unknown length
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Query Match      85.6%; Score 15.4; DB 14; Length 286178;
Best Local Similarity 82.4%; Pred. No. 1.8e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY              1 AGAGGGGCGACGCGGU 17
Db              286144 AGAGGCTCACCGCGT 286128

RESULT 39
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LOCUS           BX842654 344249 bp DNA linear BCT 17-APR-2005
DEFINITION      Bdellovibrio bacteriovorus complete genome, strain HD100; segment
9/11.
ACCESSION       BX842654 BX842601
VERSION         BX842654.1 GI:39576487
KEYWORDS        complete genome.
SOURCE          Bdellovibrio bacteriovorus HD100
ORGANISM        Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
                Bdellovibrionaceae; Bdellovibrio.
REFERENCE
AUTHORS         Rendulic,S., Jagtad,P., Rosinus,A., Eppinger,M., Baar,C., Lanz,C.,
                Keller,H., Lambert,C., Evans,K.J., Goessmann,A., Meyer,F.,
                Sockett,R.E. and Schuster,S.C.
TITLES          A predator unmasked: life cycle of Bdellovibrio bacteriovorus from
                a genomic perspective
JOURNAL         Science 303 (5658), 689-692 (2004)
PUBMED          14752164
AUTHORS         Schuster,S.C.
TITLE           Direct Submission

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JOURNAL          Submitted (26-NOV-2003) Max-Planck Institute for Developmental
FEATURES         Biology, Speemannstr. 35, 72076 Tübingen, GERMANY
SOURCE           location/Qualifiers
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LIRFPYSPVNMILIGILITRPLADMSVRQAFRVSPSPAVASITVIVPALQIPOYI
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Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGGUCCGACGCGGU 17
DB 3451 AGCGGGTCGACGCGGT 3435

RESULT 40
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DEFINITION
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segment 3/8.
ACCESSION
BX248356 BX248353
VERSION
BX248356.1 GI:38199583
KEYWORDS
complete genome.
SOURCE
Corynebacterium diptheriae
ORGANISM
Corynebacterium diptheriae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
1 (bases 1 to 347625)
Cerdano-Tarraga,A.M., Estratiou,A., Dover,L.G., Holden,M.T.,
Pallen,M., Bentley,S.D., Besra,G.S., Churcher,C., James,K.D., De
Zoyza,A., Chillingworth,T., Cronin,A., Dowd,L., Feltwell,T.,
Hamlin,N., Holtroyd,S., Jagels,K., Moule,S., Quail,M.A.,
Rabinowitch,B., Rutherford,K.M., Thomson,N.R., Unwin,L.,
Whitehead,S., Barrett,B.G. and Parkhill,J.
The complete genome sequence and analysis of Corynebacterium
diptheriae NCCTC13129
Nucleic Acids Res. 31 (22), 6516-6523 (2003)
14602910
2 (bases 1 to 347625)
Cerdano-Tarraga,A.M.
Direct Submission
Submitted (03-Oct-2003) Cerdano-Tarraga A.M., submitted on behalf
of the Pathogen Sequencing Unit, Sanger Institute, Wellcome Trust
Genome Campus, Hinxton, Cambridge CB10 1SA E-mail:
amc@sanger.ac.uk

JOURNAL
PUBMED
AUTHORS
TITLE
JOURNAL
AUTHORS
TITLE
JOURNAL

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FEATURES
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                /protein_id="CAE49241.1"
                /db_xref="GI:38199585"
                /db_xref="UniProt/TREMBL:O6N1P9"
                /translation="MDIKGFSDSPRELIVSSREDNEIIVDIRIHNAIRDAGVLDVD
                DHNRIYRNARLAAYVEGSTAPRTVGFAGA"
                487..1365
                /locus_tag="DIP0720"
                487..1365
                /locus_tag="DIP0720"
                /note="Similar to Mycobacterium tuberculosis hypothetical
                31.0 kDa protein RV3207C or MTCV07D1.19 TR:005859
                (EMBL:Z95120) (285 aa) fasta scores: E(): 1.7e-44, 46.69%
                id in 287 aa"
                /codon_start=1
                /transl_table=11
                /product="Putative membrane protein"
                /protein_id="CAE49242.1"
                /db_xref="GI:38199586"
                /db_xref="InterPro:IPR006025"
                /db_xref="UniProt/TREMBL:O6N1P8"
                /translation="MTDPAHSFPFAPADYGRAYAPVLAIVTVVLIIDVFRTPAE
                TTTATVGGPATATSAQSKGPDAPORPDALITLSPGFTKGGRYATVNA
                GAHAGQHDVFTYVIEVNGINTAYAGDDAAVAADLTLPKSKWTHDKRGFEH
                DGAVKDPDLRIQLSSVDTHGICGNIMETSCFICGNIRVIVNSRRVRAKPPQG
                DCAVROYLINHEVGGIGFPAHNSPCGKNGELAPIMOOTLSISNELRAIDANETIN
                DDGAVCSANPWPFPFA"
                535..603
                /locus_tag="DIP0720"
                /note="T1 probable transmembrane helix predicted for
                DIP0720 by TMHMM2.0"
                1165..1194
                /locus_tag="DIP0720"
                /note="ScanRegKxp hit to PS00142, Neutral zinc
                metalloproteinases, zinc-binding region signature."
                1389..2246
                /locus_tag="DIP0721"
                1389..2246
                /locus_tag="DIP0721"
                /locus_tag="DIP0721"

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gene
    CDS
        /note="Similar to Mycobacterium leprae hypothetical
        protein ML0818 TR:Q9CCG7 (EMBL:AL583919) (297 aa) fasta
        scores: E(): 1.2e-34, 39.47% id in 266 aa"
        /codon_start=1
        /transl_table=11
        /product="Conserved hypothetical protein"
        /protein_id="CAE49243.1"
        /db_xref="GI:38199587"
        /db_xref="UniProt/TREMBL:O6N1P7"
        /translation="MELQOLPOHVADAPATPTPROLGAVDYGKRVGNVAFSGVVI
        PDRSAMSAVRDKLQDGLRVVRPLKSGTIRYNGWANSREGLTARRDETVAIA
        IRLDRLADIDVPSDFSPSDSHDLFSLADHSMABRPVAVLGTVDAARVPAKQCI
        AQRLLPKIVLRLDIAPIQVTHADMFNTTISGQMFPVLDLVGAAPYGTAAVACI
        VDALAGAVDSGITDRFSHIQRRDLLRALVYRIAVHALHESSTNGTNLEWVSOT
        IMSRASVTL"
        2250..5432
        /locus_tag="DIP0722"
        2250..5432
        /locus_tag="DIP0722"
        /note="Similar to Streptomyces coelicolor putative
        ATP-dependent DNA helicase 2SC386.07 TR:Q9FCR5
        (EMBL:AJ390968) (1159 aa) fasta scores: E(): 6.2e-29,
        32.21% id in 1161 aa"
        /codon_start=1
        /transl_table=11
        /product="Putative ATP-dependent DNA helicase"
        /protein_id="CAE49244.1"
        /db_xref="GI:38199588"
        /db_xref="GOA:O6N1P6"
        /db_xref="InterPro:IPR000209"
        /db_xref="InterPro:IPR000212"
        /db_xref="InterPro:IPR010916"
        /db_xref="UniProt/TREMBL:O6N1P6"
        /translation="MDAFSTPQDSPTPTAQVIGEDLTAGIPIPLQOSFYVACRPVIEIV
        VNDHSPIREMNQCFOROGTWTWYGAAGASVTLMDTVARIRRGVSPRIIVVA
        ASRSARLRAGIARIDGSTSPASIVRSVSGSLAPLIRLSGRLITIGASODA
        VIRELLQGVDPISLAAMPARQALGLIGPARVVRPLBSGRGLPEPDELTGA
        RPPGPMWASAGKFRREYQVVMNLGGTHSILMSLVSILKLCPIIPMGWHTI11IDIAQ
        LDPOAQLQALMARTYDFTVIAGDQGVFHRGASPRELTLAPVDHEITLSSRPO
        TVEAVLVSTGQDSSEFADLRLRSHLBSGIRANDMAIVYRSPADIPSLRALLSAGVP
        VOEDSPDIIISRCRIVSALLAVRALIYQELSGOELBELAGPIGADVTYLRRLFRGL
        RAEBMAGAGNRATIRIRELIDPKSEBQTCRQVENVLTRELAIVDKIRAVYRG
        AQPSSVERLTWEINWASALSHLQVSLRGVGRQAQDDLDVAADVADGVYERK
        PTASITSPFRIABQELPGVADRRLATADAVRIYTAGSLAQQWHVTVIAGVQGTW
        PSLQGTGLTFQGEDLIDLDGSIIBENTYISRSABRLKESKLFYARTRGTRVVITA
        VSPSPDPAEBSRFLQIGASGVQGFPTDPAVOSIDIEYTHLQYVLLSVPS
        IVAKIRRELANDSPORRBOAAROLALAHQVGAAPBQMWGVGGBSETTSLD19K
        VSPSLIRNALCPLARLERLYRENTPIHMLKGTLLARPAVARGVDPNRAEQLYT
        QAFELDLDPANSLPHHMSQWSTMLQRLAHWIDVSHAQRELGVAVPVAVAPGVEL
        RGRIRLERNDAGBPHIVDPKTKQAVTKDEANERKOLLAQVQLARGLMQRNGSPA
        INTTAEQPLTVDAQVAVPYATDTKVTYTRBQAPDPADELEKFSATLLPALRLSGPO
        LVARINTQDCKIKTMCPAQPEGWVPEC"
        2250..2558
        /locus_tag="DIP0722"
        /note="ScanRegKxp hit to PS00430, TonB-dependent receptor
        proteins signature 1."
        3045..3200
        /locus_tag="DIP0722"
        /note="TMMPfam hit to PF00580, UvrD/RBP helicase"
        3285..3431
        /locus_tag="DIP0722"
        /note="TMMPfam hit to PF00580, UvrD/RBP helicase"
        4167..4199
        /locus_tag="DIP0722"
        /note="HMMPFam hit to PF00580, UvrD/RBP helicase"
        /note="ScanRegKxp hit to PS00136, Serine proteases,
        subtilase family, aspartic acid active site."
        5426..8656
        /locus_tag="DIP0723"
        5426..8656
        /locus_tag="DIP0723"
        /note="Similar to Mycobacterium tuberculosis CDC1551
        helicase, UvrD/Rep family M13295 TR:AAK47638
        (EMBL:AB007142) (1101 aa) fasta scores: E(): 2.9e-25,

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/translation="1"
/product="Putative helicase"
/protein_id="CAE49245.1"
/db_xref="GI:38199589"
/db_xref="GOA:O6NIP5"
/db_xref="InterPro:IPR000212"
/db_xref="UniProt/TREMBL:O6NIP5"
/translation="MLSPQLSCALGQKPPPTQADVISPLAFTLVVAGAGKTE
TAAARVWLVASGLVDPDVLGITFRKAQQLSKRIRDLRLQAGIDMLRDLDPGA
LATKELAPVTYSDYAGRLISEYSGGLPVSRLISQELFOIASISAHFGA
LNTNSPNTVTSTLISVSEMONHWSPDIEBSAFLAMIEDVATSKRPSKVY
KRDPTOVLENNELPIYQKTHADNMTFPGESGLARLAAKNQVASQRNROI
IMLDEYQDTHGAKVLLKSLFAGTAVTAGDQMSITGRKATNANLEFLDFPSNG
SPATKELTVSFRNPEVDILANRVSRLGVEDRFRVQLEPRLNGIVRIGF
PFSMDERSYVADHLAQAEQHDHPFLAAVLVRRKSSAIALELQORGVEVIG
LAGLGIPEVADLVATLLVRPYQAMRLIAGSVGLGAMADLMALSDRAVNLGR
DRAATTELSDPLERLKOIADPTPSDOSVGLAEVADLDRISLSDGPRYSKGS
EKLRTLAALRIYRTKNSLSNLPDLFADIERPFGITETVLQREDPSDQATGHLDR
FAEVODFSRIPEANLSLUDYSLAESSENGLEPEEVVTVADRVQILTVHAKGLEW
QHVAVLMADANTYVAKASTWLTNVAASVPALRGDADGDLVGAPEFIDTPTAEL
ARAGKAHIADFTQVAEENARLPYVAITPAEQVLVTASADPSKRPVLYEYLTALR
INPDSVEEMHERGEADYVPPAPQAVFPNPTIYVGAADVFAAMQKODLISDDL
EKREKVSALIEHEBOLSA PYAVNVTGRLTADIVNLAKNPENTQRRRRPVPEKN
STAKRTAHEMTEKRFGBALIDETELFGIGELDSDLDRLKAFIDSEMAKRTPE

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Query Match 85.6%; Score 15.4; DB 1; Length 347625;
 Best Local Similarity 82.4%; Pred. No. 1.8e+03;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCG 17
 DB 86034 AGAGGUGCGACGCGT 86018

RESULT 41
 LOCUS AR052610 17 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 8 from patent US 5831066.
 ACCESSION AR052610
 VERSION AR052610.1 GI:5975974
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Reed, J.C.
 TITLE Regulation of bcl-2 gene expression
 JOURNAL Patent: US 5831066-A 8 03-NOV-1998;
 FEATURES
 source
 1..17
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Query Match 83.3%; Score 15; DB 6; Length 17;
 Best Local Similarity 93.3%; Pred. No. 1.5e+04;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCG 15
 DB 15 AGAGGUGCGACGCG 1

RESULT 42
 LOCUS BD187523 17 bp DNA linear PAT 17-JUL-2003
 DEFINITION REGULATION OF bcl-2 GENE EXPRESSION.
 ACCESSION BD187523
 VERSION BD187523.1 GI:32997262
 KEYWORDS JP 2003026609-A/8.
 SOURCE synthetic construct

ORGANISM synthetic construct
 other sequences; artificial sequences.
 1 (bases 1 to 17)
 REFERENCE
 AUTHORS Reed, J.C.
 TITLE REGULATION OF bcl-2 GENE EXPRESSION
 JOURNAL Patent: JP 2003026609-A 8 29-JAN-2003;
 COMMENT John C REED
 OS Artificial Sequence
 PN JP 2003026609-A/8
 PD 29-JAN-2003
 PF 19-JUN-2002 JP 2002178753
 PR 20-SEP-1993 US 08/124256
 PI John C Reed
 CC Description of Artificial Sequence: Designed DNA based on bcl-2
 CC
 FH Key Location/Qualifiers
 1..17
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

QY 1 AGAGGUGCGACGCG 15
 DB 15 AGAGGUGCGACGCG 1

RESULT 43
 LOCUS BD192460 17 bp DNA linear PAT 17-JUL-2003
 DEFINITION Compositions and methods for the delivery of oligonucleotides via the alimentary canal.
 ACCESSION BD192460
 VERSION BD192460.1 GI:33002199
 KEYWORDS JP 2002510319-A/25.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Teng, C.L. and Hardee, G.
 TITLE Compositions and methods for the delivery of oligonucleotides via the alimentary canal
 JOURNAL Patent: JP 2002510319-A 25 02-APR-2002;
 COMMENT ISIS PHARMACEUTICALS INC
 OS Artificial Sequence
 PN JP 2002510319-A/25
 PD 02-APR-2002
 PF 01-JUL-1998 JP 1999507295
 PR 01-JUL-1997 US 08/866829
 PI CHING TROU TENG, GREG HARDEE
 PC C1201/68; A61K9/127; A61K48/00; C07H21/04
 CC Description of Artificial Sequence: Novel Sequence FH Key
 Location/Qualifiers
 1..17
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 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN
 Query Match 83.3%; Score 15; DB 6; Length 17;
 Best Local Similarity 93.3%; Pred. No. 1.5e+04;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCG 15
 DB 15 AGAGGUGCGACGCG 1

RESULT 44
AR630674/c
LOCUS AR630674
DEFINITION Sequence 8 from patent US 6641541.
ACCESSION AR630674
VERSION AR630674.1 GI:59766401
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Reed,J.C.
TITLE Regulation of BCL-2-gene expression
JOURNAL Patent: US 6841541-A 8 11-JAN-2005;
The Trustees of the University of Pennsylvania; Philadelphia, PA
FEATURES
source
1..17
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 83.3%; Score 15; DB 6; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.5e+04;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUCCGACCGCG 15
15 AGAGGGTCCGACCGCG 1

RESULT 45
AR653968/c
LOCUS AR653968
DEFINITION Sequence 25 from patent US 6887906.
ACCESSION AR653968
VERSION AR653968.1 GI:67584835
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Teng,C.-L. and Hardee,G.
TITLE Compositions and methods for the delivery of oligonucleotides via
JOURNAL the alimentary canal
Patent: US 6887906-A 25 03-MAY-2005;
ISISpharmaceuticals, Inc.; Carlsbad, CA
FEATURES
source
1..17
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 83.3%; Score 15; DB 6; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.5e+04;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUCCGACCGCG 15
15 AGAGGGTCCGACCGCG 1

RESULT 46
G22341
LOCUS G22341
DEFINITION human STS wt-11635, sequence tagged site.
ACCESSION G22341
VERSION G22341.1 GI:1342667
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 426)
AUTHORS Hudson,T.
TITLE Whitehead Institute/MIT Center for Genome Research, Physically
JOURNAL Mapped STS
COMMENT Unpublished (1995)

Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: AAACGAACCAACCAAAATGG
Primer B: TCTAGTCTCGACGACAGATTGG
STS size: 125
PCR profile:
Presoak:
Denaturation: 56 degrees C
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
Protocol:
Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 mM
Taq Polymerase: 0.025 units/ul
Total Vol: 20 ul

Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 9.3

Derived from dbEST (genbank accession R09557).
FEATURES
source
1..426
/organism="Homo sapiens"
/mol_type="genomic DNA"
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/map="417.8 CR from top of Chr8 linkage group"

STS
primer bind
primer_bind
complement(122..143)

ORIGIN
Query Match 83.3%; Score 15; DB 10; Length 426;
Best Local Similarity 86.7%; Pred. No. 8.8e+03;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGGUCCGACGCGCGU 17
318 AGGGTCCGACGCGGT 332

RESULT 47
BD186637
LOCUS BD186637
DEFINITION Nucleic acids isolated from neuroblastoma.
ACCESSION BD186637
VERSION BD186637.1 GI:31878837
KEYWORDS WO 02097093-A/58.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
REFERENCE 1 (bases 1 to 779)
AUTHORS Nakagawara,A.

TITLE Nucleic acids isolated from neuroblastoma
JOURNAL Patent: WO 02097093-A 58 05-DEC-2002;
COMMENT CHINA PREF,HISAMITSU PHARMACEUTICAL CO INC,AKIRA NAKAGAMARA
OS Homo sapiens (human)
PN WO 02097093-A/58
PD 05-DEC-2002
PR 30-MAY-2002 WO 2002JP005294
PR 30-MAY-2001 JP 01P 162775,24-AUG-2001 JP 01P 255226 PI
AKIRA NAKAGAMARA
PC C12N15/11,C12Q1/68,G01N33/53,G01N33/566
CC nbia-10589-f
FH Key Location/Qualifiers
FT source 1..779
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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Query Match 83.3%; Score 15; DB 6; Length 779;
Best Local Similarity 93.3%; Pred. No. 7.9e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGG 16
DB 75 GAGGGTCCGACGCGG 89
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RESULT 48
LOCUS CQ729047 1936 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 14981 from Patent WO02068579.
ACCESSION CQ729047
VERSION CQ729047.1 GI:42299514
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
1 Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kite, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 14981 06-SEP-2002;
FEATURES
source Location/Qualifiers
1..1936
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 83.3%; Score 15; DB 6; Length 1936;
Best Local Similarity 93.3%; Pred. No. 6.8e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGG 16
DB 34 GAGGGTCCGACGCGG 48
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RESULT 49
AX333656 1936 bp DNA linear PAT 09-JAN-2002
LOCUS AX333656
DEFINITION Sequence 4165 from Patent WO0194629.
ACCESSION AX333656
VERSION AX333656.1 GI:18124375
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
1 Young,P.B., Augustus,M., Carter,K.C., Edner,R., Endress,G.,
Horriggen,S., Soppet,D.R. and Weaver,Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 4165 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
source Location/Qualifiers
1..1936
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 83.3%; Score 15; DB 6; Length 1936;
Best Local Similarity 93.3%; Pred. No. 6.8e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGG 16
DB 34 GAGGGTCCGACGCGG 48
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RESULT 50
AX780022 1936 bp DNA linear PAT 14-JUL-2003
LOCUS AX780022
DEFINITION Sequence 2179 from Patent WO03039443.
ACCESSION AX780022
VERSION AX780022.1 GI:32697016
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
1 Haeflrich,T., Schoch,C., Kern,W., Kohlmann,A., Schittger,S.,
Dugas,M., Bils,R., Bros,B. and Mergenthaler,S.
TITLE Novel genetic markers for leukemias
JOURNAL Patent: WO 03039443-A 2179 15-MAY-2003;
Deutsches Krebsforschungszentrum (DB) ;
Ludwig-Maximilian-Universitaet Muenchen (DB) ; Haeflrich,Torsten,
PD Dr. Dr. (DB) ; Schoch, Claudia (DB) ; Kern, Wolfgang (DB)
FEATURES
source Location/Qualifiers
1..1936
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 83.3%; Score 15; DB 6; Length 1936;
Best Local Similarity 93.3%; Pred. No. 6.8e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGG 16
DB 34 GAGGGTCCGACGCGG 48
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Job time : 1013.54 secs

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OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:34:54 ; Search time 361.731 Seconds
(without alignments)
331.640 Million cell updates/sec

Title: US-10-800-926-1

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Sequence: 1 agagggucgcacgcgga 18

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Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 333246308 residues

Total number of hits satisfying chosen parameters: 9993994

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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4: geneeqn2001as.*
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7: geneeqn2002bs.*
8: geneeqn2003as.*
9: geneeqn2003bs.*
10: geneeqn2003cs.*
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12: geneeqn2004as.*
13: geneeqn2004bs.*
14: geneeqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	18	100.0	18	2	AAV27720 Immunost
C 3	18	100.0	18	2	AAZ41906 II-12 sec
C 4	18	100.0	18	3	AAZ41982 Immune re
C 5	18	100.0	18	3	AAZ47644 Parasitic
C 6	18	100.0	18	4	AAH50628 Natural k
C 7	18	100.0	18	4	AAH50628 Natural k
C 8	18	100.0	18	4	AAH50628 Natural k
C 9	18	100.0	18	4	AAH50628 Natural k
C 10	18	100.0	18	6	ABST77520 Angiogene
C 11	18	100.0	18	6	ABST77520 Angiogene
C 12	18	100.0	18	6	ABST77520 Angiogene
C 13	18	100.0	18	6	ABST77520 Angiogene
C 14	18	100.0	18	6	ABST77520 Angiogene
C 15	18	100.0	18	9	ACD99318 Immunost
C 16	18	100.0	18	9	ACD99318 Immunost
C 17	18	100.0	18	9	ACD99318 Immunost
C 18	18	100.0	18	10	ADG68160 Umethy1a
C 19	18	100.0	18	10	ACR36780 Immunost

C 20	18	100.0	18	12	AD101100	Ad101100 Immunost
C 21	18	100.0	18	12	ADM99069	Adm99069 Immunost
C 22	18	100.0	18	12	AD04787	Ad04787 Cpg oligo
C 23	18	100.0	18	13	ADU89320	Adu89320 Allergic
C 24	18	100.0	18	13	ADU89372	Adu89372 Allergic
C 25	18	100.0	18	14	ADU11411	Adu11411 Reverse s
C 26	18	100.0	18	14	ADW79934	Adw79934 Bacterial
C 27	18	100.0	18	14	ADZ88546	Adz88546 Cpg ODN17
C 28	18	100.0	18	14	AEI16552	Aei16552 Cpg immun
C 29	18	100.0	18	14	AEI16552	Aei16552 Cpg immun
C 30	18	100.0	18	14	AEI16552	Aei16552 Cpg immun
C 31	17	94.4	17	2	AAQ86651	AAq86651 Bcl-2 ant
C 32	17	94.4	17	2	ABR90272	ABr90272 Bcl-2 car
C 33	17	94.4	17	2	ABO78530	ABo78530 Antisense
C 34	17	94.4	17	6	ABL54157	ABl54157 Bcl-2 ant
C 35	17	94.4	17	13	ADT93917	ADt93917 Antisense
C 36	17	94.4	17	14	ADW13838	ADw13838 Bcl-2 ant
C 37	16.4	91.1	16	4	AAH48722	AAh48722 Proto-onc
C 38	15	83.3	15	2	AAO86650	AAo86650 Bcl-2 ant
C 39	15	83.3	15	2	AAV28172	AAv28172 Antisense
C 40	15	83.3	15	2	AAH18693	AAh18693 Target bc
C 41	15	83.3	15	2	AAH23684	AAh23684 Deletion
C 42	15	83.3	15	6	ABR90271	ABr90271 Bcl-2 car
C 43	15	83.3	15	6	ABO78529	ABo78529 Antisense
C 44	15	83.3	15	6	ABL54156	ABl54156 Bcl-2 ant
C 45	15	83.3	15	17	ADW13837	ADw13837 Bcl-2 ant
C 46	15	83.3	15	17	ADZ88415	ADz88415 Human bcl
C 47	15	83.3	15	11	ADM36038	Adm36038 Immunost
C 48	15	83.3	15	11	ADM35932	Adm35932 DNA oligo
C 49	15	83.3	15	12	ADQ17851	ADq17851 Human sof
C 50	15	83.3	15	12	ADQ17851	ADq17851 Human sof
C 51	15	83.3	15	12	ADQ17851	ADq17851 Human sof
C 52	15	83.3	15	14	ACL60828	ACl60828 Human col
C 53	15	83.3	15	8	ABT32212	ABt32212 Human neu
C 54	15	83.3	15	8	ABT32212	ABt32212 Human neu
C 55	15	83.3	15	8	ABT32212	ABt32212 Human neu
C 56	15	83.3	15	10	ADP81623	ADp81623 Leukaemia
C 57	15	83.3	15	12	ADQ59204	ADq59204 MSI-H car
C 58	15	83.3	15	12	ADQ22481	ADq22481 Human sof
C 59	14.8	82.2	14	10	AAH27725	AAh27725 Control o
C 60	14.8	82.2	14	10	AAH27725	AAh27725 Control o
C 61	14.8	82.2	14	13	ADX51600	ADx51600 Plant ful
C 62	14.8	82.2	14	11	ADM27081_04	ADM27081_04
C 63	14.4	80.0	14	5	AAH5473	AAh5473 Novel hum
C 64	14.4	80.0	14	4	AAK52279	AAk52279 Human pol
C 65	14.4	80.0	14	6	ABT15959	ABt15959 Aradidops
C 66	14.4	80.0	14	9	ADH02790	ADh02790 Mouse Mat
C 67	14.4	80.0	14	10	ADH73258	ADh73258 Mouse Mat
C 68	14.4	80.0	14	10	ADH73258	ADh73258 Mouse Mat
C 69	14.4	80.0	14	12	ADM74385	ADM74385 Murine ca
C 70	14.4	80.0	14	13	ADR66962	ADR66962 Mouse can
C 71	14.4	80.0	14	14	ADZ12631	ADz12631 Murine ca
C 72	14.4	80.0	14	9	AAQ89779	AAq89779 Cotranspo
C 73	14.4	80.0	14	9	AAQ89779	AAq89779 Cotranspo
C 74	14.4	80.0	14	10	ADH73257	ADh73257 Mouse Mat
C 75	14.4	80.0	14	10	ADH73257	ADh73257 Mouse Mat
C 76	14.4	80.0	14	12	ADM74384	ADM74384 Murine ca
C 77	14.4	80.0	14	14	ADH74389	ADh74389 Mycobacte
C 78	14.4	80.0	14	14	ADH74389	ADh74389 Mycobacte
C 79	14.4	80.0	14	14	ADH74389	ADh74389 Mycobacte
C 80	14.4	80.0	14	14	ADH74389	ADh74389 Mycobacte
C 81	14.4	80.0	14	14	ADH74389	ADh74389 Mycobacte
C 82	14.4	80.0	14	14	ADH74389	ADh74389 Mycobacte
C 83	14.4	80.0	14	14	ADH74389	ADh74389 Mycobacte
C 84	14.4	80.0	14	14	ADH74389	ADh74389 Mycobacte
C 85	14.4	80.0	14	14	ADH74389	ADh74389 Mycobacte
C 86	14.4	80.0	14	14	ADH74389	ADh74389 Mycobacte
C 87	14.4	80.0	14	14	ADH74389	ADh74389 Mycobacte
C 88	14.4	80.0	14	14	ADH74389	ADh74389 Mycobacte
C 89	14.4	80.0	14	14	ADH74389	ADh74389 Mycobacte
C 90	14.4	80.0	14	14	ADH74389	ADh74389 Mycobacte
C 91	14.4	80.0	14	14	ADH74389	ADh74389 Mycobacte
C 92	14.4	80.0	14	14	ADH74389	ADh74389 Mycobacte

C 93	14.4	80.0	133719	3	AAc64754	Macaca mu	C 166	13.8	76.7	2748	11	ABD09800	Abd09800 Pseudomon
C 94	14	77.8	16	14	AA8B28243	Human Bcl	C 167	13.8	76.7	2951	4	ABL14158	ABL14158 Drosophill
C 95	14	77.8	17	2	AA8B66552	AA8B6652 Bcl-2 ant	C 168	13.8	76.7	3506	13	ADW50782	ADW50782 Chinese m
C 96	14	77.8	17	2	AAV28174	AAV28174 Antisense	C 169	13.8	76.7	3768	14	ADXS8500	ADXS8500 SARS coro
C 97	14	77.8	17	2	AAV28173	AAV28173 Antisense	C 170	13.8	76.7	5973	4	ABL17320	ABL17320 Drosophill
C 98	14	77.8	17	2	AAAX18659	AAx18659 Target bc	C 171	13.8	76.7	6497	4	ABL29730	ABL29730 Drosophill
C 99	14	77.8	17	2	AAAX18694	AAx18694 Target bc	C 172	13.8	76.7	6816	6	ABSL6826	ABSL6826 Human T-c
C 100	14	77.8	17	2	AAAX23685	AAx23685 Deletion	C 173	13.8	76.7	6816	6	ABX93560	ABX93560 Human CDN
C 101	14	77.8	17	2	AAAX23686	AAx23686 Deletion	C 174	13.8	76.7	6816	12	ADH69264	ADH69264 Human TCC
C 102	14	77.8	17	6	ABK90273	Bcl-2-car	C 175	13.8	76.7	6855	6	AA516827	AA516827 Human T-t
C 103	14	77.8	17	6	ABK90273	Bcl-2-car	C 176	13.8	76.7	6855	8	ABX93561	ABX93561 Human CDN
C 104	14	77.8	17	6	ABL54158	Bcl-2 ant	C 177	13.8	76.7	6855	12	ADH69266	ADH69266 Human TCC
C 105	14	77.8	17	14	ADM13839	ADM13839 Bcl-2 ant	C 178	13.8	76.7	6866	6	ABL32667	ABL32667 Human tmm
C 106	14	77.8	17	14	ADZ84116	ADz84116 Human bcl	C 179	13.8	76.7	6866	6	ABL49320	ABL49320 Human pol
C 107	14	77.8	17	14	ADZ84117	ADz84117 Human bcl	C 180	13.8	76.7	8346	6	ABK28327	ABK28327 DNA trans
C 108	14	77.8	575	5	AAH56923	P patens	C 181	13.8	76.7	9302	4	AA531567	AA531567 Human DNA
C 109	14	77.8	575	5	AAH56923	P patens	C 182	13.8	76.7	9302	6	AB066891	AB66891 Human pol
C 110	14	77.8	1269	8	ABV77479	Abv77479 A. margin	C 183	13.8	76.7	9302	10	ADCL1178	ADCL1178 Human DNA
C 111	14	77.8	1498	13	ADX29771	Plant ful	C 184	13.8	76.7	9356	14	ABL17322	ABL17322 Drosophill
C 112	14	77.8	1498	13	ADX29771	Plant ful	C 185	13.8	76.7	10016	6	ABL17322	ABL17322 Drosophill
C 113	14	77.8	1498	13	ADX29771	Plant ful	C 186	13.8	76.7	10016	6	ABL17322	ABL17322 Drosophill
C 114	14	77.8	4317	12	ADN11920	Thanaeph	C 187	13.8	76.7	10557	6	AA518240	AA518240 Reference
C 115	14	77.8	4317	14	ADZ10196	Adz10196 Omotetic P	C 188	13.8	76.7	14180	4	ABL17324	ABL17324 Drosophill
C 116	14	77.8	6276	4	ABL29886	Ab129886 Drosophill	C 189	13.8	76.7	15782	14	ACU64631	ACU64631 M. xanthu
C 117	14	77.8	15362	8	ABK59479	ABk59479 Human mus	C 190	13.8	76.7	17082	4	ABSL4164	ABSL4164 Drosophill
C 118	14	77.8	15362	8	ABK59479	ABk59479 Human mus	C 191	13.8	76.7	25617	9	ACCS8256	ACCS8256 Novobiocl
C 119	14	77.8	15362	12	ADJ36029	Adj36029 Human mus	C 192	13.8	76.7	50000	12	ADL14227	ADL14227 Novel hum
C 120	14	77.8	15362	12	ADJ36029	Adj36029 Human mus	C 193	13.8	76.7	50000	12	ADL14227	ADL14227 Novel hum
C 121	14	77.8	15535	8	ABX59478	ABx59478 Human mus	C 194	13.8	76.7	53178	4	AA559543	AA559543 Propionib
C 122	14	77.8	15535	12	ADJ30228	Adj30228 CDNA enco	C 195	13.8	76.7	53178	8	ACRF4442	ACrf44422 Propionib

C 239	13.4	74.4	1358	3	AAc56342	AAc56342	Pinus rad
C 240	13.4	74.4	1368	14	ACI68043	ACI68043	M. xanthu
C 241	13.4	74.4	1401	13	AD548161	AD548161	Bacterial
C 242	13.4	74.4	1407	13	ACI68370	ACI68370	M. xanthu
C 243	13.4	74.4	1408	13	ACN39805	ACN39805	Tumour-as
C 244	13.4	74.4	1416	12	AD085848	AD085848	Human tum
C 245	13.4	74.4	1428	5	AAFP6113	AAFP6113	C. nasrat
C 246	13.4	74.4	1428	5	AAFP6113	AAFP6113	C. nasrat
C 247	13.4	74.4	1429	5	AAFP6110	AAFP6110	C. nasrat
C 248	13.4	74.4	1429	5	AAFP6112	AAFP6112	C. nasrat
C 249	13.4	74.4	1457	11	ADP65711	ADP65711	Human hyp
C 250	13.4	74.4	1457	11	ADP65792	ADP65792	Human CDN
C 251	13.4	74.4	1457	13	ADP25852	ADP25852	Breast ca
C 252	13.4	74.4	1500	2	AAVO1445	AAVO1445	Yeast RFL
C 253	13.4	74.4	1506	2	AAST1041	AAST1041	DNA encod
C 254	13.4	74.4	1506	5	AAAS92403	AAAS92403	DNA encod
C 255	13.4	74.4	1539	11	ACH96634	ACH96634	Klebsiell
C 256	13.4	74.4	1548	3	AAc99952	AAc99952	Human sec
C 257	13.4	74.4	1551	11	ABD06705	ABD06705	Pseudomon
C 258	13.4	74.4	1563	11	ABD17230	ABD17230	Pseudomon
C 259	13.4	74.4	1587	6	ABNS9926	ABNS9926	Novel hum
C 260	13.4	74.4	1684	5	AAAS90724	AAAS90724	DNA encod
C 261	13.4	74.4	1743	5	ABAI9813	ABAI9813	Human ner
C 262	13.4	74.4	1752	10	ADCT2652	ADCT2652	S. lepidop
C 263	13.4	74.4	1762	4	ABLO6501	ABLO6501	Drosophil
C 264	13.4	74.4	1911	6	ABST8674	ABST8674	S. carzin
C 265	13.4	74.4	1911	6	ABST8674	ABST8674	S. carzin
C 266	13.4	74.4	1911	14	ABCI10237	ABCI10237	S. carzin
C 267	13.4	74.4	1914	13	ADT42243	ADT42243	Bacterial
C 268	13.4	74.4	1953	11	ABD17159	ABD17159	Pseudomon
C 269	13.4	74.4	2000	8	ADAT73016	ADAT73016	Rice gene
C 270	13.4	74.4	2000	11	ACI34849	ACI34849	Rice stre
C 271	13.4	74.4	2000	11	ACI37580	ACI37580	Rice stre
C 272	13.4	74.4	2145	12	ADQ64772	ADQ64772	Novel hum
C 273	13.4	74.4	2340	14	AAAS4358	AAAS4358	Pseudomon
C 274	13.4	74.4	2340	8	ACA42750	ACA42750	Prokaryot
C 275	13.4	74.4	2514	14	ADW16799	ADW16799	Pinus rad
C 276	13.4	74.4	2576	8	AA049613	AA049613	Human cyt
C 277	13.4	74.4	2576	8	ACC44326	ACC44326	Gene encod
C 278	13.4	74.4	2655	5	AAFP6114	AAFP6114	C. nasrat
C 279	13.4	74.4	2727	2	AAO65489	AAO65489	Human NMD
C 280	13.4	74.4	2763	13	ADSS7060	ADSS7060	Bacterial
C 281	13.4	74.4	2835	2	AAO65490	AAO65490	Human NMD
C 282	13.4	74.4	2888	4	ABLI16825	ABLI16825	Drosophil
C 283	13.4	74.4	2916	2	AAO66669	AAO66669	Human NMD
C 284	13.4	74.4	3007	2	AAQ79395	AAQ79395	Human NMD
C 285	13.4	74.4	3007	2	AAV82904	AAV82904	Human N-m
C 286	13.4	74.4	3007	3	AAZ38718	AAZ38718	Human NMD
C 287	13.4	74.4	3007	3	AAA95027	AAA95027	Human N-m
C 288	13.4	74.4	3007	6	AB191814	AB191814	Human NMD
C 289	13.4	74.4	3007	6	AA147371	AA147371	Human NMD
C 290	13.4	74.4	3007	6	ABX77675	ABX77675	Human N-m
C 291	13.4	74.4	3007	9	ACD98340	ACD98340	Human NMD
C 292	13.4	74.4	3007	9	ADDS9672	ADDS9672	Human NMD
C 293	13.4	74.4	3007	10	ABX98530	ABX98530	Human N-m
C 294	13.4	74.4	3007	10	ABX92879	ABX92879	Human N-m
C 295	13.4	74.4	3070	2	AAQ79398	AAQ79398	Human N-m
C 296	13.4	74.4	3070	2	AAV82907	AAV82907	N-methyl-
C 297	13.4	74.4	3070	2	AAZ38721	AAZ38721	Human NMD
C 298	13.4	74.4	3070	3	AAAS95030	AAAS95030	Human N-m
C 299	13.4	74.4	3070	6	AB191817	AB191817	Human NMD
C 300	13.4	74.4	3070	6	AA147374	AA147374	Human NMD
C 301	13.4	74.4	3070	6	ABX77678	ABX77678	Human N-m
C 302	13.4	74.4	3070	9	ACD98343	ACD98343	Human NMD
C 303	13.4	74.4	3070	10	ADDS9675	ADDS9675	Human NMD
C 304	13.4	74.4	3070	10	ABX98533	ABX98533	Human N-m
C 305	13.4	74.4	3070	10	ABX92882	ABX92882	Human N-m
C 306	13.4	74.4	3109	6	ABZ53338	ABZ53338	Human gen
C 307	13.4	74.4	3155	2	AAQ79385	AAQ79385	Human N-m
C 308	13.4	74.4	3155	2	AAV82894	AAV82894	Human N-m
C 309	13.4	74.4	3155	3	AAZ38708	AAZ38708	Human NMD
C 310	13.4	74.4	3155	3	AAAS9017	AAAS9017	Human N-m
C 311	13.4	74.4	3155	6	AB1919174	AB1919174	Human NMD
C 312	13.4	74.4	3155	6	AA147361	AA147361	Human NMD
C 313	13.4	74.4	3155	9	ABX77665	ABX77665	Human N-m
C 314	13.4	74.4	3155	10	ACD98330	ACD98330	Human CDN
C 315	13.4	74.4	3155	10	ADDS9662	ADDS9662	Human NMD
C 316	13.4	74.4	3155	10	ABX98520	ABX98520	Human N-m
C 317	13.4	74.4	3155	10	ABX92869	ABX92869	Human N-m
C 318	13.4	74.4	3211	2	AAQ79389	AAQ79389	Human NMD
C 319	13.4	74.4	3211	2	AAV82898	AAV82898	Human NMD
C 320	13.4	74.4	3211	3	AAZ38712	AAZ38712	Human N-m
C 321	13.4	74.4	3211	3	AAAS9021	AAAS9021	Human N-m
C 322	13.4	74.4	3211	6	AB1919178	AB1919178	Human NMD
C 323	13.4	74.4	3211	6	AA147365	AA147365	Human NMD
C 324	13.4	74.4	3211	6	ABX77669	ABX77669	Human N-m
C 325	13.4	74.4	3211	9	ACD98334	ACD98334	Human NMD
C 326	13.4	74.4	3211	10	ADDS9666	ADDS9666	Human NMD
C 327	13.4	74.4	3211	10	ABX98524	ABX98524	Human N-m
C 328	13.4	74.4	3211	10	ABX98524	ABX98524	Human N-m
C 329	13.4	74.4	3211	10	ABX92873	ABX92873	Human N-m
C 330	13.4	74.4	3274	2	AAQ79397	AAQ79397	Human NMD
C 331	13.4	74.4	3274	2	AAV82906	AAV82906	Human N-m
C 332	13.4	74.4	3274	3	AAZ38720	AAZ38720	Human N-m
C 333	13.4	74.4	3274	3	AAA95029	AAA95029	Human N-m
C 334	13.4	74.4	3274	6	AB191816	AB191816	Human NMD
C 335	13.4	74.4	3274	6	AA147373	AA147373	Human NMD
C 336	13.4	74.4	3274	8	ABX77677	ABX77677	Human N-m
C 337	13.4	74.4	3274	9	ACD98342	ACD98342	Human NMD
C 338	13.4	74.4	3274	10	ADDS9674	ADDS9674	Human NMD
C 339	13.4	74.4	3274	10	ABX98532	ABX98532	Human N-m
C 340	13.4	74.4	3351	11	ABD17267	ABD17267	Pseudomon
C 341	13.4	74.4	3428	12	ADQ63985	ADQ63985	Novel hum
C 342	13.4	74.4	3546	4	ABLI12658	ABLI12658	Drosophil
C 343	13.4	74.4	3622	4	ABLI18286	ABLI18286	Drosophil
C 344	13.4	74.4	3657	11	ABD09694	ABD09694	Pseudomon
C 345	13.4	74.4	3663	12	ADJ95524	ADJ95524	Equine he
C 346	13.4	74.4	3731	2	AAV82903	AAV82903	Human NMD
C 347	13.4	74.4	3731	2	AAQ79394	AAQ79394	Human NMD
C 348	13.4	74.4	3731	3	AAZ38717	AAZ38717	Human NMD
C 349	13.4	74.4	3731	3	AAA95026	AAA95026	Human N-m
C 350	13.4	74.4	3731	6	AB191813	AB191813	Human NMD
C 351	13.4	74.4	3731	6	AA147370	AA147370	Human NMD
C 352	13.4	74.4	3731	8	ABX77674	ABX77674	Human NMD
C 353	13.4	74.4	3731	8	ACD98339	ACD98339	Human NMD
C 354	13.4	74.4	3731	10	ADDS9671	ADDS9671	Human NMD
C 355	13.4	74.4	3731	10	ABX98529	ABX98529	Human N-m
C 356	13.4	74.4	3731	10	ABX92878	ABX92878	Human N-m
C 357	13.4	74.4	3750	8	ABX34706	ABX34706	Human mid
C 358	13.4	74.4	3794	2	AAQ79392	AAQ79392	Human NMD
C 359	13.4	74.4	3794	2	AAV82901	AAV82901	N-methyl-
C 360	13.4	74.4	3794	3	AAZ38715	AAZ38715	Human NMD
C 361	13.4	74.4	3794	3	AAA95024	AAA95024	Human N-m
C 362	13.4	74.4	3794	6	AB191811	AB191811	Human NMD
C 363	13.4	74.4	3794	6	AA147368	AA147368	Human NMD
C 364	13.4	74.4	3794	8	ABX77672	ABX77672	Human N-m
C 365	13.4	74.4	3794	9	ACD98337	ACD98337	Human NMD
C 366	13.4	74.4	3794	10	ADDS9669	ADDS9669	Human NMD
C 367	13.4	74.4	3794	10	ABX98527	ABX98527	Human N-m
C 368	13.4	74.4	3794	10	ABX92876	ABX92876	Human N-m
C 369	13.4	74.4	3831	11	ACA42615	ACA42615	Prokaryot
C 370	13.4	74.4	3861	11	ABD09414	ABD09414	Pseudomon
C 371	13.4	74.4	3903	11	ACI27178	ACI27178	Rice abdo
C 372	13.4	74.4	3935	2	AAQ79388	AAQ79388	Human NMD
C 373	13.4	74.4	3935	2	AAV82897	AAV82897	Human N-m
C 374	13.4	74.4	3935	2	AAZ38711	AAZ38711	Human NMD
C 375	13.4	74.4	3935	3	AAA95020	AAA95020	Human N-m
C 376	13.4	74.4	3935	3	AAAS9177	AAAS9177	Human NMD
C 377	13.4	74.4	3935	6	AA147364	AA147364	Human NMD
C 378	13.4	74.4	3935	9	ABX77668	ABX77668	Human N-m
C 379	13.4	74.4	3935	9	ACD98333	ACD98333	Human NMD
C 380	13.4	74.4	3935	10	ADDS9665	ADDS9665	Human NMD
C 381	13.4	74.4	3935	10	ABX98523	ABX98523	Human N-m
C 382	13.4	74.4	3935	10	ABX92872	ABX92872	Human N-m
C 383	13.4	74.4	3998	2	AAQ79396	AAQ79396	Human NMD
C 384	13.4	74.4	3998	2	AAV82905	AAV82905	Human N-m

C 385	13.4	74.4	3998	3	AAZ8719	AAZ8719 Human NMD	458	13.4	74.4	17654	14	ACL64698	ACL64698 M. xanthu
C 386	13.4	74.4	3998	3	AAA55028	AAA55028 Human N-m	C 459	13.4	74.4	22118	8	ADAI4746	ADAI4746 Mouse 45S
C 387	13.4	74.4	3998	6	ABL27162	ABL27162 Drosophila	C 460	13.4	74.4	22118	8	ABX11085	ABX11085 Mouse rib
C 388	13.4	74.4	3998	6	ABI99185	ABI99185 Human NMD	C 461	13.4	74.4	22118	9	ADA37415	ADA37415 Origin of
C 389	13.4	74.4	3998	6	AAI47372	AAI47372 Human NMD	C 462	13.4	74.4	22118	10	AD61410	AD61410 Mouse rib
C 390	13.4	74.4	3998	8	ABX7676	ABX7676 Human N-m	C 463	13.4	74.4	22118	10	ADFI0518	ADFI0518 Mouse rib
C 391	13.4	74.4	3998	9	ACD98341	ACD98341 Human NMD	C 464	13.4	74.4	22118	10	ACCA4629	ACCA4629 Mouse rib
C 392	13.4	74.4	3998	10	AA059673	AA059673 Human NMD	C 465	13.4	74.4	22118	13	ADRA3948	ADRA3948 Mouse pre
C 393	13.4	74.4	3998	10	ABX98531	ABX98531 Human N-m	C 466	13.4	74.4	22118	14	ABE25474	ABE25474 Mouse 45S
C 394	13.4	74.4	3998	10	ABX92880	ABX92880 Human N-m	C 467	13.4	74.4	22115	9	ADA02852	ADA02852 Human CBX
C 395	13.4	74.4	4094	2	AA079393	AA079393 Human NMD	C 468	13.4	74.4	22715	10	ADB72590	ADB72590 Human CBX
C 396	13.4	74.4	4094	2	AA082902	AA082902 Human N-m	C 469	13.4	74.4	22715	10	ADCE8531	ADCE8531 Mouse Cbx
C 397	13.4	74.4	4094	2	AAZ8716	AAZ8716 Human NMD	C 470	13.4	74.4	22715	12	ADM74447	ADM74447 Human car
C 398	13.4	74.4	4094	3	AAA95025	AAA95025 Human N-m	C 471	13.4	74.4	24683	13	ABD33069	ABD33069 Murine ca
C 399	13.4	74.4	4094	6	ABI99182	ABI99182 Human NMD	C 472	13.4	74.4	25733	13	ACL64752	ACL64752 M. xanthu
C 400	13.4	74.4	4094	6	AAI47369	AAI47369 Human NMD	C 473	13.4	74.4	26659	14	ACL64774	ACL64774 M. xanthu
C 401	13.4	74.4	4094	6	ABX7673	ABX7673 Human N-m	C 474	13.4	74.4	26729	9	AAI60439	AAI60439 Human kin
C 402	13.4	74.4	4094	9	ACD98338	ACD98338 Human NMD	C 475	13.4	74.4	28320	14	ACL64759	ACL64759 M. xanthu
C 403	13.4	74.4	4094	10	AA059670	AA059670 Human NMD	C 476	13.4	74.4	28533	11	ACN44308	ACN44308 Mouse gen
C 404	13.4	74.4	4094	10	ABX98528	ABX98528 Human N-m	C 477	13.4	74.4	47670	4	ABLI6824	ABLI6824 Drosophila
C 405	13.4	74.4	4094	10	ABX92877	ABX92877 Human N-m	C 478	13.4	74.4	50368	4	ABLI6768	ABLI6768 Drosophila
C 406	13.4	74.4	4157	2	AA079391	AA079391 Human NMD	C 479	13.4	74.4	65952	12	ADQ59527	ADQ59527 Human can
C 407	13.4	74.4	4157	2	AA082900	AA082900 Human N-m	C 480	13.4	74.4	66009	14	ADZ13908	ADZ13908 Murine ca
C 408	13.4	74.4	4157	3	AAZ8714	AAZ8714 Human NMD	C 481	13.4	74.4	67674	12	ADP81772	ADP81772 Human MD-
C 409	13.4	74.4	4157	3	AAA95023	AAA95023 Human N-m	C 482	13.4	74.4	70583	9	AAI60437	AAI60437 Human kin
C 410	13.4	74.4	4157	6	ABI99180	ABI99180 Human NMD	C 483	13.4	74.4	71887	11	ACNA4950	ACNA4950 Human gen
C 411	13.4	74.4	4157	6	AAI47367	AAI47367 Human NMD	C 484	13.4	74.4	103765	4	AAI99683_43	AAI99683_43 Continuation (44 o
C 412	13.4	74.4	4157	8	ABX7671	ABX7671 Human N-m	C 485	13.4	74.4	110000	12	ADN46845_07	ADN46845_07 Continuation (14 o
C 413	13.4	74.4	4157	9	ACD98336	ACD98336 Human NMD	C 486	13.4	74.4	110000	12	ADN47591_13	ADN47591_13 Continuation (14 o
C 414	13.4	74.4	4157	10	AA059668	AA059668 Human NMD	C 487	13.4	74.4	110000	12	ADN47591_13	ADN47591_13 Continuation (14 o
C 415	13.4	74.4	4157	10	ABX98526	ABX98526 Human N-m	C 488	13.4	74.4	110000	12	ADN46123_07	ADN46123_07 Continuation (14 o
C 416	13.4	74.4	4157	10	ABX92875	ABX92875 Human N-m	C 489	13.4	74.4	110000	12	ADN47209_13	ADN47209_13 Continuation (14 o
C 417	13.4	74.4	4158	11	ABD06744	ABD06744 Pseudomon	C 490	13.4	74.4	110000	12	ADN46464_07	ADN46464_07 Continuation (14 o
C 418	13.4	74.4	4287	13.4	ABL06500	ABL06500 Drosophila	C 491	13.4	74.4	110000	12	ADN47960_13	ADN47960_13 Continuation (14 o
C 419	13.4	74.4	4298	2	AA079370	AA079370 Human N-m	C 492	13.4	74.4	149158	12	ADP74211	ADP74211 Equine he
C 420	13.4	74.4	4298	2	AA082867	AA082867 Human N-m	C 493	13.4	74.4	149261	12	ADP74212	ADP74212 Equine he
C 421	13.4	74.4	4298	3	AAZ8701	AAZ8701 Human NMD	C 494	13.4	74.4	150071	12	ADP74216	ADP74216 Equine he
C 422	13.4	74.4	4298	3	AAA95010	AAA95010 Human N-m	C 495	13.4	74.4	150223	12	ADP74201	ADP74201 Equine he
C 423	13.4	74.4	4298	6	ABI99167	ABI99167 Human NMD	C 496	13.4	74.4	309400	5	AAH68534	AAH68534 C. glutam
C 424	13.4	74.4	4298	6	AAI47354	AAI47354 Human NMD	C 497	13.2	73.3	25	ACI81324	ACI81324 Human mtc	
C 425	13.4	74.4	4298	8	ABX7658	ABX7658 DNA encod	C 498	13.2	73.3	29	AAQ3869	AAQ3869 Sequence	
C 426	13.4	74.4	4298	9	ACD98323	ACD98323 Human CDN	C 499	13.2	73.3	54	AAQ47266	AAQ47266 Lactate d	
C 427	13.4	74.4	4298	9	AA059655	AA059655 Human NMD	C 500	13.2	73.3	100	ACD77872	ACD77872 E. coli X	
C 428	13.4	74.4	4298	10	ABX98513	ABX98513 Human N-m	C 501	13.2	73.3	100	ACD77871	ACD77871 E. coli K	
C 429	13.4	74.4	4298	10	ABX92862	ABX92862 Human N-m	C 502	13.2	73.3	100	ABQ84336	ABQ84336 DPPIII gen	
C 430	13.4	74.4	4361	2	AA079390	AA079390 Human NMD	C 503	13.2	73.3	100	ABQ84337	ABQ84337 DPPIII gen	
C 431	13.4	74.4	4361	2	AA082899	AA082899 Human N-m	C 504	13.2	73.3	125	AACT10486	AACT10486 Human sec	
C 432	13.4	74.4	4361	3	AAZ8713	AAZ8713 Human NMD	C 505	13.2	73.3	192	ADP91968	ADP91968 Novel S.	
C 433	13.4	74.4	4361	3	AAA95022	AAA95022 Human N-m	C 506	13.2	73.3	192	ABAS5838	ABAS5838 Streptoco	
C 434	13.4	74.4	4361	6	ABI99179	ABI99179 Human NMD	C 507	13.2	73.3	197	AA664683	AA664683 DNA encod	
C 435	13.4	74.4	4361	6	AAI47366	AAI47366 Human NMD	C 508	13.2	73.3	197	AA688140	AA688140 DNA encod	
C 436	13.4	74.4	4361	8	ABX7670	ABX7670 Human N-m	C 509	13.2	73.3	197	AA688994	AA688994 DNA encod	
C 437	13.4	74.4	4361	9	ACD98335	ACD98335 Human NMD	C 510	13.2	73.3	197	AA667026	AA667026 DNA encod	
C 438	13.4	74.4	4361	10	AA059667	AA059667 Human NMD	C 511	13.2	73.3	197	AA680086	AA680086 DNA encod	
C 439	13.4	74.4	4361	10	ABX98525	ABX98525 Human N-m	C 512	13.2	73.3	206	ABQ84298	ABQ84298 Human DPP	
C 440	13.4	74.4	4361	10	ABX92874	ABX92874 Human N-m	C 513	13.2	73.3	327	ABK76591	ABK76591 Bacillus	
C 441	13.4	74.4	4494	14	ACL71069	ACL71069 M. xanthu	C 514	13.2	73.3	330	ABK79782	ABK79782 Bacillus	
C 442	13.4	74.4	4599	2	AA070131	AA070131 NMDAR1-1	C 515	13.2	73.3	380	ADV78134	ADV78134 Zoogloea	
C 443	13.4	74.4	4599	2	AA099964	AA099964 Human exc	C 516	13.2	73.3	387	ABX36272	ABX36272 Human sec	
C 444	13.4	74.4	4599	2	ABX94241	ABX94241 cDNA encod	C 517	13.2	73.3	394	ABX88139	ABX88139 DNA encod	
C 445	13.4	74.4	4663	6	ABX53058	ABX53058 cDNA encod	C 518	13.2	73.3	394	AA684682	AA684682 DNA encod	
C 446	13.4	74.4	5022	11	ABD06623	ABD06623 Pseudomon	C 519	13.2	73.3	394	AA667025	AA667025 DNA encod	
C 447	13.4	74.4	5022	12	AA099970	AA099970 Human exc	C 520	13.2	73.3	400	ACF05800	ACF05800 Streptoco	
C 448	13.4	74.4	5636	8	AA659561	AA659561 Propionib	C 521	13.2	73.3	400	ADO49127	ADO49127 S. pneumo	
C 449	13.4	74.4	5636	8	ACF64490	ACF64490 Propionib	C 522	13.2	73.3	402	AA657353	AA657353 S. pneumo	
C 450	13.4	74.4	6600	14	ABLI6769	ABLI6769 Drosophila	C 523	13.2	73.3	402	AA657356	AA657356 S. pneumo	
C 451	13.4	74.4	6988	14	ACI64270	ACI64270 M. xanthu	C 524	13.2	73.3	414	ACH94487	ACH94487 Klebsiell	
C 452	13.4	74.4	7282	10	ACC49359	ACC49359 Human NMI	C 525	13.2	73.3	418	AACT6880	AACT6880 Human ORF	
C 453	13.4	74.4	7796	3	AAAC64578	AAAC64578 T. gondii	C 526	13.2	73.3	426	AAAC43330	AAAC43330 Arabidops	
C 454	13.4	74.4	8663	5	AAAC30133	AAAC30133 Human lun	C 527	13.2	73.3	426	AAH65562	AAH65562 C. glutam	
C 455	13.4	74.4	8663	10	ADB33470	ADB33470 Human nov	C 528	13.2	73.3	468	ACA000019	ACA000019 C. glutam	
C 456	13.4	74.4	16387	14	ACI64653	ACI64653 M. xanthu	C 529	13.2	73.3	474	ADP92657	ADP92657 Cotton ex	
C 457	13.4	74.4	17384	10	ACC44721	ACC44721 Cosmid pf	C 530	13.2	73.3	490	ABV10781	ABV10781 Human pro	

531	13.2	73.3	505	9	ACH34904	ACH34904 Human end	c 604	13.2	73.3	1542	13	ADR65495	ADR65495 Aspergill
532	13.2	73.3	506	6	ABK77059	ABK77059 Bacillus	c 605	13.2	73.3	1550	12	AD116275	AD116275 Human nuc
533	13.2	73.3	512	6	ABQ44041	ABQ44041 Oligonuc	c 606	13.2	73.3	1590	11	ACH94615	ACH94615 Klebsiell
534	13.2	73.3	512	6	ABQ44040	ABQ44040 Oligonuc	c 607	13.2	73.3	1591	13	ACH8435	ACH8435 Arabidops
535	13.2	73.3	514	6	ABQ18920	ABQ18920 Oligonuc	c 608	13.2	73.3	1611	12	ADQ23250	ADQ23250 Human sof
536	13.2	73.3	514	6	ABQ18921	ABQ18921 Oligonuc	c 609	13.2	73.3	1617	5	AA930364	AA930364 DNA encod
537	13.2	73.3	521	12	ADQ18372	ADQ18372 Human sof	c 610	13.2	73.3	1668	15	AA669002	AA669002 DNA encod
538	13.2	73.3	525	6	ABQ39241	ABQ39241 Oligonuc	c 611	13.2	73.3	1668	14	ADM16710	ADM16710 Buncalyptu
539	13.2	73.3	525	6	ABQ39240	ABQ39240 Oligonuc	c 612	13.2	73.3	1682	13	ADR64908	ADR64908 Aspergill
540	13.2	73.3	531	12	ACH72965	ACH72965 Human gen	c 613	13.2	73.3	1702	6	ADD33055	ADD33055 Human bec
541	13.2	73.3	543	8	ABZ36885	ABZ36885 Human GEN	c 614	13.2	73.3	1756	6	ABV23578	ABV23578 Human pro
542	13.2	73.3	552	11	ABD10266	ABD10266 Pseudomon	c 615	13.2	73.3	1779	8	ACA25210	ACA25210 Prokaryot
543	13.2	73.3	577	6	ABQ43770	ABQ43770 Oligonuc	c 616	13.2	73.3	1815	12	ADJ62773	ADJ62773 Human CDN
544	13.2	73.3	577	6	ABQ43771	ABQ43771 Oligonuc	c 617	13.2	73.3	1815	14	ADZ80550	ADZ80550 Syntaxin
545	13.2	73.3	589	6	ABQ46551	ABQ46551 Oligonuc	c 618	13.2	73.3	1854	13	ADT44511	ADT44511 Bacterial
546	13.2	73.3	589	6	ABQ46550	ABQ46550 Oligonuc	c 619	13.2	73.3	1867	6	ABE67923	ABE67923 Ovary can
547	13.2	73.3	621	5	ABV53182	ABV53182 Human pro	c 620	13.2	73.3	1867	6	ABK83449	ABK83449 Human CDN
548	13.2	73.3	624	10	ADK59637	ADK59637 Plant DNA	c 621	13.2	73.3	1883	5	AA669005	AA669005 DNA encod
549	13.2	73.3	629	4	AAK58047	AAK58047 Human imm	c 622	13.2	73.3	1888	9	ACE25366	ACE25366 Human eyrn
550	13.2	73.3	629	4	AAK58047	AAK58047 Human cDN	c 623	13.2	73.3	1901	5	AA682469	AA682469 DNA encod
551	13.2	73.3	637	12	ADD43160	ADD43160 Plant CDN	c 624	13.2	73.3	1928	13	ADR98766	ADR98766 Lung spec
552	13.2	73.3	647	13	ADRI5017	ADRI5017 Rat elect	c 625	13.2	73.3	1944	14	ADW64698	ADW64698 Gluconace
553	13.2	73.3	647	14	ABE47944	ABE47944 Rat growt	c 626	13.2	73.3	1965	14	ACT172528	ACT172528 M. xanthu
554	13.2	73.3	666	6	ABQ49000	ABQ49000 Oligonuc	c 627	13.2	73.3	1970	6	ABQ81544	ABQ81544 Gene up-r
555	13.2	73.3	666	6	ABQ49001	ABQ49001 Oligonuc	c 628	13.2	73.3	1981	4	ABU17135	ABU17135 Drosophi
556	13.2	73.3	667	6	ABT07870	ABT07870 Human lun	c 629	13.2	73.3	2000	8	ADA71568	ADA71568 Rice gene
557	13.2	73.3	690	10	ADP00829	ADP00829 Bacterial	c 630	13.2	73.3	2044	13	ADS48703	ADS48703 Bacterial
558	13.2	73.3	714	3	AAK45660	AAK45660 Arabidops	c 631	13.2	73.3	2059	10	ADBS8542	ADBS8542 Toxicity-
559	13.2	73.3	715	3	AAK33148	AAK33148 Arabidops	c 632	13.2	73.3	2059	10	ADBS3150	ADBS3150 Primary r
560	13.2	73.3	716	3	AAK52027	AAK52027 Arabidops	c 633	13.2	73.3	2099	13	ADVA1338	ADVA1338 Rat cardi
561	13.2	73.3	740	3	AAAT9339	AAAT9339 Buncalyptu	c 634	13.2	73.3	2155	10	ADCO8395	ADCO8395 Rice DNA
562	13.2	73.3	752	5	AA94177	AA94177 DNA encod	c 635	13.2	73.3	2155	10	ADCO8342	ADCO8342 Rice DNA
563	13.2	73.3	773	4	AAK57140	AAK57140 Human imm	c 636	13.2	73.3	2212	5	AA667036	AA667036 DNA encod
564	13.2	73.3	774	5	AA91490	AA91490 DNA encod	c 637	13.2	73.3	2297	2	AAV63562	AAV63562 DNA encod
565	13.2	73.3	780	14	ADV78127	ADV78127 Zoolgoea	c 638	13.2	73.3	2297	4	AAE24904	AAE24904 Nucleoicd
566	13.2	73.3	786	6	ABQ22326	ABQ22326 Oligonuc	c 639	13.2	73.3	2298	2	AAZ32678	AAZ32678 Human ves
567	13.2	73.3	786	6	ABQ22327	ABQ22327 Oligonuc	c 640	13.2	73.3	2322	5	AAE78441	AAE78441 Corynebac
568	13.2	73.3	814	5	AA588148	AA588148 DNA encod	c 641	13.2	73.3	2338	5	AAO40408	AAO40408 Rice phen
569	13.2	73.3	815	8	ACR23777	ACR23777 Prokaryot	c 642	13.2	73.3	2413	5	AA930357	AA930357 DNA encod
570	13.2	73.3	844	12	ADI82274	ADI82274 Human DNA	c 643	13.2	73.3	2427	13	ADS46097	ADS46097 Bacterial
571	13.2	73.3	845	2	AAV83887	AAV83887 Promoter	c 644	13.2	73.3	2504	4	AAQ87446	AAQ87446 Triboiliu
572	13.2	73.3	882	11	ABD10373	ABD10373 Pseudomon	c 645	13.2	73.3	2646	12	ADO57328	ADO57328 DNA encod
573	13.2	73.3	900	5	AA588147	AA588147 DNA encod	c 646	13.2	73.3	2650	14	ABE51127	ABE51127 Pseudomon
574	13.2	73.3	940	8	ABZ52514	ABZ52514 Aspergill	c 647	13.2	73.3	2684	4	ABU04951	ABU04951 Drosophi
575	13.2	73.3	994	6	ABQ32082	ABQ32082 Oligonuc	c 648	13.2	73.3	2747	4	ABU10709	ABU10709 Drosophi
576	13.2	73.3	994	6	ABQ32083	ABQ32083 Oligonuc	c 649	13.2	73.3	2987	4	ABR08622	ABR08622 Human str
577	13.2	73.3	1020	4	ABU101888	ABU101888 Human rep	c 650	13.2	73.3	3002	11	ABE86037	ABE86037 DNA damag
578	13.2	73.3	1020	4	ABU97181	ABU97181 Human tee	c 651	13.2	73.3	3077	10	ADBS8072	ADBS8072 Rat gene
579	13.2	73.3	1023	12	ADM36193	ADM36193 Candida a	c 652	13.2	73.3	3077	10	ADBS8068	ADBS8068 Rat gene
580	13.2	73.3	1032	3	AAK38509	AAK38509 Arabidops	c 653	13.2	73.3	3319	5	AA664698	AA664698 DNA encod
581	13.2	73.3	1035	6	ABQ40400	ABQ40400 Oligonuc	c 654	13.2	73.3	3321	5	AA585592	AA585592 DNA encod
582	13.2	73.3	1035	6	ABQ40401	ABQ40401 Oligonuc	c 655	13.2	73.3	3367	2	AAV63191	AAV63191 CDNA fctm
583	13.2	73.3	1036	6	ABQ45043	ABQ45043 Oligonuc	c 656	13.2	73.3	3367	6	ABQ92041	ABQ92041 Human pol
584	13.2	73.3	1036	6	ABQ45042	ABQ45042 Oligonuc	c 657	13.2	73.3	3369	2	AAV52175	AAV52175 Streptoco
585	13.2	73.3	1044	8	ACR48211	ACR48211 Prokaryot	c 658	13.2	73.3	3420	13	ADBS5852	ADBS5852 Bacterial
586	13.2	73.3	1079	6	ABQ27779	ABQ27779 Oligonuc	c 659	13.2	73.3	3558	10	ADBS6087	ADBS6087 C. neofo
587	13.2	73.3	1079	6	ABQ27778	ABQ27778 Oligonuc	c 660	13.2	73.3	3777	6	ADD33048	ADD33048 Human bec
588	13.2	73.3	1098	5	AA580090	AA580090 DNA encod	c 661	13.2	73.3	3789	14	ADX02206	ADX02206 Human cod
589	13.2	73.3	1101	4	AA565186	AA565186 Salmonell	c 662	13.2	73.3	3794	5	AA593067	AA593067 Human encod
590	13.2	73.3	1101	8	ACA52127	ACA52127 Prokaryot	c 663	13.2	73.3	3800	2	AAK28141	AAK28141 CCoAOMT p
591	13.2	73.3	1119	3	ADBS56810	ADBS56810 Bacterial	c 664	13.2	73.3	3800	3	AAZ60808	AAZ60808 Nucleoicd
592	13.2	73.3	1131	10	ADT75855	ADT75855 DNA homol	c 665	13.2	73.3	3907	10	ADBS6088	ADBS6088 C. neofo
593	13.2	73.3	1215	2	AAV04470	AAV04470 Gallus ga	c 666	13.2	73.3	3921	13	ADU01914	ADU01914 Novel hum
594	13.2	73.3	1215	9	ACF06116	ACF06116 Bacterial	c 667	13.2	73.3	4237	5	AA586660	AA586660 DNA encod
595	13.2	73.3	1269	13	ADBS55410	ADBS55410 Bacterial	c 668	13.2	73.3	4268	4	AA667040	AA667040 DNA encod
596	13.2	73.3	1272	13	AD849896	AD849896 Bacterial	c 669	13.2	73.3	4340	5	ABU17134	ABU17134 Drosophi
597	13.2	73.3	1315	5	AA664693	AA664693 DNA encod	c 670	13.2	73.3	4746	4	AAK52577	AAK52577 Human pol
598	13.2	73.3	1357	13	ADP17063	ADP17063 plant cDN	c 671	13.2	73.3	4860	5	AA584894	AA584894 DNA encod
599	13.2	73.3	1434	5	AA665653	AA665653 DNA encod	c 672	13.2	73.3	4874	6	AB878711	AB878711 Human CDN
600	13.2	73.3	1434	5	AA666659	AA666659 DNA encod	c 673	13.2	73.3	4927	6	AB878720	AB878720 Human CDN
601	13.2	73.3	1434	5	AA663062	AA663062 DNA encod	c 674	13.2	73.3	4986	4	ABU10708	ABU10708 Drosophi
602	13.2	73.3	1452	13	ADBS58692	ADBS58692 Bacterial	c 675	13.2	73.3	5093	10	ADBS5876	ADBS5876 Primary r
603	13.2	73.3	1539	10	ABZ40437	ABZ40437 N. gonorr	c 676	13.2	73.3	5197	4	AAK71813	AAK71813 Human imm

677	13.2	73.3	5197	4	AAI62920	Adi13520 Human can	c 750	13.2	72.3	170506	14	ADZ13520	Adi13520 Human can
678	13.2	73.3	5891	6	ABNL3439	Adt05874 Cercopit	c 751	13.2	72.3	171096	13	ADT05874	Adt05874 Cercopit
679	13.2	73.3	6089	6	ABN80255	Adg97957 Human che	c 752	13.2	72.3	191284	12	ADG97957	Adg97957 Human che
c 680	13.2	73.3	7682	13	ADMR4321	Adc44331 Aspergill	c 753	13.2	73.3	227448	13	ADM4321	Adm4321 Aspergill
681	13.2	73.3	10607	13	ADM27018	Adc44331 Aspergill s	754	13.2	73.3	339734	12	ADM27018	Adm27018 Aspergill s
682	13.2	73.3	10682	14	ACR64497	Abi164497 M. xanthu	755	13.2	73.3	339234	14	ADM27018	Adm27018 Aspergill s
683	13.2	73.3	13154	4	ABLI19201	Abi19201 Drosophill	756	13.2	73.3	349980	5	AAH68525	AAH68525 C glutam
c 684	13.2	73.3	13836	5	ABLA16631	Abal16631 Human ner	c 757	13.2	72.2	20	2	AAH68525	AAH68525 C glutam
c 685	13.2	73.3	14417	4	AAK87584	AAK87584 Human imm	c 758	13	72.2	20	2	AAH68525	AAH68525 C glutam
c 686	13.2	73.3	14417	4	AAK87586	AAK87586 Human imm	c 759	13	72.2	20	2	AAH68525	AAH68525 C glutam
c 687	13.2	73.3	14417	4	AAK73113	AAK73113 Human imm	c 760	13	72.2	20	2	AAH68525	AAH68525 C glutam
c 688	13.2	73.3	14417	4	AAK73113	AAK73113 Human imm	c 761	13	72.2	20	2	AAH68525	AAH68525 C glutam
c 689	13.2	73.3	14417	8	AAI62923	AAI62923 Human gen	c 762	13	72.2	20	2	AAH68525	AAH68525 C glutam
c 690	13.2	73.3	14417	10	ABZ74674	Abz74674 Secreted	c 763	13	72.2	20	10	AAH68525	AAH68525 C glutam
c 691	13.2	73.3	14426	4	AAK87586	AAK87586 Human imm	c 764	13	72.2	20	13	AAH68525	AAH68525 C glutam
c 692	13.2	73.3	14426	4	AAK73099	AAK73099 Human imm	c 765	13	72.2	20	13	AAH68525	AAH68525 C glutam
c 693	13.2	73.3	14426	4	AAK87568	AAK87568 Human imm	c 766	13	72.2	20	14	AAH68525	AAH68525 C glutam
c 694	13.2	73.3	14426	4	AAK71817	AAK71817 Human imm	c 767	13	72.2	228	13	AAH68525	AAH68525 C glutam
c 695	13.2	73.3	14426	4	AAK85290	AAK85290 Human imm	c 768	13	72.2	228	13	AAH68525	AAH68525 C glutam
c 696	13.2	73.3	14426	4	AAK85290	AAK85290 Human imm	c 769	13	72.2	234	6	AAH68525	AAH68525 C glutam
c 697	13.2	73.3	14426	4	AAK73115	AAK73115 Human imm	c 770	13	72.2	849	5	AAH68525	AAH68525 C glutam
c 698	13.2	73.3	14426	4	AAI62921	AAI62921 Human gen	c 771	13	72.2	972	4	AAH68525	AAH68525 C glutam
c 699	13.2	73.3	14426	4	AAI62924	AAI62924 Human gen	c 772	13	72.2	1335	5	AAH68525	AAH68525 C glutam
c 700	13.2	73.3	14426	8	ABZ74676	Abz74676 Secreted	c 773	13	72.2	1608	8	AAH68525	AAH68525 C glutam
c 701	13.2	73.3	14426	8	ABZ74673	Abz74673 Secreted	c 774	13	72.2	1617	8	AAH68525	AAH68525 C glutam
c 702	13.2	73.3	14426	10	ABZ68198	Abz68198 Human sec	c 775	13	72.2	1902	6	AAH68525	AAH68525 C glutam
c 703	13.2	73.3	14426	10	ABZ68195	Abz68195 Human sec	c 776	13	72.2	1905	13	AAH68525	AAH68525 C glutam
c 704	13.2	73.3	14448	4	AAK71815	AAK71815 Human imm	c 777	13	72.2	2019	6	AAH68525	AAH68525 C glutam
c 705	13.2	73.3	14448	4	AAK87580	AAK87580 Human imm	c 778	13	72.2	2160	10	AAH68525	AAH68525 C glutam
c 706	13.2	73.3	14448	4	AAK73111	AAK73111 Human imm	c 779	13	72.2	2160	10	AAH68525	AAH68525 C glutam
c 707	13.2	73.3	14448	4	AAI62922	AAI62922 Human gen	c 780	13	72.2	2160	10	AAH68525	AAH68525 C glutam
c 708	13.2	73.3	14451	4	AAK73116	AAK73116 Human imm	c 781	13	72.2	3083	2	AAH68525	AAH68525 C glutam
c 709	13.2	73.3	14451	4	AAK71818	AAK71818 Human imm	c 782	13	72.2	3285	4	AAH68525	AAH68525 C glutam
c 710	13.2	73.3	14451	4	AAK87587	AAK87587 Human imm	c 783	13	72.2	3612	4	AAH68525	AAH68525 C glutam
c 711	13.2	73.3	14451	4	AAI62925	AAI62925 Human gen	c 784	13	72.2	3612	13	AAH68525	AAH68525 C glutam
c 712	13.2	73.3	16680	4	ABLI19202	Abli19202 Drosophill	c 785	13	72.2	6324	2	AAH68525	AAH68525 C glutam
c 713	13.2	73.3	16680	4	ABLI19202	Abli19202 Drosophill	c 786	13	72.2	10095	2	AAH68525	AAH68525 C glutam
c 714	13.2	73.3	20188	12	ADN33950	Adn33950 Human CDN	c 787	13	72.2	31328	3	AAH68525	AAH68525 C glutam
c 715	13.2	73.3	20190	10	ADCT1539	Adct1539 Human NOV	c 788	13	72.2	36292	13	AAH68525	AAH68525 C glutam
c 716	13.2	73.3	20190	12	ADQ42304	Adq42304 Human NOV	c 789	13	72.2	36292	13	AAH68525	AAH68525 C glutam
c 717	13.2	73.3	22129	4	AAAS59632	AAAS59632 Proplonib	c 790	13	72.2	36412	10	AAH68525	AAH68525 C glutam
c 718	13.2	73.3	22129	8	ACF64561	Acf64561 Proplonib	c 791	13	72.2	76363	12	AAH68525	AAH68525 C glutam
c 719	13.2	73.3	22612	13	ADM67003	Adm67003 Mouse can	c 792	13	72.2	76363	12	AAH68525	AAH68525 C glutam
c 720	13.2	73.3	22612	14	ADZ12852	Adz12852 Murline ca	c 793	13	72.2	76363	12	AAH68525	AAH68525 C glutam
c 721	13.2	73.3	30390	8	AAAS59520	AAAS59520 Proplonib	c 794	13	72.2	76363	12	AAH68525	AAH68525 C glutam
c 722	13.2	73.3	30390	8	ACF64449	Acf64449 Proplonib	c 795	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 723	13.2	73.3	33303	3	AAAB1514	AAAB1514 N. mening	c 796	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 724	13.2	73.3	45265	2	AAZ46508	AAZ46508 Sequence	c 797	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 725	13.2	73.3	49999	2	AAZ23902	AAZ23902 Human LOB	c 798	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 726	13.2	73.3	51837	13	ABD33453	Abd33453 Human can	c 799	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 727	13.2	73.3	54929	11	AAAS59436	AAAS59436 Mouse gen	c 800	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 728	13.2	73.3	56050	11	AAAS59436	AAAS59436 Mouse gen	c 801	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 729	13.2	73.3	56050	8	ACF64478	Acf64478 Proplonib	c 802	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 730	13.2	73.3	57137	11	ACN44300	Acn44300 Mouse gen	c 803	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 731	13.2	73.3	58540	11	ACN44640	Acn44640 Mouse gen	c 804	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 732	13.2	73.3	71292	11	ACN45142	Acn45142 Human gen	c 805	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 733	13.2	73.3	71292	11	ACN45142	Acn45142 Human gen	c 806	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 734	13.2	73.3	104644	6	ABOQ9653	Abog9653 Human MS4	c 807	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 735	13.2	73.3	110000	4	AAAB1489_0	AAAB1489 N. mening	c 808	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 736	13.2	73.3	110000	4	AAI99682_20	AAI99682_20 Human gen	c 809	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 737	13.2	73.3	110000	8	ABX16390_4	ABX16390_4 Human gen	c 810	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 738	13.2	73.3	110000	10	ABSS6454_02	ABSS6454_02 Human gen	c 811	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 739	13.2	73.3	110000	11	ADM27081_15	ADM27081_15 Human gen	c 812	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 740	13.2	73.3	110000	11	ADM27081_15	ADM27081_15 Human gen	c 813	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 741	13.2	73.3	110000	11	ACN44150_2	ACN44150_2 Human gen	c 814	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 742	13.2	73.3	110000	13	ABD3267_0	ABD3267_0 Mouse can	c 815	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 743	13.2	73.3	123230	11	ACN44816	Acn44816 Mouse can	c 816	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 744	13.2	73.3	123230	14	ACN44816	Acn44816 Mouse can	c 817	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 745	13.2	73.3	128668	11	ACN44074	Acn44074 Murline ca	c 818	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 746	13.2	73.3	131680	10	ADP29092	ADP29092 Human gen	c 819	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 747	13.2	73.3	135005	12	ADQ19501	Adq19501 Human eof	c 820	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 748	13.2	73.3	135005	12	ADP67269	Adp67269 Human chr	c 821	13	72.2	103599	4	AAH68525	AAH68525 C glutam
c 749	13.2	73.3	170489	13	ABD33314	Abd33314 Human can	c 822	13	72.2	103599	4	AAH68525	AAH68525 C glutam

C 823	12.8	71.1	243	8	ABZ56063	Abz56063	Apergill	C 896	12.8	71.1	583	6	ABQ55663	AbQ55663	Human ova
C 824	12.8	71.1	244	4	AAK53931	Aak53931	Murine re	C 897	12.8	71.1	583	10	ACA10301	AcA10301	Rice leaf
C 825	12.8	71.1	251	2	AAK12443	Aak12443	Human bia	C 898	12.8	71.1	583	13	ADU53415	AdU53415	Pseudomon
C 826	12.8	71.1	254	3	AACT0110	Aac10110	Human sec	C 899	12.8	71.1	583	14	ADZ91418	AdZ91418	Fusarium
C 827	12.8	71.1	276	6	ABN17900	Abn17900	Human ORF	C 900	12.8	71.1	585	6	ABQ36158	AbQ36158	Oligonucle
C 828	12.8	71.1	287	10	ABX8742	Abx8742	Corn ear-	C 901	12.8	71.1	585	6	ABQ36159	AbQ36159	Oligonucle
C 829	12.8	71.1	289	2	AAH87219	Aah87219	Human ear-	C 902	12.8	71.1	589	6	ABK54739	AbK54739	Human col
C 830	12.8	71.1	293	10	ABX8989	Abx8989	Corn ear-	C 903	12.8	71.1	594	6	ABQ49814	AbQ49814	Oligonucle
C 831	12.8	71.1	300	2	AAK98239	Aak98239	Human ear-	C 904	12.8	71.1	594	6	ABQ49815	AbQ49815	Oligonucle
C 832	12.8	71.1	303	12	ADK64500	Adk64500	Human cat	C 905	12.8	71.1	595	14	ADY98049	AdY98049	Fungal IT
C 833	12.8	71.1	315	13	ADQ18669	Adq18669	Cotton CD	C 906	12.8	71.1	597	6	ABN16686	AbN16686	Human ORF
C 834	12.8	71.1	319	5	AD175465	Ad175465	Human ova	C 907	12.8	71.1	597	13	ADQ53310	AdQ53310	Novel can
C 835	12.8	71.1	319	5	AD169118	Ad169118	Human ova	C 908	12.8	71.1	599	14	ADY98052	AdY98052	Fungal IT
C 836	12.8	71.1	343	6	ABN77427	Abn77427	Human ORF	C 909	12.8	71.1	601	6	ABQ50119	AbQ50119	Oligonucle
C 837	12.8	71.1	347	6	ABN22254	Abn22254	Human ORF	C 910	12.8	71.1	601	6	ABQ50118	AbQ50118	Oligonucle
C 838	12.8	71.1	352	4	AAH22400	Aah22400	Human rac	C 911	12.8	71.1	607	6	ABQ54458	AbQ54458	Human ova
C 839	12.8	71.1	365	2	AAV70847	Aav70847	Sequence	C 912	12.8	71.1	609	4	AAU00402	AAU00402	Human rep
C 840	12.8	71.1	378	7	ADG31202	Adg31202	Human gen	C 913	12.8	71.1	609	4	ABA07480	ABa07480	Human ova
C 841	12.8	71.1	378	7	ADY36590	Ady36590	HTRA gene	C 914	12.8	71.1	629	6	ABQ98527	AbQ98527	Human ORF
C 842	12.8	71.1	382	3	AAAT72782	Aa72782	5.8S rRNA	C 915	12.8	71.1	646	4	AAH06561	AAH06561	Human ORF
C 843	12.8	71.1	387	3	AAH30645	Aah30645	Human col	C 916	12.8	71.1	660	4	AB1022323	AB1022323	Human CDN
C 844	12.8	71.1	389	14	ADK25718	Adk25718	Novel cel	C 917	12.8	71.1	660	5	ABV37051	ABV37051	Human pro
C 845	12.8	71.1	390	8	ACA25967	Ac25967	Prokaryot	C 918	12.8	71.1	660	6	ABQ39008	AbQ39008	Oligonucle
C 846	12.8	71.1	390	8	ACA23244	Ac23244	Prokaryot	C 919	12.8	71.1	660	6	ABQ33847	AbQ33847	Oligonucle
C 847	12.8	71.1	397	3	ACG98648	Acg98648	Human col	C 920	12.8	71.1	660	6	ABQ39009	AbQ39009	Oligonucle
C 848	12.8	71.1	402	6	ABN75080	Abn75080	Human ORF	C 921	12.8	71.1	660	6	ABQ33846	AbQ33846	Oligonucle
C 849	12.8	71.1	405	5	ABN13625	Abn13625	Human ner	C 922	12.8	71.1	672	14	ADY98023	AdY98023	Fungal IT
C 850	12.8	71.1	405	5	ABN19982	Abn19982	Human ner	C 923	12.8	71.1	675	4	AAH51989	AAH51989	Human pro
C 851	12.8	71.1	411	8	ACA00388	Ac00388	C. glutam	C 924	12.8	71.1	676	14	ADY98020	AdY98020	Fungal IT
C 852	12.8	71.1	411	5	AAH61611	Aah61611	C. glutam	C 925	12.8	71.1	682	6	ABQ14059	AbQ14059	Oligonucle
C 853	12.8	71.1	414	3	ACG98274	Acg98274	Human col	C 926	12.8	71.1	682	6	ABQ14058	AbQ14058	Oligonucle
C 854	12.8	71.1	414	3	AAAC28334	Aac28334	Human sec	C 927	12.8	71.1	701	2	ABT22310	ABT22310	Breast ca
C 855	12.8	71.1	427	5	ABV07110	Abv07110	Human pro	C 928	12.8	71.1	734	6	ABQ26163	AbQ26163	Oligonucle
C 856	12.8	71.1	432	8	AAQ48961	Aaq48961	Human met	C 929	12.8	71.1	734	6	ABQ26162	AbQ26162	Oligonucle
C 857	12.8	71.1	435	14	ACL70921	ACL70921	M. xanthu	C 930	12.8	71.1	735	11	ABD16493	ABD16493	Pseudomon
C 858	12.8	71.1	459	9	AAZ16771	Aaz16771	Human adu	C 931	12.8	71.1	751	6	ABQ18300	AbQ18300	Oligonucle
C 859	12.8	71.1	476	2	ACX14573	Acx14573	Human gen	C 932	12.8	71.1	751	6	ABQ18301	AbQ18301	Oligonucle
C 860	12.8	71.1	484	13	ACN52654	Acn52654	Cotton an	C 933	12.8	71.1	752	10	ADCI3584	ADCI3584	Human NOV
C 861	12.8	71.1	485	6	ABH83718	Abh83718	Human ova	C 934	12.8	71.1	762	13	ADCI3586	ADCI3586	Human NOV
C 862	12.8	71.1	486	9	ACH15331	Ach15331	Human adu	C 935	12.8	71.1	763	13	ADSB8607	ADSB8607	Human hou
C 863	12.8	71.1	492	12	ACH87023	ACH87023	Human gen	C 936	12.8	71.1	763	13	ADU60286	ADu60286	Housekeep
C 864	12.8	71.1	493	12	ACH94062	ACH94062	Human gen	C 937	12.8	71.1	771	13	ADT43154	ADT43154	Bacterial
C 865	12.8	71.1	494	9	ACH37883	Ach37883	Human end	C 938	12.8	71.1	784	6	ABQ37285	AbQ37285	Oligonucle
C 866	12.8	71.1	499	5	ABV11655	Abv11655	Human pro	C 939	12.8	71.1	784	6	ABQ37284	AbQ37284	Oligonucle
C 867	12.8	71.1	507	3	AAFI6380	Aafi6380	Human pro	C 940	12.8	71.1	785	10	ADF28876	ADF28876	Human nor
C 868	12.8	71.1	510	6	ABQ42192	Abq42192	Oligonucle	C 941	12.8	71.1	786	8	AC04819	AC04819	CDNA ento
C 869	12.8	71.1	510	6	ABQ42193	Abq42193	Oligonucle	C 942	12.8	71.1	795	4	AAI23802	AAI23802	Human bre
C 870	12.8	71.1	511	6	ABX93641	Abx93641	New asper	C 943	12.8	71.1	795	4	AAH07870	AAH07870	Human CDN
C 871	12.8	71.1	513	12	ACH73293	Ach73293	Human gen	C 944	12.8	71.1	813	11	ACL29508	ACL29508	Rice abio
C 872	12.8	71.1	526	13	ADU12508	Adu12508	Solid tum	C 945	12.8	71.1	845	6	ABQ22604	AbQ22604	Oligonucle
C 873	12.8	71.1	526	14	ABE53260	Abe53260	Human pro	C 946	12.8	71.1	845	6	ABQ22605	AbQ22605	Oligonucle
C 874	12.8	71.1	528	6	ABQ44954	Abq44954	Oligonucle	C 947	12.8	71.1	852	10	ACF67588	ACF67588	Photornab
C 875	12.8	71.1	528	6	ABQ44955	Abq44955	Oligonucle	C 948	12.8	71.1	858	5	AA577901	AA577901	DNA encod
C 876	12.8	71.1	535	12	ACH80362	ACH80362	Human gen	C 949	12.8	71.1	867	4	AAI02813	AAI02813	Human rep
C 877	12.8	71.1	537	14	ACL66935	ACL66935	M. xanthu	C 950	12.8	71.1	881	13	ADX31657	ADX31657	Human ste
C 878	12.8	71.1	538	6	ABQ49665	Abq49665	Oligonucle	C 951	12.8	71.1	886	8	ACC57556	ACC57556	Human ste
C 879	12.8	71.1	538	6	ABQ49664	Abq49664	Oligonucle	C 952	12.8	71.1	900	2	ART71596	ART71596	Mycobacte
C 880	12.8	71.1	540	4	AAI00061	Aai00061	Human rep	C 953	12.8	71.1	900	10	AAU59705	AAU59705	M. tuberc
C 881	12.8	71.1	551	3	AACT6609	Aac6609	Human ORF	C 954	12.8	71.1	900	13	ADU64256	ADU64256	Mycobacte
C 882	12.8	71.1	552	12	ADQ24957	Adq24957	Human sof	C 955	12.8	71.1	918	11	ABDI6236	ABDI6236	Pseudomon
C 883	12.8	71.1	555	4	AAI02812	Aai02812	Human rep	C 956	12.8	71.1	924	11	ACL27592	ACL27592	Rice abio
C 884	12.8	71.1	562	6	ABQ52559	Abq52559	Oligonucle	C 957	12.8	71.1	942	13	ADR12609	ADR12609	Gene vacc
C 885	12.8	71.1	562	6	ABQ52558	Abq52558	Oligonucle	C 958	12.8	71.1	952	2	AAV63923	AAV63923	Mycobacte
C 886	12.8	71.1	569	6	ABQ21069	Abq21069	Oligonucle	C 959	12.8	71.1	952	2	AAH81026	AAH81026	Nucleotid
C 887	12.8	71.1	569	6	ABQ21068	Abq21068	Oligonucle	C 960	12.8	71.1	967	6	ABQ42625	AbQ42625	Oligonucle
C 888	12.8	71.1	573	6	ABQ23260	Abq23260	Oligonucle	C 961	12.8	71.1	967	6	ABQ42624	AbQ42624	Oligonucle
C 889	12.8	71.1	573	6	ABQ23261	Abq23261	Oligonucle	C 962	12.8	71.1	970	2	AAZ41416	AAZ41416	Human nor
C 890	12.8	71.1	573	12	ADJ39109	Adj39109	Plant CDN	C 963	12.8	71.1	971	6	ABQ16240	ABQ16240	Oligonucle
C 891	12.8	71.1	577	10	ADD13732	Add13732	C. glutam	C 964	12.8	71.1	971	6	ABQ16241	ABQ16241	Oligonucle
C 892	12.8	71.1	578	10	ABT22373	ABT22373	Breast ca	C 965	12.8	71.1	976	6	ABK93132	ABK93132	DNA seque
C 893	12.8	71.1	579	6	ABQ42902	Abq42902	Oligonucle	C 966	12.8	71.1	993	11	ABD03398	ABD03398	Pseudomon
C 894	12.8	71.1	579	6	ABQ42903	Abq42903	Oligonucle	C 967	12.8	71.1	996	14	ADZ75692	ADZ75692	Xanthomon
C 895	12.8	71.1	583	3	AAFO9374	Aaf09374	Fusarium	C 968	12.8	71.1	999	12	ADQ85696	ADQ85696	Human tum

C 969	12.8	71.1	999	13	ADG86772	Human tum
C 970	12.8	71.1	999	13	ADG82260	Plant ful
C 971	12.8	71.1	1008	6	ABL61976	Colon ade
C 972	12.8	71.1	1008	10	ADG76529	Novel hum
C 973	12.8	71.1	1010	4	AA160629	Novel hum
C 974	12.8	71.1	1010	13	ADG97395	Human pol
C 975	12.8	71.1	1015	4	AA158843	Human pol
C 976	12.8	71.1	1015	5	ADG99064	DNA encod
C 977	12.8	71.1	1015	4	ADG48824	Novel hum
C 978	12.8	71.1	1018	3	AA188922	Human bre
C 979	12.8	71.1	1020	11	AD131337	Human CDN
C 980	12.8	71.1	1020	13	ADG83404	Human lym
C 981	12.8	71.1	1023	8	ACA25958	Prokaryot
C 982	12.8	71.1	1043	14	ADG49508	Insulin s
C 983	12.8	71.1	1047	5	AA585011	DNA encod
C 984	12.8	71.1	1047	10	ADG53767	Alcohol d
C 985	12.8	71.1	1047	12	AD188257	Corynebac
C 986	12.8	71.1	1047	14	ADG69576	Corynebac
C 987	12.8	71.1	1047	14	AC167776	M. xanthu
C 988	12.8	71.1	1052	14	ADG62795	Human CDN
C 989	12.8	71.1	1052	14	ADG15209	DNA encod
C 990	12.8	71.1	1052	14	ADG49144	Insulin s
C 991	12.8	71.1	1065	14	AC173167	M. xanthu
C 992	12.8	71.1	1069	11	AC127795	Rice abio
C 993	12.8	71.1	1084	6	ABQ47759	Oligonuc
C 994	12.8	71.1	1084	6	ABQ47758	Oligonuc
C 995	12.8	71.1	1103	3	AA18132	Lung canc
C 996	12.8	71.1	1123	6	ABQ38699	Oligonuc
C 997	12.8	71.1	1123	6	ABQ38698	Oligonuc
C 998	12.8	71.1	1152	12	ADG46685	DNA encod
C 999	12.8	71.1	1155	6	ABQ94237	FL011 gen
C 1000	12.8	71.1	1158	6	AA138737	Coryneb

ALIGNMENTS

RESULT 1
AAV52546/c
ID AAV52546 standard; DNA, 18 BP.

AC AAV52546;
DT 20-NOV-1998 (first entry)

XX Unmethylated CpG dinucleotide 1761.

XX Unmethylated CpG dinucleotide; immune response; bacterial meningitis;
XX natural killer cell activation; NK cell; Th2 response; neonatal sepsis;
XX pulmonary disorder; asthma; environmentally induced airway disease;
XX bacterial infection; endotoxaemia; therapy; cystic fibrosis;
XX inflammatory bowel disease; ss.

OS Synthetic.
XX WO9837919-A1.
XX 03-SEP-1998.
XX 25-FEB-1998; 98WO-US003678.
XX 28-FEB-1997; 97US-0039405P.
XX (IOWA) UNIV IOWA RES FOUND.
XX Schwartz DA, Krieg AM;
XX WPI; 1998-480941/41.
XX Use of nucleic acids containing an unmethylated CpG - for treating a
XX subject having or at risk of having an acute decrement in air flow or
XX inhibiting an inflammatory response.

PS Example 4; Page 35; 65pp; English.
XX This sequence represents an unmethylated CpG dinucleotide, and can be
CC having, in the method of the invention. The method is for treating a subject
CC using, or at risk of having an acute decrement in air flow, comprising
CC administering a nucleic acid sequence containing at least one
CC unmethylated CpG. The nucleic acid contains an unmethylated CpG
CC dinucleotide affect an immune response in a subject by activating natural
CC killer cells (NK) or redirecting a subject's immune response from a Th2
CC to a Th1 response by inducing monocytic and other cells to produce Th1
CC cytokines. They can be used to treat pulmonary disorders having an
CC immunologic component, such as asthma or environmentally induced airway
CC disease. They can also be used to treat diseases associated with Gram-
CC positive bacterial infections or endotoxaemia including bacterial
CC meningitis, neonatal sepsis, cystic fibrosis, inflammatory bowel disease
CC and liver cirrhosis, Gram-negative pneumonia, Gram-negative abdominal
CC abscesses, haemorrhagic shock, disseminated intravascular coagulation, or
CC an inflammatory response to lipopolysaccharide

SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 88.9%; Pred. No. 10;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGCGCGACCGGTA 18
DB 18 AGAGGCGCGACCGGTA 1

RESULT 2
AAV27720/c
ID AAV27720 standard; DNA, 18 BP.

AC AAV27720;
DT 01-OCT-1998 (first entry)

XX Immunostimulatory oligodeoxyribonucleotide of the invention.

XX Immunostimulatory; oligodeoxyribonucleotide; ODN;
XX unmethylated CpG dinucleotide; activate; lymphocyte; immune response;
XX Th2; cytokine; treatment; prevention; asthma; autoimmune disease;
XX desensitisation therapy; artificial adjuvant; antibody generation; ss.

OS Synthetic.
XX WO9818810-A1.
XX 07-MAY-1998.
XX 30-OCT-1997; 97WO-US019791.
XX 30-OCT-1996; 96US-00738652.

XX (IOWA) UNIV IOWA RES FOUND.

XX Krieg AM, Kline JN;
XX WPI; 1998-272127/24.

XX New immunostimulatory nucleic acid molecules - which contain at least one
XX unmethylated CpG dinucleotide, used for treating e.g. tumours, infections
XX or autoimmune disease.

PS Disclosure; Page 49; 109pp; English.

XX AAV27641-751 represent immunostimulatory oligodeoxyribonucleotides (ODNs)
XX of the invention. The ODNs contain at least one unmethylated CpG
XX dinucleotide, and have the formula: 5' N1X1CGX2N2 3', where at least one
XX nucleotide separates consecutive CpGs, N1 is adenine, guanine, or
XX thymine, X2 is cytosine or thymine, N2 is any nucleotide and N1+N2 is 0-26
XX bases with the provision that N1 and N2 does not contain a CCGG tetramer

CC or more than one CCG or CCG trimer OR 5' NX1X2CGX3X4N 3', where at least
 CC one nucleotide separates consecutive Cpgs, X1 and X2 are selected from
 CC GpT, GpC, GpA, ApgT and ApgA, X3 and X4 are selected from Tpt or Cpt, N is
 CC any nucleotide and NXN2 is 0-26 bases with the provision that N1 and N2
 CC does not contain a CCGG tetramer or more than one CCG or CCG trimer. The
 CC ODNs activate lymphocytes in a subject and redirect a subject's immune
 CC response from a Th2 to a Th1 (e.g. by inducing monocyte cells and other
 CC cells to produce Th1 cytokines, including IL-12, IFN-gamma and GM-CSF).
 CC The ODNs can be used to treat or prevent an asthmatic disorder,
 CC autoimmune diseases, in desensitisation therapy, as an artificial
 CC adjuvant during antibody generation in a mammal such as a mouse or a
 CC human

SO Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 18;
 Best Local Similarity 88.9%; Pred. No. 10;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGGCACGCGGUA 18
 |||||:|||||:|
 DB 18 AGAGGUGGCACGCGGUA 1

RESULT 3

AAZ41906/C
 ID AAZ41906 standard; DNA; 18 BP.

AC AAZ41906;

DT 24-JAN-2000 (first entry)

DE IL-12 secretion inducing Cpg oligonucleotide 51.

KW Cpg oligonucleotide; phosphorothioate; interleukin-12; IL-12; secretion;
 KW human PMBC; immune response; cancer; HIV; bacterial disease; asthma;
 KW neoplastic disorder; jaagsiekte; B cell; NK cell; ss; cytokine;
 KW antigen presenting cell; infection; allergic disease.

OS Synthetic.

PN WO951259-A2.

PD 14-OCT-1999.

PF 02-APR-1999; 99WO-US007335.

PR 03-APR-1999; 98US-0080729P.

PA (IOWA) UNIV IOWA RES FOUND.

PI Kriegl AM, Welner G;

WPI; 1999-620169/53.

PT Novel synergistic combinations of immunostimulatory oligonucleotides and
 PT immunopotentiating cytokines are useful for stimulating the immune
 PT system.

PS Example 8; Page 80; 91pp; English.

CC Sequences AAZ41856-241949 are phosphorothioate Cpg oligonucleotides which
 CC are used in the invention to induce interleukin-12 (IL-12) secretion from
 CC human PMBC. The invention comprises stimulating an immune response in a
 CC subject comprising administering to a subject exposed to an antigen, an
 CC immunopotentiating cytokine and an immunostimulatory Cpg oligonucleotide
 CC to induce a synergistic antigen specific immune response. The methods are
 CC useful for treating cancer by stimulating an antigen specific immune
 CC response against a cancer antigen. The methods can also be used to treat
 CC neoplastic disorders in humans, including but not limited to: sarcoma,
 CC carcinoma, fibroma, lymphoma, melanoma, neuroblastoma, retinoblastoma,
 CC and glioma. The methods are also useful for treating infectious diseases,
 CC e.g. viral diseases such as HIV, bacterial diseases, and fungal diseases.

CC The methods may also be used to treat allergic diseases, e.g. asthma. The
 CC methods and compositions may also be applied to treat cancer and tumours
 CC in non human subjects, e.g. cats and dogs. Neoplasias affecting
 CC agricultural livestock may also be treated and include leukaemia,
 CC haemangioepithelioma and bovine ocular neoplasia. Chronic, infectious,
 CC contagious diseases of sheep and goats caused by the bacterium
 CC Corynebacterium pseudotuberculosis, and contagious lung tumour of sheep
 CC caused by jaagsiekte may also be treated. Cpg oligonucleotides can be
 CC useful in activating B cells, NK cells, and antigen presenting cells,
 CC such as monocytes and macrophages. Cpg oligonucleotides enhance antibody
 CC dependent cellular cytotoxicity and can be used as an adjuvant in
 CC conjunction with tumour antigens to protect against a tumour challenge

SO Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 18;
 Best Local Similarity 88.9%; Pred. No. 10;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGGCACGCGGUA 18
 |||||:|||||:|
 DB 18 AGAGGUGGCACGCGGUA 1

RESULT 4

AAZ47982/C
 ID AAZ47982 standard; DNA; 18 BP.

AC AAZ47982;

DT 08-MAR-2000 (first entry)

DE Immune remodeling inducing Cpg oligonucleotide SEQ ID NO:60.

KW Haematopoiesis; regulation; Cpg oligonucleotide; phosphorothioate;
 KW immune remodeling; thrombopoiesis; anaemia; immune system; cancer;
 KW immune response; allergic reaction; infectious disease; asthma;
 KW thrombocytopaenia; immunohaemolytic disorder; genetic disorder;
 KW haemoglobinopathy; kidney failure; chronic inflammatory disorder;
 KW rheumatoid arthritis; ss.

OS Synthetic.

PN WO9558118-A2.

PD 18-NOV-1999.

PF 14-MAY-1999; 99WO-1B001285.

PR 14-MAY-1999; 98US-0085516P.

PR 02-FEB-1999; 99US-00241653.

PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

PA (CPGI-) CPG IMMUNOPHARMACEUTICALS INC.

PI Wagner H, Lipford G;

WPI; 2000-062261/05.

PT Use of Cpg containing oligonucleotides for, e.g. inducing an antigen-
 PT specific immune response.

PS Example 1; Page 66; 116pp; English.

CC The present invention describes a method using Cpg containing
 CC oligonucleotides (ONs) for regulating immune system remodeling and for
 CC regulating haematopoiesis. The method for inducing an antigen-specific
 CC immune response comprises: (1) administering an ON having a sequence
 CC including at least the formula (1), and (2) exposing the subject to an
 CC antigen at least 3 days after the ON is administered to the subject to
 CC produce an antigen-specific immune response; 5' X1CGX2 3' (1), where the
 CC ON = includes at least 8 nucleotides; C and G = unmethylated, and X1 and
 CC X2 = nucleotides. The method can be used for inducing an immune response

CC against an antigen such as cells, cell extracts, proteins,
CC polyaccharides, polyaccharide conjugates, lipids, glycolipids,
CC carbohydrate, viral extracts, viruses, bacteria, fungi, parasites and
CC allergens. It can be used in a subject at risk of developing cancer or an
CC allergic reaction. It can also be used for treating an infectious
CC disease, allergic diseases and asthma, as well as thrombocytopaenia which
CC is drug-induced, due to an autoimmune disorder such as idiopathic
CC thrombocytopenic purpura, or resulting from accidental or therapeutic
CC radiation exposure. It can also be used for treating anaemia such as drug
CC -induced anaemia, immunohaemolytic disorder, genetic disorders such as
CC haemoglobinopathy and inherited haemolytic anaemia, inadequate production
CC despite adequate iron stores, chronic disease such as kidney failure, and
CC chronic inflammatory disorder such as rheumatoid arthritis, or anaemia
CC resulting from accidental or therapeutic radiation exposure. AA247932 to
CC AA248029 represent phosphorothioate Cpg oligonucleotides used in the
CC exemplification of the present invention

SO Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 88.9%; Pred. No. 10;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGUGCGACGCGGTA 1

RESULT 5
ID AA247644 standard; DNA; 18 BP.
AC AA247644;
XX
XX
DT 01-MAR-2000 (first entry)
XX
XX
DB Parasitic infection preventing exemplary oligonucleotide SEQ ID NO:50.
XX
XX
KW Immune system; immunostimulatory; parasitic infection; parasite;
KW Cpg oligonucleotide; antigen presenting cell; natural killer cell;
KW granulocyte; malaria; helminth disease; tick; mite; ss.
XX
XX
OS Synthetic.
XX
XX
PN MO956755-A1.
XX
XX
PD 11-NOV-1999.
XX
XX
PF 06-MAY-1999; 99MO-US009863.
XX
XX
PR 06-MAY-1998; 98US-0084512P.
XX
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (OTTA-) OTTAWA CIVIC LOEB RES INST.
PA (USNA) US SEC OF NAVY.
XX
XX
PI Gramzinski RA, Krieg AM, Davis HU, Hoffman SL;
XX
XX
DR WPI; 2000-062123/05.
XX
XX
PT Treating and preventing parasitic infections using Cpg oligonucleotides.
XX
XX
PS Disclosure; Page 20; 74pp; English.
XX
XX
CC The present invention describes a method for treating and preventing
CC parasitic infection by administration of unmethylated Cpg
CC oligonucleotides. The Cpg oligonucleotides are able to stimulate the
CC innate immune system via the activation of immune cells, such as antigen
CC presenting cells, natural killer cells and granulocytes. The Cpg
CC oligonucleotides and the method can be used to treat and prevent
CC parasitic diseases, such as malaria, helminth diseases, tick and mites in
CC humans, animals and poultry. The oligonucleotides may be administered in
CC conjunction with parasitocides or other therapeutic compounds after an

CC organism has been diagnosed to be infected with parasites. Diseases which
CC can be treated or prevented include those caused by Plasmodium
CC falciparum, P. ovale, P. malariae, P. vivax, P. knowlesi, Babesia
CC microti, B. divergens, Trypanosoma cruzi, T. gambiense, T. rhodesiense,
CC Schistosoma mansoni, Toxoplasma gondii, Trichinella spiralis, Leishmania
CC major, L. donovani, L. braziliensis, and L. tropica. The parasite is
CC especially capable of causing malaria. The present sequence represents a
CC parasitic infection preventing exemplary oligonucleotide sequence from
CC the present invention

SO Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 88.9%; Pred. No. 10;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGUGCGACGCGGTA 1

RESULT 6
ID AAH50628 standard; DNA; 18 BP.
AC AAH50628;
XX
XX
DT 22-AUG-2001 (first entry)
XX
XX
DB Natural killer cell lytic activity inducing oligonucleotide SEQ ID NO:60.
XX
XX
KW Immunostimulatory; inducing; natural killer cell; lytic activity;
KW unmethylated Cpg dinucleotide; immune response; B cell proliferation;
KW Th1; immune activation; interleukin 6; IL-6; interferon gamma; IFN-gamma;
KW cytokine; ss.
XX
XX
OS Homo sapiens.
XX
XX
OS Synthetic.
XX
XX
PN US6239116-B1.
XX
XX
PD 29-MAY-2001.
XX
XX
PF 30-OCT-1997; 97US-00960774.
XX
XX
PR 30-OCT-1996; 96US-00738652.
XX
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEBY PHARM GROUP INC.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX
PI Krieg AM, Kline JN;
XX
XX
DR WPI; 2001-380456/40.
XX
XX
PT Methods for inducing IL-6, interferon-gamma or IL-12, or stimulating
PT natural killer cell lytic activity in a human, comprise administering to
PT the subject or exposing a natural killer cell to immunostimulatory
PT nucleic acids.
XX
XX
PS Disclosure; Col 32; 74pp; English.
XX
XX
XX
CC The present invention describes methods for inducing interleukin 6 (IL-
CC 6), interferon-gamma (IFN-gamma) or IL-12, or for stimulating natural
CC killer cell lytic activity. The methods comprise administering to the
CC subject or exposing a natural killer cell to an immunostimulatory nucleic
CC acid. Also described are: (1) inducing IL-6 in a subject comprising
CC administering to the subject to induce IL-6 in the subject the
CC immunostimulatory nucleic acid; (2) stimulating natural killer cell lytic
CC activity comprising exposing a natural killer cell to the
CC immunostimulatory nucleic acid to stimulate natural killer cell lytic
CC activity; (3) inducing interferon-gamma in a subject to treat an immune
CC system deficiency comprising administering to the subject to induce

CC interferon-gamma production, the immunostimulatory nucleic acid; and (4)
 CC inducing IL-12 in a subject comprising administering to the subject the
 CC immunostimulatory nucleic acid. The methods are useful for inducing IL-6,
 CC interferon-gamma or IL-12, or stimulating natural killer cell lytic
 CC activity in a subject, particularly a human. The methods are particularly
 CC useful for modulating an immune response. AAH50571 to AAH50671 represent
 CC oligonucleotide sequences used in the exemplification of the present
 CC invention
 CC
 XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 18; DB 4; Length 18;
 Best Local Similarity 88.9%; Pred. No. 10;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGAGGUGCGCAGCGGUA 18
 DB 18 AGAGGUGCGCAGCGGUA 1
 RESULT 7
 AAF98931/c
 ID AAF98931 standard; DNA; 18 BP.
 AC AAF98931;
 XX
 XX 12-JUN-2001 (first entry)
 DT
 XX Immunostimulatory nucleic acid #47.
 DE
 XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
 KW immunostimulatory; tumour; viral infection; bacterial infection;
 KW fungal infection; parasitic infection; cancer; asthma;
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
 XX
 XX Synthetic.
 XX WO200122972-A2.
 PN
 XX 05-APR-2001.
 PD
 XX 25-SEP-2000; 2000MO-US026383.
 PF
 XX 25-SEP-1999; 99US-015613P.
 PR 27-SEP-1999; 99US-015613P.
 PR 23-AUG-2000; 2000US-0227436P.
 XX
 PA (IOWA) UNITV IOWA RES FOUND.
 PA (COLE-) COLEY PHARM GMBH.
 XX
 PI Krieg AM, Schetter C, Vollmer J;
 PI
 XX WPI; 2001-273485/28.
 DR
 XX
 XX Vaccinating against tumors, infectious diseases, allergies and asthma
 PT using immunostimulatory Py-rich and TG nucleic acids.
 PS
 XX Disclosure; Page 39; 338pp; English.
 PS
 XX The present invention relates to a method for stimulating an immune
 CC response. The method comprises administering an immunostimulatory nucleic
 CC acid to a non-rodent subject in sufficient quantity to stimulate an
 CC immune response. The present sequence is one such immunostimulatory
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
 CC also useful for preventing cancer, asthma, infectious disease, allergy or
 CC immune deficiency. The present sequence can also be used to redirect a
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the
 CC present sequence may have a phosphorothioate backbone

XX
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 4; Length 18;
 Best Local Similarity 88.9%; Pred. No. 10;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGAGGUGCGCAGCGGUA 18
 DB 18 AGAGGUGCGCAGCGGUA 1
 RESULT 8
 AAF98888/c
 ID AAF98888 standard; DNA; 18 BP.
 AC AAF98888;
 XX
 XX 12-JUN-2001 (first entry)
 DT
 XX Immunostimulatory nucleic acid #4.
 DE
 XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
 KW immunostimulatory; tumour; viral infection; bacterial infection;
 KW fungal infection; parasitic infection; cancer; asthma;
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
 XX
 XX Synthetic.
 XX WO200122972-A2.
 PN
 XX 05-APR-2001.
 PD
 XX 25-SEP-2000; 2000MO-US026383.
 PF
 XX 25-SEP-1999; 99US-015613P.
 PR 27-SEP-1999; 99US-015613P.
 PR 23-AUG-2000; 2000US-0227436P.
 XX
 PA (IOWA) UNITV IOWA RES FOUND.
 PA (COLE-) COLEY PHARM GMBH.
 XX
 PI Krieg AM, Schetter C, Vollmer J;
 PI
 XX WPI; 2001-273485/28.
 DR
 XX
 XX Vaccinating against tumors, infectious diseases, allergies and asthma
 PT using immunostimulatory Py-rich and TG nucleic acids.
 PS
 XX Disclosure; Page 38; 338pp; English.
 PS
 XX The present invention relates to a method for stimulating an immune
 CC response. The method comprises administering an immunostimulatory nucleic
 CC acid to a non-rodent subject in sufficient quantity to stimulate an
 CC immune response. The present sequence is one such immunostimulatory
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
 CC also useful for preventing cancer, asthma, infectious disease, allergy or
 CC immune deficiency. The present sequence can also be used to redirect a
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the
 CC present sequence may have a phosphorothioate backbone
 SQ
 Query Match 100.0%; Score 18; DB 4; Length 18;
 Best Local Similarity 88.9%; Pred. No. 10;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGAGGUGCGCAGCGGUA 18

Db 18 AGAGGCTCGACGCGGTA 1

RESULT 9

ABST77572/C
ID ABST77572 standard; DNA; 18 BP.

AC ABS77572;

DT 13-DEC-2002 (first entry)

XX Angiogenesis inhibitory oligonucleotide #56.

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KM tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KM diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KM corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KM rubecosis; Osler-Webber Syndrome; myocardial angiogenesis;
KM plaque neovascularisation; telangiectasia; haemophilic joint;
KM angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KM scleroderma; hypertrophic scar.

XX Synthetic.

PN WO200253141-A2.

PD 11-JUL-2002.

PF 14-DEC-2001; 2001WO-US048458.

PR 14-DEC-2000; 2000US-0255534P.

PA (COLE-) COLEY PHARM GROUP INC.

PI Bratzler RL;

DR WPI; 2002-566690/60.

XX Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.

PS Claim 2; Page 20; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubecosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 18;

Best Local Similarity 88.9%; Pred. No. 10;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGCTCGACGCGGTA 18
DB 18 AGAGGCTCGACGCGGTA 1

RESULT 10

ABST77520/C
ID ABST77520 standard; DNA; 18 BP.

XX ABS77520;

DT 13-DEC-2002 (first entry)

XX Angiogenesis inhibitory oligonucleotide #4.

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KM tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KM diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KM corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KM rubecosis; Osler-Webber Syndrome; myocardial angiogenesis;
KM plaque neovascularisation; telangiectasia; haemophilic joint;
KM angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KM scleroderma; hypertrophic scar.

XX Synthetic.

PN WO200253141-A2.

PD 11-JUL-2002.

PF 14-DEC-2001; 2001WO-US048458.

PR 14-DEC-2000; 2000US-0255534P.

PA (COLE-) COLEY PHARM GROUP INC.

PI Bratzler RL;

DR WPI; 2002-566690/60.

XX Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.

PS Claim 2; Page 19; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubecosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 18;

Best Local Similarity 88.9%; Pred. No. 10;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGCTCGACGCGGTA 18
DB 18 AGAGGCTCGACGCGGTA 1

RESULT 11

ABL39077/C
ID ABL39077 standard; DNA; 18 BP.

AC ABL39077;

DT 16-APR-2002 (first entry)

XX Immunostimulatory nucleic acid SEQ ID NO: 485.

XX 15-UTL-1994; 94US-00276358.
 PR 07-FEB-1995; 95US-00386063.
 PR 30-OCT-1996; 96US-00738652.
 PR 30-OCT-1997; 97US-00960774.
 XX (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Krieg AM, Hartmann G;
 DR WPI; 2002-689667/74.
 XX
 PT Activating a dendritic cell for cancer immunotherapy or for treating
 PT infectious or allergy disease, by contacting a dendritic cell with an
 PT isolated nucleic acid containing at least one unmethylated CpG
 PT dinucleotide.
 XX
 PS Example 6; Col 32; 52pp; English.
 XX
 CC This invention relates to a novel method for activating or causing
 CC maturation of a dendritic cell. The method comprises contacting a
 CC dendritic cell with an isolated nucleic acid containing at least one
 CC unmethylated CpG dinucleotide in an amount effective to activate or cause
 CC maturation of the dendritic cell, where the activation is performed ex
 CC vivo. The method of the invention may have cytostatic or antiallergic
 CC activities. The method of the invention is useful for cancer
 CC immunotherapy or for treating an infectious disease or allergy, by
 CC administering an activated dendritic cell that expresses a specific cancer,
 CC microbial or allergy causing antigen, to a subject having a cancer
 CC including the cancer antigen, to a subject having an infection with a
 CC microorganism including the microbial antigen or to a subject having an
 CC allergic reaction to the allergy causing antigen, where the activated
 CC dendritic cell is prepared using the method of the invention. The method
 CC is useful for generating a high yield of dendritic cells by administering
 CC an isolated nucleic acid containing at least one unmethylated CpG
 CC dinucleotide, where the nucleic acid is 8-80 bases in length in an amount
 CC effective to activate the dendritic cells to a subject, and isolating
 CC dendritic cells from the subject. The use of CpG allows the generation of
 CC mature dendritic cells from peripheral blood within two days in a well
 CC defined system. The application of CpG for this purpose is superior to
 CC granulocyte macrophage-colony stimulating factor (GM-CSF), which is
 CC currently used for this purpose. CpG oligonucleotides have a longer half
 CC life, are less expensive, and show a greater magnitude of immune effects.
 CC The present sequence represents a CpG oligonucleotide used in the method
 CC of the invention
 CC
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
 CC
 Query Match 100.0%; Score 18; DB 6; Length 18;
 Best Local Similarity 88.9%; Pred. No. 10;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGAGGCGCGACGCGGUA 18
 Db |||||:|||||:|||||:
 18 AGAGGCGCGACGCGGTA 1
 RESULT 14
 ACD99318/c
 ID ACD99318 standard; DNA; 18 BP.
 AC ACD99318;
 XX
 DT 25-SEP-2003 (first entry)
 XX
 DE Immunostimulatory nucleic acid #4.
 XX
 KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
 KW anticancer; gene therapy; vaccine; non-allergic inflammatory disease;
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
 XX
 XX Synthetic.

XX US2003050268-A1.
 PN
 XX 13-MAR-2003.
 PD
 XX 29-MAR-2002; 2002US-00112653.
 XX
 XX 29-MAR-2001; 2001US-0279642P.
 PR
 XX (KRIE/) KRIEG A M.
 PA (BERG/) BERG D J.
 XX
 PI Krieg AM, Berg DJ;
 DR WPI; 2003-521815/49.
 XX
 PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
 PT disease by administering an immunostimulatory nucleic acid.
 XX
 PS Disclosure; Page 8; 229pp; English.
 XX
 CC The invention describes a method of treating non-allergic inflammatory
 CC disease comprising administering to a subject having or at risk of
 CC developing a non-allergic inflammatory disease an immunostimulatory
 CC nucleic acid for prevention or treatment of the disease. The method is
 CC useful for treating non-allergic inflammatory diseases, such as
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
 CC This sequence represents an immunostimulatory nucleic acid
 CC
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
 CC
 Query Match 100.0%; Score 18; DB 9; Length 18;
 Best Local Similarity 88.9%; Pred. No. 10;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGAGGCGCGACGCGGUA 18
 Db |||||:|||||:|||||:
 18 AGAGGCGCGACGCGGTA 1
 RESULT 15
 ADB36390/c
 ID ADB36390 standard; DNA; 18 BP.
 AC ADB36390;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Immunostimulatory nucleic acid #4.
 XX
 KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
 KW hypo-responsive subject; immunostimulatory.
 XX
 XX Synthetic.
 OS
 XX US2003087848-A1.
 PN
 XX 08-MAY-2003.
 PD
 XX 02-FEB-2001; 2001US-00776479.
 XX
 PR 03-FEB-2000; 2000US-0179991P.
 XX
 PA (BRAT/) BRATZLER R L.
 PA (PETER/) PETERSEN D M.
 PA (FOUR/) FOURON Y.
 XX
 PI Bratzler RL, Petersen DM, Fouron Y;
 DR WPI; 2003-657977/62.
 XX

PT Treating and/or preventing allergy or asthma using an immunostimulatory
nucleic acid alone or in combination with an asthma/allergy medicament.
XX
XX
PS Disclosure; Page 5; 221pp; English.
CC The invention relates to a method of treating or preventing allergy or
asthma which comprises administering to a subject a poly-G nucleic acid
in an aerosol formulation. The methods and compositions of the present
invention are useful for diagnosing and/or treating asthma and allergy
especially in a hypo-responsive subject. The present sequence represents
an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 9; Length 18;
Best Local Similarity 88.9%; Pred. No. 10;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGUGCGACGCGGUA 1
RESULT 16
ADB36433/c
ID ADB36433 standard; DNA; 18 BP.
XX
AC ADB36433;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #47.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
hypo-responsive subject; immunostimulatory.
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 6; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
asthma which comprises administering to a subject a poly-G nucleic acid
in an aerosol formulation. The methods and compositions of the present
invention are useful for diagnosing and/or treating asthma and allergy
especially in a hypo-responsive subject. The present sequence represents
an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 9; Length 18;
Best Local Similarity 88.9%; Pred. No. 10;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGAGGUGCGACGCGGUA 18

DB 18 AGAGGUGCGACGCGGUA 1
RESULT 17
AAD60215/c
ID AAD60215 standard; DNA; 18 BP.
XX
AC AAD60215;
XX
DT 18-DEC-2003 (first entry)
XX
DE Oligonucleotide 1761 used for activating dendritic cells.
XX
KW Dendritic cell activation; cancer immunotherapy; infectious disease;
allergy; cell therapy; ss.
OS Unidentified.
XX
PN US2003100527-A1.
XX
PD 29-MAY-2003.
XX
PF 03-JUN-2002; 2002US-00161229.
XX
PR 15-JUN-1994; 94US-00276358.
PR 07-FEB-1995; 95US-00386063.
PR 30-OCT-1996; 96US-00738652.
PR 30-OCT-1997; 97US-00960774.
PR 13-NOV-1998; 98US-00191170.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Krieg AM, Hartmann G;
XX
DR WPI; 2003-706674/67.
XX
PT Activating a dendritic cell useful for treating cancer, infectious
diseases or allergies, comprises contacting the dendritic cell with an
amount of an isolated nucleic acid that contains at least one
unmethylated CpG dinucleotide.
XX
PS Example 6; Page 18; 51pp; English.
XX
CC The invention relates to a method of activating a dendritic cell. The
method involves contacting the dendritic cell with an isolated nucleic
acid containing at least one unmethylated CpG dinucleotide, where the
nucleic acid is about 8-80 bases in length, in an amount that activates
the dendritic cell. The compositions and methods of the invention are
useful for cancer immunotherapy, or for treating an infectious disease
(e.g. viral, bacterial or fungal infections) or allergy. The invention is
useful in cell therapy. The present sequence is an oligonucleotide used
for activating dendritic cells
XX
SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 10; Length 18;
Best Local Similarity 88.9%; Pred. No. 10;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGUGCGACGCGGUA 1
RESULT 18
ADG68160/c
ID ADG68160 standard; DNA; 18 BP.
XX
AC ADG68160;
XX
DT 11-MAR-2004 (first entry)
XX

XX OS Unidentified.
XX PN US653292-B1.
XX PD 25-NOV-2003.
XX 21-JUN-1999; 99US-00337619.
XX 15-JUL-1994; 94US-00276358.
XX 07-FEB-1995; 95US-00386063.
XX 30-OCT-1996; 96US-00738652.
XX 30-OCT-1997; 97US-00960774.
XX (IOWA) UNITV IOWA RES FOUND.
XX Krieger AM, Welner G;
XX WPI; 2004-088215/09.
XX
XX Treatment and/or prevention of cancer and other disorders, e.g. tumor and
XX viral infection, involves administering an immunostimulatory nucleic
XX acid.
XX
XX Disclosure; SEQ ID NO 60; 71pp; English.
XX
XX The invention relates to a novel method whereby cancer is treated and/or
XX prevented by administering an immunostimulatory nucleic acid. The method
XX of the invention has cytostatic, virucide, fungicide, antibacterial,
XX antiparasitic and antineoplastic activities and may be useful for treating
XX colon cancer, including brain, lung, ovary, breast, prostate and
XX colon cancers, as well as leukemia, carcinoma, sarcoma and tumour.
XX Furthermore, the method may be utilized to address viral, fungal,
XX bacterial or parasitic infection and asthmatic disorders. The current
XX sequence is that of the immunostimulatory Cpg (unmethylated cytosine-
XX guanine)-related oligodeoxynucleotide (ODN) of the invention.
XX
XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 12; Length 18;
Best Local Similarity 88.9%; Pred. No. 10;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGAGGUGCGACGCGGTA 18
DB 18 AGAGGUGCGACGCGGTA 1
RESULT 21
ADM99069/C
ID ADM99069 standard; DNA; 18 BP.
XX
XX ADM99069;
XX
XX 29-JUL-2004 (first entry)
XX
XX Immunostimulatory Cpg containing oligonucleotide seqid 60.
XX
XX anti-allergic; antiarthritic; antineoplastic; antibacterial;
XX anti-inflammatory; antiparasitic; antipsoriatic; antithyroid; cytostatic;
XX dermatological; fungicide; gastrointestinal; immunosuppressive; virucide;
XX unethylated Cpg dinucleotide; asthmatic disorder; cancer; infection;
XX allergy; endosomal acidification; autoimmune disorder;
XX Cpg associated disorder; systemic lupus erythematosus; sepsis;
XX inflammatory bowel disease; psoriasis; gingivitis; arthritis;
XX Crohn's disease; Grave's disease; asthma; lymphocyte activation;
XX Th1 immune response; Th2 immune response; ss.
XX
XX Synthetic.
XX
XX US2004087538-A1.
XX
XX 06-MAY-2004.

XX 21-NOV-2003; 2003US-00719493.
XX 15-JUL-1994; 94US-00276358.
XX 07-FEB-1995; 95US-00386063.
XX 30-OCT-1996; 96US-00738652.
XX 30-OCT-1997; 97US-00960774.
XX 21-JUN-1999; 99US-00337619.
XX (IOWA) UNITV IOWA RES FOUND.
XX Krieger AM, Welner G;
XX WPI; 2004-374746/35.
XX
XX New isolated nucleic acid sequence containing at least one unethylated
XX Cpg dinucleotide, useful for treating autoimmune or other Cpg associated
XX disorder, e.g. systemic lupus erythematosus, sepsis, psoriasis,
XX gingivitis, asthma.
XX
XX Disclosure; SEQ ID NO 60; 70pp; English.
XX
XX The invention describes an isolated nucleic acid sequence containing at
XX least one unethylated Cpg dinucleotide. The nucleic acid is useful for
XX treating an asthmatic disorder, and may also be used for treating cancer,
XX viral, fungal, bacterial, or parasitic infections. The nucleic acid may
XX also be used for treating allergies, and as a synthetic adjuvant.
XX Administration of an inhibitor of endosomal acidification is useful for
XX treating autoimmune or other Cpg associated disorders, such as systemic
XX lupus erythematosus, sepsis, inflammatory bowel disease, psoriasis,
XX gingivitis, arthritis, Crohn's disease, Grave's disease and asthma. This
XX sequence represents an immunostimulatory Cpg containing oligonucleotide
XX of the invention.
XX
XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 12; Length 18;
Best Local Similarity 88.9%; Pred. No. 10;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGAGGUGCGACGCGGTA 18
DB 18 AGAGGUGCGACGCGGTA 1
RESULT 22
AD004787/C
ID AD004787 standard; DNA; 18 BP.
XX
XX AD004787;
XX
XX 26-AUG-2004 (first entry)
XX
XX Cpg oligonucleotide #60 tested for immunostimulatory activity.
XX
XX Unethylated Cpg dinucleotide; immune response; T helper cell; Th;
XX immune activation; cytokine production;
XX natural killer cell lytic activity; NK; B cell proliferation;
XX asthmatic disorder; autoimmune disorder; Cpg associated disorder;
XX systemic lupus erythematosus; sepsis; inflammatory bowel disease;
XX psoriasis; gingivitis; arthritis; parasitic; Crohn's disease;
XX cancer; viral; fungal; bacterial; parasitic; anti-inflammatory;
XX dermatological; immunosuppressive; antibacterial; antipsoriatic;
XX antiarthritic; antithyroid; cytostatic; virucide; fungicide;
XX antiparasitic; ss.
XX
XX Synthetic.
XX
XX US2004106568-A1.
XX
XX 03-JUN-2004.
XX
XX 25-JUL-2003; 2003US-00627331.

XX 15-JUL-1994; 94US-00276358.
 PR 07-FEB-1995; 95US-00386063.
 PR 30-OCT-1996; 96US-00738652.
 PR 30-OCT-1997; 97US-00960774.
 PR 31-JUL-2000; 2000US-00630319.
 PR 02-JUL-2002; 2002US-00187489.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (COLE-) COLEY PHARM GROUP INC.
 PI Krieg AM, Kliman D, Steinberg AD;
 DR WPI; 2004-419485/39.
 XX
 PT New nucleic acid sequence containing unmethylated cytosine-guanine (Cpg)
 PT dinucleotide, useful for modulating immune response, e.g. stimulating Th1
 PT pattern of immune activation, cytokine production, or B cell
 PT proliferation.
 PS Disclosure; SEQ ID NO 60; 72pp; English.
 XX
 CC The present invention relates to oligonucleotide sequences containing at
 CC least one unmethylated Cpg dinucleotide that are able of modulating an
 CC immune response such as stimulating T helper cell (Th) pattern of immune
 CC activation, cytokine production, natural killer cell (NK) lytic activity,
 CC and B cell proliferation in a subject, preferably human. The
 CC immunostimulatory oligonucleotides of the invention are useful for
 CC treating asthmatic disorders, autoimmune or other Cpg associated
 CC disorders (e.g. systemic lupus erythematosus, sepsis, inflammatory bowel
 CC disease, psoriasis, gingivitis, arthritis, Crohn's disease, Grave's
 CC disease), cancer, and viral, fungal, bacterial, and parasitic diseases.
 CC The present sequence represents an unmethylated Cpg dinucleotide
 CC oligonucleotide that is tested for its ability to modulate an immune
 CC response.
 CC
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 100.0%; Score 18; DB 12; Length 18;
 Best Local Similarity 88.9%; Pred. No. 10;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGAGGGUCCGACGCGGUA 18
 Db 18 AGAGGGTCCGACGCGGTA 1
 XX
 RESULT 23
 ADU89320/c
 ID ADU89320 standard; DNA; 18 BP.
 XX
 AC ADU89320;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE Allergic response suppressor oligonucleotide #4.
 XX
 KW ss; antiasthmatic; antiallergic; dermatological; antiinflammatory;
 KW antibacterial; virucide; immunoglobulin B antagonist; allergy;
 KW immunostimulator; asthma; rhinitis; urticaria; dermatitis;
 KW bacterial infection; viral infection.
 XX
 OS Synthetic.
 XX
 PN US2004235774-A1.
 XX
 PD 25-NOV-2004.
 XX
 PF 23-APR-2004; 2004US-00831778.
 XX
 PR 03-FEB-2000; 2000US-0179991P.
 XX
 PR 02-FEB-2001; 2001US-00776479.

XX (BRAT/) BRATZLER R L.
 PA (PETE/) PETERSEN D M.
 PA (FOUR/) FOURON Y.
 XX
 PI Bratzler RL, Petersen DM, Fouron Y;
 DR WPI; 2004-833006/82.
 XX
 PT Suppressing allergies, including asthma, rhinitis, urticaria and atopic
 PT dermatitis, in a subject, comprises administering a first and second dose
 PT of an immunostimulatory nucleic acid.
 PS Disclosure; SEQ ID NO 4; 235pp; English.
 XX
 CC The invention relates to a method of suppressing a symptom of an allergic
 CC response in a subject by administering a first and second dose of an
 CC immunostimulatory nucleic acid that comprises a nucleotide sequence
 CC comprising 5'-cg-3', and where the second dose is administered from 1 day
 CC to 8 weeks after the first dose. The methods and compositions of the
 CC present invention are useful for the treatment or prevention of asthma
 CC and allergy, including rhinitis, urticaria and atopic dermatitis, using
 CC an immunostimulatory nucleic acid alone or in combination with other
 CC medications. They can also be used in preventing bacterial and viral
 CC infections. This sequence represents an oligonucleotide used in the
 CC method of the invention.
 CC
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 100.0%; Score 18; DB 13; Length 18;
 Best Local Similarity 88.9%; Pred. No. 10;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGAGGGUCCGACGCGGUA 18
 Db 18 AGAGGGTCCGACGCGGTA 1
 XX
 RESULT 24
 ADU89372/c
 ID ADU89372 standard; DNA; 18 BP.
 XX
 AC ADU89372;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE Allergic response suppressor oligonucleotide #56.
 XX
 KW ss; antiasthmatic; antiallergic; dermatological; antiinflammatory;
 KW antibacterial; virucide; immunoglobulin B antagonist; allergy;
 KW immunostimulator; asthma; rhinitis; urticaria; dermatitis;
 KW bacterial infection; viral infection.
 XX
 OS Synthetic.
 XX
 PN US2004235774-A1.
 XX
 PD 25-NOV-2004.
 XX
 PF 23-APR-2004; 2004US-00831778.
 XX
 PR 03-FEB-2000; 2000US-0179991P.
 XX
 PR 02-FEB-2001; 2001US-00776479.
 XX
 PA (BRAT/) BRATZLER R L.
 PA (PETE/) PETERSEN D M.
 PA (FOUR/) FOURON Y.
 XX
 PI Bratzler RL, Petersen DM, Fouron Y;
 DR WPI; 2004-833006/82.
 XX
 PT Suppressing allergies, including asthma, rhinitis, urticaria and atopic

PT dermatitis, in a subject, comprises administering a first and second dose
 PT of an immunostimulatory nucleic acid.
 PS Disclosure; SEQ ID NO 56; 235pp; English.
 XX
 CC The invention relates to a method of suppressing a symptom of an allergic
 CC response in a subject by administering a first and second dose of an
 CC immunostimulatory nucleic acid that comprises a nucleotide sequence
 CC comprising 5'-cg-3', and where the second dose is administered from 1 day
 CC to 8 weeks after the first dose. The methods and compositions of the
 CC present invention are useful for the treatment or prevention of asthma
 CC and allergy, including rhinitis, urticaria and atopic dermatitis, using
 CC an immunostimulatory nucleic acid alone or in combination with other
 CC medicaments. They can also be used in preventing bacterial and viral
 CC infections. This sequence represents an oligonucleotide used in the
 CC method of the invention.
 CC
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 13; Length 18;
 Best Local Similarity 88.9%; Pred. No. 10;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AGAGGUGCCAGCGCGUA 18
 |||||:|||||:|||||:
 18 AGAGGTCGACGCGGTA 1
 DB
 RESULT 25
 ADV11411/c
 ID ADV11411 standard; DNA; 18 BP.
 AC
 AC ADV11411;
 DT 24-FEB-2005 (first entry)
 XX
 DE Reverse sequence of Bcl-2 antisense DNA.
 XX
 KW Oligonucleic acid-bearing composite; liposome;
 KW 2-O-(2-diehyllaminoethyl)carbamoyl-1,3-O-dioleoylglycerol;
 KW pharmaceutical; oncogene; bcl-2; cancer; viral infection; inflammation;
 KW cytostatic; virucide; antiinflammatory; gene therapy; phosphorothioate;
 KW ds.
 XX
 OS Synthetic.
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..17
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER=Phosphorothioate backbone"
 XX
 PN WO2004105774-A1.
 XX
 PD 09-DEC-2004.
 XX
 PF 28-MAY-2004; 2004WO-JP007785.
 XX
 PR 30-MAY-2003; 2003JP-00154798.
 PR 12-NOV-2003; 2003JP-00382819.
 PR 31-MAR-2004; 2004JP-00104036.
 XX
 PA (INNSH) NIPPON SHINYAKU CO LTD.
 XX
 PI Yano J, Hirabayashi K, Yamaguchi T, Sonoke S;
 XX
 DR MPI; 2005-031376/03.
 XX
 PT Oligonucleic acid-bearing composite, useful for treating cancer,
 PT comprises cationic liposome composed of 2-O-(2-
 PT diehyllaminoethyl)carbamoyl-1,3-O-dioleoylglycerol and phospholipid as
 PT active ingredient with oligonucleic acid.

XX
 PS Disclosure; SEQ ID NO 6; 55pp; Japanese.
 XX
 CC The invention relates to an oligonucleic acid-bearing composite
 CC comprising a cationic liposome composed of 2-O-(2-
 CC diehyllaminoethyl)carbamoyl-1,3-O-dioleoylglycerol and phospholipid as an
 CC active ingredient, with the oligonucleic acid having 10-15 bases. Also
 CC disclosed is a pharmaceutical composition for preventing and/or treating
 CC disease, comprising the oligonucleic acid-bearing composite, where the
 CC target molecule for the oligonucleic acid-bearing composite, includes
 CC target DNA, target RNA or target protein. The oligonucleic acid-bearing
 CC composite has an average particle diameter of 10-100 nm. In the preferred
 CC oligonucleic acid-bearing composite the phospholipid is lecithin, the
 CC oligonucleotide is RNA, DNA or its derivative, preferably siRNA (short
 CC interfering RNA), shRNA, antisense DNA, antisense RNA, DNA enzyme,
 CC ribozyme or an aptamer. The oligo double-stranded RNA comprises an
 CC antisense and sense RNA strand with 2 DNA bases at the 3' terminal ends.
 CC The oligonucleic acid-bearing composite is delivered into a cell
 CC containing a target molecule (e.g. target DNA, RNA or protein). The
 CC target molecule of the oligonucleotide includes a viral gene of HIV,
 CC Hepatitis C virus and Hepatitis B virus, an oncogene such as bcl-2, c-myc
 CC and bcr-abl gene, and an inflammation related gene such as TNFalpha
 CC (tumor necrosis factor alpha) and Fas gene, their transcription product,
 CC translation product and the non-coding region of genomic DNA of arbitrary
 CC protein. The oligonucleic acid-bearing composite is useful for preparing
 CC a pharmaceutical composition for treating or preventing diseases such as
 CC cancer, viral disease or inflammatory disease. The oligonucleic acid
 CC enables efficient biological activity with respect to the target molecule
 CC (e.g. target DNA, RNA or protein). This sequence represents the reverse
 CC sequence of Bcl-2 antisense DNA.
 CC
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 14; Length 18;
 Best Local Similarity 88.9%; Pred. No. 10;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AGAGGUGCCAGCGCGUA 18
 |||||:|||||:|||||:
 18 AGAGGTCGACGCGGTA 1
 DB
 RESULT 26
 ADM79934
 ID ADM79934 standard; RNA; 18 BP.
 AC
 AC ADM79934;
 DT 21-APR-2005 (first entry)
 XX
 DE Bacterial immunomodulatory Cpg oligoribonucleotide, SEQ ID NO:1.
 XX
 KW Immune modulation; immune stimulation; bacterial infection; infection;
 KW endotoxic shock; antibacterial; antimicrobial; immunomodulator;
 KW immunostimulant; adjuvant; ss.
 XX
 OS Bacteria.
 OS
 XX
 FH Key Location/Qualifiers
 FT misc_feature 12..13
 FT /*tag= a
 FT /note= "Cpg dinucleotide"
 FT misc_feature 14..15
 FT /*tag= b
 FT /note= "Cpg dinucleotide"
 XX
 PN US2005032731-A1.
 XX
 PD 10-FEB-2005.
 XX
 PF 15-MAR-2004; 2004US-00800926.
 PF 11-MAY-1993; 93US-00059745.
 XX

PR 20-JAN-1995; 95US-00376175.
 PR 18-APR-1995; 95US-00517016.
 PR 29-OCT-1996; 96US-00739264.
 PR 17-NOV-1998; 98US-00193653.
 PR 18-JUN-2001; 2001US-00883550.
 XX
 PA (MARS/) MARSHALL W E.
 XX
 PI Marshall WE;
 XX
 DR WPI; 2005-161694/17.
 XX
 PT Composition for modulating and/or stimulating immune system of animal
 PT useful for withstanding microbial infections and lethality of endotoxic
 PT shock, comprises low molecular weight oligoribonucleotide from bacteria.
 XX
 PS Claim 5; SEQ ID NO 1; 17pp; English.
 XX
 CC The invention relates to a composition for modulating and/or stimulating
 CC the immune system of an animal, comprising bacterial oligoribonucleotides
 CC (ORN) with a molecular weight of less than 10 kD. The bacterial ORNs are
 CC preferably ADM79934-ADM79936, contain CPG motifs and are resistant to
 CC RNase. Bacteria produce RNase-resistant CPG ORNs in response to stresses
 CC such as a change in environment, including the neutral pH they encounter
 CC when they colonize animals. The immune systems of animals have co-evolved
 CC to recognize such CPG ORNs as being derived from bacteria, and has
 CC adapted a non-toxic alerting response to their release from bacteria. The
 CC invention also relates to a method for the preparation of the bacterial
 CC ORNs by subjecting bacteria to one or more periods of stress, separating
 CC the ORNs and media from the bacteria, and filtering the separated product
 CC to remove substances with a molecular weight of more than 10 kD; and a
 CC method of using the filtrate to modulate/stimulate the immune system of
 CC an animal to withstand microbial infection. The composition and methods
 CC of the invention are useful for modulating and/or stimulating the immune
 CC system of animals (including humans, poultry and livestock), particularly
 CC to withstand microbial infections or the onset of endotoxic shock. The
 CC compositions may be administered orally (e.g., as a food supplement) or
 CC parenterally, and may also be administered as an adjuvant for oral or
 CC parenteral vaccines. The compositions may additionally be used topically
 CC to protect against ear, nose and vaginal infections. They may further be
 CC used to extend the viability of monocytes, thereby improving their
 CC ability to mature into macrophages to fight infection, and may be used to
 CC downregulate the cytotoxicity of macrophages to prevent them from
 CC destroying normal T-cells in people with HIV infections. The composition
 CC of the invention contains ORNs released by either harmless or pathogenic
 CC bacteria, but is free from bacterial cells. Unlike CPG
 CC oligodeoxyribonucleotides (ODNs), the bacterial CPG ORNs and compositions
 CC containing them are non-toxic. The present sequence represents a
 CC specifically claimed bacterial CPG oligoribonucleotide present in
 CC compositions of the invention.
 XX
 SQ Sequence 18 BP; 4 A; 4 C; 8 G; 0 T; 2 U; 0 Other;
 Query Match 100.0%; Score 18; DB 14; Length 18;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGAGGGUCCGACGCGGUA 18
 DB 1 AGAGGGUCCGACGCGGUA 18
 AC
 AC ADZ88546;
 XX
 DT 14-JUL-2005 (first entry)
 XX
 DE CPG ODN1761, to induce NK cell lytic activity, SEQ ID NO: 60 #1.
 XX Immune stimulation; immunotherapy; nucleic acid vaccine;

KW papillomavirus infection; virucide; infection;
 KW systemic lupus erythematosus; antiinflammatory; dermatological;
 KW immunosuppressive; dermatological disease; immune disorder;
 KW metabolic disorder; musculoskeletal disease; tumor; cytostatic;
 KW fungal infection; fungicide; parasitic infection; antiparasitic;
 KW bacterial infection; antibacterial; asthma; antiaesthetic; inflammation;
 KW respiratory disease; leukemia; hematological disease; allergy;
 KW antiallergic; ss.
 XX
 OS Unidentified.
 XX
 XX US2005101554-A1.
 XX
 PD 12-MAY-2005.
 XX
 PF 25-JUL-2003; 2003US-00627413.
 XX
 PR 15-JUL-1994; 94US-00276358.
 PR 07-FEB-1995; 95US-00386063.
 PR 30-OCT-1996; 96US-00738652.
 PR 30-OCT-1997; 97US-00960774.
 PR 31-JUL-2000; 2000US-00630319.
 PR 02-JUL-2002; 2002US-00187489.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 PA (COLE-) COLEY PHARM GROUP INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Krieg AM, Klimman D, Steinberg AD;
 XX
 DR WPI; 2005-345416/35.
 XX
 PT Treating, preventing or ameliorating a papilloma virus infection
 PT comprises administering to the subject a composition containing
 PT unmethylated CPG dinucleotide.
 XX
 PS Disclosure; SEQ ID NO 60; 72pp; English.
 XX
 CC The invention relates to unmethylated cytosine-guanine (CpG)
 CC dinucleotides that activate lymphocytes and redirect a subject's immune
 CC response from a antibody (humoral) immune response (Th2) to cellular
 CC immune response (Th1) thus acting as immunostimulatory compounds. The
 CC invention is useful for treating, preventing or ameliorating a papilloma
 CC virus infection, autoimmune disorders (particularly systemic lupus
 CC erythematosus) and other disorders such as tumor or cancer, viral,
 CC fungal, bacterial or parasitic infection, asthmatic disorder, allergic
 CC reaction and leukemia and for stimulating immune activation. The nucleic
 CC acid sequences of the invention are useful as an adjuvant for generating
 CC antibodies and in the production of vaccines. The invention is also
 CC useful in immunotherapy. The present sequence is a Cpg oligonucleotide
 CC involved in induction of natural killer (NK) cell lytic activity. Note:
 CC The present sequence is the SEQ ID NO: 60 which is given in the sequence
 CC listing. This sequence differs from the SEQ ID NO: 60 shown in the
 CC disclosure (page 19) of the specification.
 XX
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 14; Length 18;
 Best Local Similarity 88.9%; Pred. No. 10;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGAGGGUCCGACGCGGUA 18
 DB 18 AGAGGGUCCGACGCGGUA 1
 AC
 AC ABA1652;
 XX
 DT 14-JUL-2005 (first entry)
 XX

XX Cpg immunostimulatory oligo, S-ODN 1761 SEQ ID NO: 60.
 XX
 XX Immune stimulation; immunotherapy; nucleic acid vaccine; allergy;
 XX anti-allergic; eczema; dermatological; anti-inflammatory;
 XX dermatological disease; immune disorder; common cold; virus; vaccine;
 XX ear, nose, throat disease; infection; respiratory disease;
 XX allergic rhinitis; inflammation; urticaria; autoimmune disease;
 XX immunosuppressive; systemic lupus erythematosus; metabolic disorder;
 XX musculoskeletal disease; tumor; cancer; cytotoxic; neoplasm; leukemia;
 XX hematological disease; viral infection; bacterial infection;
 XX antibacterial; fungal infection; fungicide; parasitic infection;
 XX antiparasitic; asthma; antiasthmatic; phosphorothioate; ss.

XX Unidentified.

XX Key Location/Qualifiers
 XX modified_base 1.18
 XX /tag= a
 XX /mod_base= OTHER
 XX /note= "Phosphorothioate backbone"

XX US2005101557-A1.

XX 12-MAY-2005.

XX 18-AUG-2004; 2004US-00921086.

XX 15-JUL-1994; 94US-00276358.

XX 07-FEB-1995; 95US-00386063.

XX 30-OCT-1996; 96US-00738652.

XX 30-OCT-1997; 97US-00960774.

XX 21-JUN-1999; 99US-00337584.

XX (IOWA) UNIV IOWA RES FOUND.

XX Krieg AM, Kline JN;

XX WPI; 2005-345417/35.

XX Desensitizing a subject against the occurrence of an allergic reaction

XX comprises administering to a subject an amount an immunostimulatory

XX nucleic acid.

XX Disclosure; SEQ ID NO 60; 72pp; English.

XX The present invention relates to nucleic acid sequences containing at

XX least one unethylyated Cpg dinucleotide which are immunostimulatory. The

XX invention also provides a method for desensitizing a subject against the

XX occurrence of an allergic reaction in response to contact with an

XX allergen. The method involves administering to a subject an amount for

XX desensitizing the subject against the occurrence of an allergic reaction

XX of an immunostimulatory nucleic acid. The invention is useful for

XX treating or preventing allergy and allergic conditions selected from

XX eczema, allergic rhinitis, allergic colitis, hay fever, urticaria and food

XX allergy. The invention is also useful for treating autoimmune disorder

XX particularly systemic lupus erythematosus and other disorders, e.g. tumor

XX or cancer, viral, bacterial, fungal, or parasitic infection, asthmatic

XX disorder, or leukemia in a subject and for producing vaccine. The present

XX sequence is a Cpg immunostimulatory phosphorothioate modified

XX oligodeoxynucleotide (S-ODN).

RESULT 29
 AEC16249/C
 ID AEC16249 standard; DNA; 18 BP.
 XX
 XX AEC16249;
 AC
 XX
 XX 20-OCT-2005 (first entry)
 DT
 XX
 XX NK lytic activity inducing Cpg oligo, ODN 1761, SEQ ID NO: 60.
 DE
 XX
 XX Immune stimulation; cell proliferation; immunotherapy; cancer;
 XX cytostatic; neoplasm; infection; antimicrobial; phosphorothioate; ss.
 XX
 XX Unidentified.
 OS
 XX
 XX US2005182017-A1.
 PN
 XX
 XX 18-AUG-2005.
 PD
 XX
 XX 03-MAR-2005; 2005US-00071836.
 PP
 XX
 XX 30-OCT-1997; 97US-00960774.
 PR
 XX 21-JUN-1999; 99US-00337893.
 PR
 XX 14-JUL-2003; 2003US-00619279.
 XX
 XX (IOWA) UNIV IOWA RES FOUND.
 PA
 XX
 XX Krieg AM;
 PI
 XX
 XX WPI; 2005-590434/60.
 DR
 XX
 XX New oligonucleotide, useful for stimulating an immune response including
 PT a Th1 pattern of immune activation, cytokine production, NK lytic
 PT activity and B cell proliferation, in a subject having cancer or an
 PT infectious disease.
 PT
 XX
 XX Disclosure; SEQ ID NO 60; 70pp; English.
 PS
 XX
 XX The invention relates to an immunostimulatory oligonucleotide that
 CC modulates an immune response including a Th1 pattern of immune
 CC activation, cytokine production, natural killer (NK) lytic activity and B
 CC cell proliferation. The oligonucleotide is useful for stimulating an
 CC immune response including a Th1 pattern of immune activation, cytokine
 CC production, NK lytic activity and B cell proliferation, in a subject
 CC having cancer or an infectious disease. The invention is also useful as a
 CC synthetic adjuvant and in immunotherapy. The present sequence is a Cpg
 CC oligonucleotide involved in the induction of NK lytic activity.
 CC
 XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
 SO
 Query Match 100.0%; Score 18; DB 14; Length 18;
 Best Local Similarity 88.9%; Pred. No. 10;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGAGGUGCGACGCGGUA 18
 DB 18 AGAGGUGCGACGCGGUA 1
 ID ABR90354 standard; DNA; 57 BP.
 AC ABR90354;
 XX
 XX 21-OCT-2002 (first entry)
 DT
 XX
 XX Bcl-2/Cb1 hybrid antisense oligonucleotide BKL-PS-1084.
 DE
 XX
 XX Antisense; ss; probe; Bcl-2; cell proliferative disorder; cancer; CRE;
 XX CAMP response element; bacterial infection; viral infection;
 XX inflammation; anaphylaxis; allergy; arthritis; asthma; cytostatic;
 XX autoimmune disorder; parasitic infection; virus; hyperplasia;

KW tumorigenesis; hepatitis B infection; human.
 XX Homo sapiens.
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT modified_base 1..57
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "phosphorothioate backbone"
 XX
 PN WO200257480-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 22-JAN-2002; 2002WO-US001967.
 XX
 PR 22-JAN-2001; 2001US-0263244P.
 XX
 PA (GENT-) GENTA INC.
 XX
 PI Klem RE;
 XX
 DR WPI; 2002-590754/63.
 XX
 PT Hybrid oligomer comprises a cyclic AMP response element sequence and a
 PT sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for
 PT preventing or treating cell-proliferative disorders e.g., cancer.
 XX
 PS Example 1; Page 58; 78pp; English.
 XX
 CC The invention relates to a hybrid oligomer comprising a cyclic AMP
 CC response element (CRE) sequence and a sequence that hybridizes to the bcl
 CC -2 pre-mRNA or mRNA. Also included are: (1) inhibiting the growth of
 CC cancer cells in vitro, which comprises contacting the cancer cells with a
 CC hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer;
 CC (2) treating or preventing cancer in a human, which comprises
 CC administering a hybrid oligomer or a bcl-2 antisense oligomer and a CRE
 CC decoy oligomer; and (3) a pharmaceutical composition comprising a hybrid
 CC oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer and a
 CC carrier. The pharmaceutical composition of the invention is useful for
 CC preventing or treating cell-proliferative disorders e.g., cancer;
 CC hyperplasia or tumorigenesis and also bacterial infection, viral
 CC infection, inflammation, anaphylaxis, allergy, arthritis, asthma,
 CC autoimmune disorders and parasitic infection. The CRE decoy oligomer and
 CC bcl-2 antisense oligomer are also useful for preventing or treating
 CC hepatitis B virus infection. The hybrid oligomers can also be used for
 CC screening candidate transcription factors or other molecules e.g., gene
 CC regulatory proteins or for diagnostic assays. The present sequence is a
 CC Bcl-2/CRE hybrid antisense oligonucleotide
 XX
 SQ Sequence 57 BP; 12 A; 17 C; 18 G; 10 T; 0 U; 0 Other;
 XX
 Query Match 100.0%; Score 18; DB 6; Length 57;
 Best Local Similarity 88.9%; Pred. No. 11;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 AGAGGUGCCACGCGGUA 18
 |||||:|||||:|||||:
 Db 37 AGAGGCTCCGACGCGGTA 54
 |||||:|||||:|||||:
 XX
 RESULT 31
 AAQ86651/c
 ID AAQ86651 standard; DNA; 17 BP.
 XX
 AC AAQ86651;
 XX
 XX 25-MAR-2003 (revised)
 DT 27-SEP-1995 (first entry)
 XX
 DE Bcl-2 antisense oligonucleotide.
 XX

KW Anticode oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
 KW lymphoma; programmed cell death; ss.
 XX
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT misc_feature 1..17
 FT /tag= a
 FT /note= "3'-5' (antisense) sequence"
 XX
 PN WO9508350-A1.
 XX
 PD 30-MAR-1995.
 XX
 PF 20-SEP-1994; 94WO-US010725.
 XX
 PR 20-SEP-1993; 93US-00124256.
 XX
 PA (REED/) REED J C.
 XX
 PI Reed JC;
 XX
 DR WPI; 1995-139394/18.
 XX
 PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment of human
 PT solid tumours, esp. breast cancer.
 XX
 PS Example 12; Page 33; 108pp; English.
 XX
 CC Antisense oligonucleotides were tested for their ability to induce
 CC programmed cell death (DNA fragmentation) in the human lymphoma cell line
 CC RS1846. The oligonucleotides are phosphodiester targeted against the
 CC translation initiation site (AAQ86650-55) or the 5'-cap region (AAQ86656-
 CC 58) of human bcl-2 pre-mRNAs. The AAQ86651 oligonucleotide provided
 CC pronounced DNA fragmentation. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 94.4%; Score 17; DB 2; Length 17;
 Best Local Similarity 88.2%; Pred. No. 35;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 2 GAGGUGCCACGCGGUA 18
 |||||:|||||:|||||:
 Db 17 GAGGCTCCGACGCGGTA 1
 |||||:|||||:|||||:
 XX
 RESULT 32
 ABR90272/c
 ID ABR90272 standard; DNA; 17 BP.
 XX
 AC ABR90272;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Bcl-2-targeting antisense oligonucleotide #9.
 XX
 KW Antisense; ss; probe; Bcl-2; cell proliferative disorder; cancer; CRE;
 KW CAMP response element; bacterial infection; viral infection;
 KW inflammation; anaphylaxis; allergy; arthritis; asthma; cytostatic;
 KW autoimmune disorder; parasitic infection; virucide; hyperplasia;
 KW tumorigenesis; hepatitis B infection; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200257480-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 22-JAN-2002; 2002WO-US001967.
 XX
 PR 22-JAN-2001; 2001US-0263244P.
 XX

XX (GENT-) GENTA INC.
XX Klem RE;
XX WPI; 2002-590754/63.
XX
XX Hybrid oligomer comprises a cyclic AMP response element sequence and a
PT sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for
XX preventing or treating cell-proliferative disorders e.g., cancer.
XX
XX Disclosure; Page 13; 78pp; English.
XX
XX The invention relates to a hybrid oligomer comprising a cyclic AMP
CC response element (CRE) sequence and a sequence that hybridizes to the bcl-
CC -2 pre-mRNA or mRNA. Also included are: (1) inhibiting the growth of
CC cancer cells in vitro, which comprises contacting the cancer cells with a
CC hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer;
CC (2) treating or preventing cancer in a human, which comprises
CC administering a hybrid oligomer or a bcl-2 antisense oligomer and a CRE
CC decoy oligomer; and (3) a pharmaceutical composition comprising a hybrid
CC oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer and a
CC carrier. The pharmaceutical composition of the invention is useful for
CC preventing or treating cell-proliferative disorders e.g., cancer,
CC hyperplasia or tumorigenesis and also bacterial infection, viral
CC infection, inflammation, anaphylaxis, allergy, arthritis, asthma,
CC autoimmune disorders and parasitic infection. The CRE decoy oligomer and
CC bcl-2 antisense oligomer are also useful for preventing or treating
CC hepatitis B virus infection. The hybrid oligomers can also be used for
CC screening candidate transcription factors or other molecules e.g., gene
CC regulatory proteins or for diagnostic assays. The present sequence is a
CC Bcl-2 antisense oligonucleotide
XX
SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
XX
Query Match 94.4%; Score 17; DB 6; Length 17;
Best Local Similarity 88.2%; Pred. No. 35;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 2 GAGGGUCCGACCGCGUA 18
DB 17 GAGGGTCCGACCGCGTA 1
XX
RESULT 33
ABQ78530/c
ID ABQ78530 standard; DNA; 17 BP.
XX
XX ABQ78530;
AC
XX 25-NOV-2002 (first entry)
DT
XX
XX Antisense oligodeoxynucleotide of the human bcl-2 gene.
DE
XX
XX Antisense oligonucleotide; B cell lymphoma/leukemia-2 gene; bcl-2 gene;
KW cancer; lymphoma; leukemia; chemotherapeutic agent; bone marrow purging;
KW autoimmune disease; ss.
XX
XX Homo sapiens.
OS
XX
XX US6414134-B1.
PN
XX 02-JUL-2002.
PD
XX
XX 28-NOV-2000; 2000US-00724426.
PF
XX
XX 22-DEC-1998; 88US-00288692.
PR
XX 21-FEB-1992; 92US-00840716.
PR
XX 20-SEP-1993; 93US-00124256.
PR
XX 05-JUN-1995; 95US-00465485.
PR
XX 18-MAY-1998; 98US-00080285.
PR
XX 17-AUG-1999; 99US-00375514.
XX

PA (UYPE-) UNIV PENNSYLVANIA.
XX
XX Reed JC;
XX
XX WPI; 2002-641579/69.
XX
XX
XX Novel antisense oligonucleotide complementary to B cell lymphoma/leukemia
PT -2 mRNA, useful for inhibiting cancer cell growth, for treating
PT autoimmune disorders, and for ex vivo bone marrow purging.
XX
XX
XX Claim 1; Col 17; 41pp; English.
XX
XX The present sequence represents an antisense oligonucleotide
CC complementary to B cell lymphoma/leukemia-2 (bcl-2) mRNA. The antisense
CC oligonucleotide is useful for inhibiting cancer cell (lymphoma or
CC leukemia cells) growth, for increasing the sensitivity of cancer cells to
CC cancer chemotherapeutic agents, or for inducing cancer cell death alone
CC or in combination with any one or more cancer chemotherapeutic agents. It
CC is also useful for reducing the bcl-2 gene expression or impairing bcl-2
CC protein function, for ex vivo bone marrow purging, for removing residual
CC malignant cells from the bone marrow, for inhibiting cancer of neoplastic
CC cell growth, and for treating autoimmune disease
XX
SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
XX
Query Match 94.4%; Score 17; DB 6; Length 17;
Best Local Similarity 88.2%; Pred. No. 35;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 2 GAGGGUCCGACCGCGUA 18
DB 17 GAGGGTCCGACCGCGTA 1
XX
RESULT 34
ABL54157/c
ID ABL54157 standard; DNA; 17 BP.
XX
XX ABL54157;
AC
XX
XX 12-JUL-2002 (first entry)
DT
XX
XX Bcl-2 antisense oligonucleotide.
DE
XX
XX B cell lymphoma/leukemia-2; bcl-2; oncogene; antisense; lymphoma;
KW leukaemia; colon carcinoma; rectal carcinoma; pancreatic cancer;
KW breast cancer; ovarian cancer; prostate cancer; renal cell carcinoma;
KW hepatoma; bile duct carcinoma; choriocarcinoma; cervical cancer;
KW testicular cancer; lung carcinoma; bladder carcinoma; melanoma;
KW head and neck cancer; brain cancer; cytostatic; human; gene therapy; ss.
XX
XX
XX Homo sapiens.
OS
XX
XX WO200217852-A2.
PN
XX
XX 07-MAR-2002.
PD
XX
XX 23-AUG-2001; 2001WO-US026414.
PF
XX
XX 25-AUG-2000; 2000US-0227970P.
PR
XX 29-SEP-2000; 2000US-0237009P.
PR
XX 10-NOV-2000; 2000US-00709170.
XX
XX (GENT-) GENTA INC.
XX
XX Warrel RP, Klem RE, Fingert H;
XX
XX WPI; 2002-371796/40.
XX
XX Treating or preventing cancer, tumors and carcinomas, comprises
PT administering B cell lymphoma/leukemia-2 antisense oligonucleotide at
PT high doses for short period for time with one or more cancer
PT therapeutics.

CC The invention relates to a novel method for treating cancer in a human,
 CC comprising the administration of anticode oligomers for treating bcl-2
 CC gene expressing cancer cells. The invention further comprises: a
 CC pharmaceutical composition comprising an anticode oligomer, and a
 CC pharmaceutical carrier; and increasing the sensitivity of a tumor cell to
 CC a chemotherapeutic agent. The anticode oligomers have cytostatic
 CC activity. The oligomers may be used in gene therapy to treat cancer. The
 CC method is also useful for increasing the sensitivity of a tumor cell to a
 CC chemotherapeutic agent. The types of treatable cancer include non-
 CC Hodgkin's lymphoma, prostate cancer, breast cancer, gastro-intestinal
 CC cancer, or colon cancer. The anticode oligomers are useful for inhibiting
 CC growth of cancer cells or killing tumor cells. This polynucleotide
 CC sequence represents a bcl-2 oligodeoxynucleotide of the invention.

XX
 SQ Sequence 17 BP, 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 94.4%; Score 17; DB 14; Length 17;
 Best Local Similarity 88.2%; Pred. No. 35;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 GAGGGTCCACCGCGTA 18
 |||||:|||||:|
 DB 17 GAGGGTCCACCGCGTA 1

RESULT 37
 AAH48722/c
 ID AAH48722 standard; DNA; 20 BP.

XX
 AC AAH48722;

XX 19-OCT-2001 (first entry)

XX Proto-oncogene bcl-2 associated primer SEQ ID 3.

XX
 KW Primer: phosphorothioate; somatostatin; cytostatic; virocid; asthma;
 KW antiinflammatory; antiaesthatic; cardiant; antisense therapy; cancer;
 KW viral disease; inflammatory process; somatostatin receptor;
 KW central nervous system disease; cardiovascular disease; SSTR;
 KW proto-oncogene; bcl-2; ss.

XX Unidentified.

XX
 PH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "phosphorothioate"

XX DE10006572-A1.

XX 23-AUG-2001.

XX 14-FEB-2000; 2000DE-01006572.

XX 14-FEB-2000; 2000DE-01006572.

XX (DEKR-) DEUT KREBSFORSCHUNGSGEZENTRUM.

XX Bisenhut M, Mier W, Britia R, Haberkorn U;

XX WPI; 2001-530596/59.

XX
 PT New conjugates of oligonucleotides with somatostatin analogs, useful in
 PT antisense therapy, e.g. of viral, inflammatory or asthmatic disease or
 PT especially tumors overexpressing the somatostatin receptor.

XX Example 3; Page 9; 16pp; German.

XX This invention describes a novel oligonucleotide conjugate (1) comprising
 CC (a) an oligonucleotide, at least part of the sequence of which is
 CC complementary to part of an intracellular nucleic acid sequence; and (b)
 CC a somatostatin analog. The products of the invention have cytostatic.

CC virocid, antiinflammatory, antiaesthatic and cardiant activity. The use
 CC of (1) is claimed in antisense therapy, especially of cancer, viral
 CC disease, inflammatory processes or asthmatic, central nervous system or
 CC cardiovascular disease. (1) are especially used for therapy of tumors
 CC overexpressing the somatostatin receptor (SSTR) (e.g. small-cell lung
 CC tumors, breast tumors, brain tumors or other endocrine tumors), but are
 CC also useful for treating viral diseases (e.g. herpes simplex-1
 CC infection), inflammatory disease (typical target RNA the NF-kappa-B),
 CC asthmatic disease (typical target RNA the adenosine A1 receptor), central
 CC nervous system disease (typical target RNA the dopamine receptor), or
 CC cardiovascular disease (typical target RNA c-myc). (1) are efficiently
 CC taken up by cells and incorporated in target cells (via the SSTR) and are
 CC highly selective for cells overexpressing SSTRs. This sequence
 CC represents a primer used to illustrate the method of the invention

XX
 SQ Sequence 20 BP, 2 A; 7 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 4; Length 20;
 Best Local Similarity 83.3%; Pred. No. 73;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 AGAGGGTCCACCGCGTA 18
 |||||:|||||:|
 DB 18 AGAGGGTCCACCGCGTA 1

RESULT 38
 AAQ86650/c
 ID AAQ86650 standard; DNA; 17 BP.

XX AAQ86650;

XX 25-MAR-2003 (revised)

XX 27-SEP-1995 (first entry)

XX Bcl-2 antisense oligonucleotide.

XX Anticod oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
 KW lymphoma; programmed cell death; ss.

XX Synthetic.

XX
 PH Key Location/Qualifiers
 FT misc_feature 1..17
 FT /*tag= a
 FT /note= "3'-5' (antisense) sequence"

XX WO9508350-A1.

XX 30-MAR-1995.

XX 20-SEP-1994; 94WO-US010725.

XX 20-SEP-1993; 93US-00124256.

XX (REED/) REED J C.

XX Reed JC;

XX WPI; 1995-139394/18.

XX
 PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment of human
 PT solid tumors, esp. breast cancer.

XX Example 12; Page 33; 108pp; English.

XX Antisense oligonucleotides were tested for their ability to induce
 CC programmed cell death (DNA fragmentation) in the human lymphoma cell line
 CC RS11846. The oligonucleotides are phosphodiester targeted against the
 CC translation initiation site (AAQ86650-55) or the 5'-cap region (AAQ86656-
 CC 58) of human bcl-2 pre-mRNAs. (Updated on 25-MAR-2003 to correct PN
 CC field.)

SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 2; Length 17;
 Best Local Similarity 93.3%; Pred. No. 4e+02;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUCCGACGCG 15
 |||||:|||||
 DB 15 AGAGGGTCCGACGCG 1

RESULT 39
 AAV28172/C
 ID AAV28172 standard; DNA; 17 BP.
 XX
 AC AAV28172;
 XX
 DT 08-OCT-1998 (first entry)
 XX
 DE Antisense oligonucleotide to bcl-2 mRNA.
 XX
 KW Purification; oligonucleotide; matrix; affinity unit;
 KM affinity purification; antisense; bcl-2; ss.
 XX
 OS Synthetic.
 XX
 PN WO9827425-A1.
 XX
 PD 25-JUN-1998.
 XX
 PF 18-DEC-1997; 97WO-US023284.
 XX
 PR 19-DEC-1996; 96US-00769951.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Chen D, Srivatsa GS, Cole DL;
 XX
 DR WPI; 1998-362922/31.
 XX
 PT Matrix for selective separation of oligonucleotide - useful for, e.g.
 PT large scale purification of anti-sense agents from their deletion
 PT derivatives formed during synthesis.
 XX
 PS Disclosure; Page 79; 183pp; English.
 XX
 CC AAV28155-268 represent oligonucleotides which can be purified using the
 CC method of the invention. The specification describes a matrix that
 CC comprises a support and an affinity unit that specifically and reversibly
 CC binds a target oligonucleotide, and comprises a sequence of bases having
 CC the reverse complement of a hybridising portion of the target
 CC oligonucleotide. The matrix is used for affinity purification of
 CC synthetic oligonucleotides, specifically antisense agents, for treatment
 CC of hyperproliferative diseases, for treating a non-pathogen, non-
 CC hyperproliferative disease, e.g. Alzheimer's, for modulating expression
 CC of cell surface proteins, and to inhibit a eukaryotic pathogen,
 CC retrovirus or other viruses
 XX
 SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 2; Length 17;
 Best Local Similarity 93.3%; Pred. No. 4e+02;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUCCGACGCG 15
 |||||:|||||
 DB 15 AGAGGGTCCGACGCG 1

RESULT 40
 AAX18693/C
 ID AAX18693 standard; DNA; 17 BP.
 XX

AC AAX18693;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 DE Target bcl-2 antisense oligonucleotide #25.
 XX
 KW Cellular adhesion protein; proliferation; antisense oligonucleotide;
 KM alimentary canal; transport; gastrointestinal mucosa; cancer;
 KM Alzheimer's disease; beta-thalassemia; malaria; viral infection; HIV;
 KM inflammation; ss.
 XX
 OS Synthetic.
 XX
 PN WO9901579-A1.
 XX
 PD 14-JAN-1999.
 XX
 PF 01-JUL-1998; 98WO-US013574.
 XX
 PR 01-JUL-1997; 97US-00868629.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Teng C, Hardee G;
 XX
 DR WPI; 1999-106077/09.
 XX
 PT Composition comprising nucleic acid and penetration enhancer - used
 PT particularly for delivering therapeutic antisense oligonucleotides across
 PT the gastrointestinal mucosa, provides high bioavailability.
 XX
 PS Example 2; Page 84; 115pp; English.
 XX
 CC A pharmaceutical composition has been developed which comprises a nucleic
 CC acid and at least one penetration enhancer. The compositions are used:
 CC (i) to treat or prevent any disease or disorder that can be treated with
 CC the nucleic acid, e.g. cancer, Alzheimer's disease, beta-thalassemia,
 CC malaria, viral infections (including human immune deficiency virus
 CC (HIV)), inflammation, in human or animal medicine; (ii) to investigate
 CC the role of a gene or gene product in non-human animals; and (iii) to
 CC modulate gene expression in cells, tissues or organs. The compositions
 CC provide bioavailability of at least 15, preferably 17-35%. The
 CC penetration enhancer improves: (i) transport of the nucleic acid across
 CC the mucosa of the alimentary canal and into cells; and (ii) increases
 CC stability of the nucleic acid. Oral administration avoids the
 CC complications and expense of intravenous or other methods of
 CC administration. AAX18693 to AAX18799 and AAX18801 represent antisense
 CC oligonucleotides which can be used as the nucleic acid in the method of
 CC the invention
 XX
 SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 2; Length 17;
 Best Local Similarity 93.3%; Pred. No. 4e+02;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUCCGACGCG 15
 |||||:|||||
 DB 15 AGAGGGTCCGACGCG 1

RESULT 41
 AAX23684/C
 ID AAX23684 standard; DNA; 17 BP.
 XX
 AC AAX23684;
 XX
 DT 18-JUN-1999 (first entry)
 XX
 DE Deletion sequence oligonucleotide 137.
 XX
 KW Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
 KM probe; cellular adhesion modulator; cellular proliferation modulator;

KM human retrovirus; human immunodeficiency virus; non-human retrovirus;
 KW HIV; primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9911820-A1.
 XX
 PD 11-MAR-1999.
 XX
 PF 01-SEP-1998; 98WO-US018084.
 XX
 PR 02-SEP-1997; 97US-00923771.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Chen D, Srivatsa GS;
 XX
 DR WPI; 1999-205198/17.
 XX
 PT New compositions comprising sensor arrays made up of unique probe
 PT oligonucleotides - useful for characterizing a sample of target deletion
 PT oligonucleotides.
 PS
 PS Example 9; Page 149; 163pp; English.
 XX
 CC This invention describes a novel composition comprising a number of
 CC sensor arrays, where each array comprises a unique probe oligonucleotide,
 CC which is the reverse complement of part of a unique target
 CC oligonucleotide present in a mixture of target deletion sequence
 CC oligonucleotides. The compositions form a method for characterizing a
 CC sample of target deletion oligonucleotides which are labelled and
 CC hybridize with the probe oligonucleotides of the sensor arrays. Such
 CC oligonucleotides and their targets are represented in AMX3548-X23709.
 CC Oligonucleotides characterized by the method form pharmaceutical
 CC compositions that are useful for modulating cellular adhesion or
 CC proliferation, and being active against a eukaryotic pathogen, a human
 CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
 CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
 CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
 CC characterization of deletion sequence oligonucleotides having related,
 CC but different nucleobase sequences, and quantification of different
 CC species of deletion sequence ("target") oligonucleotides in a mixture.
 CC Also, if the specificity of the oligonucleotide's nucleobase sequence for
 CC its reverse complement is not modified, the method may be performed using
 CC oligodeoxynucleotides
 CC
 SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
 XX
 QY Query Match 83.3%; Score 15; DB 2; Length 17;
 Best Local Similarity 93.3%; Pred. No. 4e+02; 0; Indels 0; Gaps 0;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 DB 1 AGAGGUGCCACGCG 15
 15 AGAGGCTCCGACGCG 1
 XX
 RESULT 42
 ABR90271/c
 ID ABR90271 standard; DNA; 17 BP.
 XX
 AC ABR90271;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Bcl-2-targeting antisense oligonucleotide #8.
 XX
 KM Antisense; ss; probe; Bcl-2; cell proliferative disorder; cancer; CRB;
 KM CAMP response element; bacterial infection; viral infection;
 KM inflammation; anaphylaxis; allergy; arthritis; asthma; cytostatic;
 KM autoimmune disorder; parasitic infection; vitruclide; hyperplasia;
 KM tumorigenesis; hepatitis B infection; human.
 XX

OS Homo sapiens.
 XX
 PN WO200257480-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 22-JAN-2002; 2002WO-US001967.
 XX
 PR 22-JAN-2001; 2001US-0263244P.
 XX
 PA (GENT-) GENTA INC.
 XX
 PI Klem RB;
 XX
 DR WPI; 2002-590754/63.
 XX
 PT Hybrid oligomer comprises a cyclic AMP response element sequence and a
 PT sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for
 PT preventing or treating cell-proliferative disorders e.g., cancer.
 XX
 PS Disclosure; Page 13; 78pp; English.
 XX
 CC The invention relates to a hybrid oligomer comprising a cyclic AMP
 CC response element (CRE) sequence and a sequence that hybridizes to the bcl
 CC -2 pre-mRNA or mRNA. Also included are: (1) inhibiting the growth of
 CC cancer cells in vitro, which comprises contacting the cancer cells with a
 CC hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer;
 CC (2) treating or preventing cancer in a human, which comprises
 CC administering a hybrid oligomer or a bcl-2 antisense oligomer and a CRE
 CC decoy oligomer; and (3) a pharmaceutical composition comprising a hybrid
 CC oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer and a
 CC carrier. The pharmaceutical composition of the invention is useful for
 CC preventing or treating cell-proliferative disorders e.g., cancer,
 CC hyperplasia or tumorigenesis and also bacterial infection, viral
 CC infection, inflammation, anaphylaxis, allergy, arthritis, asthma,
 CC autoimmune disorders and parasitic infection. The CRE decoy oligomer and
 CC bcl-2 antisense oligomer are also useful for preventing or treating
 CC hepatitis B virus infection. The hybrid oligomers can also be used for
 CC screening candidate transcription factors or other molecules e.g., gene
 CC regulatory proteins or for diagnostic assays. The present sequence is a
 CC Bcl-2 antisense oligonucleotide
 CC
 SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
 XX
 QY Query Match 83.3%; Score 15; DB 6; Length 17;
 Best Local Similarity 93.3%; Pred. No. 4e+02; 0; Indels 0; Gaps 0;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 DB 1 AGAGGUGCCACGCG 15
 15 AGAGGCTCCGACGCG 1
 XX
 RESULT 43
 ABR78529/c
 ID ABR78529 standard; DNA; 17 BP.
 XX
 AC ABR78529;
 XX
 DT 25-NOV-2002 (first entry).
 XX
 DE Antisense oligodeoxynucleotide of the human bcl-2 gene.
 XX
 KM Antisense oligonucleotide; B cell lymphoma/leukemia-2 gene; bcl-2 gene;
 KM cancer; lymphoma; leukemia; chemotherapeutic agent; bone marrow purging;
 KM autoimmune disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6414134-B1.
 XX
 PD 02-JUL-2002.
 XX

PF 28-NOV-2000; 2000US-00724426.
 XX
 XX 22-DEC-1988; 88US-00288692.
 PR 21-FEB-1992; 92US-00840716.
 PR 20-SEP-1993; 93US-00124256.
 PR 05-JUN-1995; 95US-00465485.
 PR 18-MAY-1998; 98US-00080285.
 PR 17-AUG-1999; 99US-00375514.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Reed JC;
 XX
 DR WPI; 2002-641579/69.
 XX
 XX Novel antisense oligonucleotide complementary to B cell lymphoma/leukemia
 PT -2 mRNA, useful for inhibiting cancer cell growth, for treating
 PT autoimmune disorders, and for ex vivo bone marrow purging.
 XX
 PS Example 12; Col 17; 41pp; English.
 XX
 XX The present sequence represents an antisense oligonucleotide
 CC complementary to B cell lymphoma/leukemia-2 (bcl-2) mRNA. The antisense
 CC oligonucleotide is useful for inhibiting cancer cell (lymphoma or
 CC leukemia cells) growth, for increasing the sensitivity of cancer cells to
 CC cancer chemotherapeutic agents, or for inducing cancer cell death alone
 CC or in combination with any one or more cancer chemotherapeutic agents. It
 CC is also useful for reducing the bcl-2 gene expression or impairing bcl-2
 CC protein function, for ex vivo bone marrow purging, for removing residual
 CC malignant cells from the bone marrow, for inhibiting cancer of neoplastic
 CC cell growth, and for treating autoimmune disease
 XX
 SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 83.3%; Score 15; DB 6; Length 17;
 Best Local Similarity 93.3%; Pred. No. 4e+02; Indels 0; Gaps 0;
 Matches 14; Conservative 1; Mismatches 0;
 QY 1 AGAGGGGCGCAGCG 15
 Db 15 AGAGGGGCGCAGCG 1
 XX
 RESULT 44
 ABL54156/c
 ID ABL54156 standard; DNA; 17 BP.
 XX
 AC ABL54156;
 XX
 DT 12-JUL-2002 (first entry)
 XX
 DE Bcl-2 antisense oligonucleotide.
 XX
 XX B cell lymphoma/leukemia-2; bcl-2; oncogene; antisense; lymphoma;
 KW leukemia; colon carcinoma; rectal carcinoma; pancreatic cancer;
 KW breast cancer; ovarian cancer; prostate cancer; renal cell carcinoma;
 KW hepatoma; bile duct carcinoma; choriocarcinoma; cervical cancer;
 KW testicular cancer; lung carcinoma; bladder carcinoma; melanoma;
 KW head and neck cancer; brain cancer; cytostatic; human; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200217852-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 23-AUG-2001; 2001WO-US026414.
 XX
 XX 25-AUG-2000; 2000US-0227970P.
 PR 29-SEP-2000; 2000US-0237009P.
 PR 10-NOV-2000; 2000US-00709170.
 XX
 XX (GENT-) GENTA INC.
 PA

XX
 PI Warrel RP, Klem RE, Finger H;
 XX
 DR WPI; 2002-371796/40.
 XX
 XX Treating or preventing cancer, tumors and carcinomas, comprises
 PT administering B cell lymphoma/leukemia-2 antisense oligonucleotide at
 PT high doses for short period for time with one or more cancer
 PT therapeutics.
 XX
 PS Disclosure; Page 54; 64pp; English.
 XX
 XX The present sequence is that of a B cell lymphoma/leukemia-2 (bcl-2)
 CC antisense oligonucleotide. The present invention is directed to the use
 CC of bcl-2 antisense oligomers, particularly G3139 (see ABL54148), to treat
 CC and prevent bcl-2 related disorders. Administration at high doses results
 CC in significant therapeutic responses, including low toxicity, high
 CC tolerance and prolonged survival. Administration at high doses for short
 CC periods of time (less than 14 days) also provides significant therapeutic
 CC responses in the treatment of cancer. The bcl-2 antisense oligomer may
 CC also be used to increase the sensitivity of a subject to cancer
 CC therapeutics, and in combination with hormone treatment or gene therapy.
 CC Conditions that may be treated or prevented include cancer of the
 CC hematopoietic system, skin, bone and soft tissue, reproductive system,
 CC genitourinary system, breast, endocrine system, brain, central nervous
 CC system, peripheral nervous system, kidney, lung, respiratory system,
 CC thorax, gastrointestinal and alimentary canal, lymph nodes, pancreas,
 CC hepatobiliary system, or cancer of unknown primary site, non-Hodgkin's
 CC lymphoma, Hodgkin's lymphoma, leukemia, colon carcinoma, rectal
 CC carcinoma, pancreatic, breast, ovarian, prostate, cervical, testicular,
 CC head and neck or brain cancer, renal cell carcinoma, hepatoma, bile duct
 CC carcinoma, choriocarcinoma, lung carcinoma, bladder carcinoma and
 CC melanoma (all claimed)
 XX
 SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 83.3%; Score 15; DB 6; Length 17;
 Best Local Similarity 93.3%; Pred. No. 4e+02; Indels 0; Gaps 0;
 Matches 14; Conservative 1; Mismatches 0;
 QY 1 AGAGGGGCGCAGCG 15
 Db 15 AGAGGGGCGCAGCG 1
 XX
 RESULT 45
 ADW13837/c
 ID ADW13837 standard; DNA; 17 BP.
 XX
 AC ADW13837;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE Bcl-2 antisense oligodeoxynucleotide, SEQ ID 8.
 XX
 XX cancer; bcl-2; chemotherapy; cytostatic; gene therapy;
 KW non-hodgkin lymphoma; prostate tumor; breast tumor;
 KW gastrointestinal tumor; colon tumor; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6841541-B1.
 XX
 PD 11-JAN-2005.
 XX
 PF 28-NOV-2000; 2000US-00724425.
 XX
 XX 21-FEB-1992; 92US-00840716.
 PR 20-SEP-1993; 93US-00124256.
 PR 05-JUN-1995; 95US-00465485.
 PR 18-MAY-1998; 98US-00080285.
 PR 22-DEC-1998; 98US-00288692.
 PR 17-AUG-1999; 99US-00375514.
 XX

XX (UTPR-) UNTV PENNSYLVANIA.
 XX Reed JC;
 XX WPI; 2005-072307/08.
 XX Treating cancer, e.g. non-Hodgkin's lymphoma, prostate cancer, or breast
 PT cancer, by administering an amount of anticodon oligomer for treating the
 PT cancer.
 XX Example 12; SEQ ID NO 8; 41pp; English.
 XX The invention relates to a novel method for treating cancer in a human,
 CC comprising the administration of anticodon oligomers for treating bcl-2
 CC gene expressing cancer cells. The invention further comprises: a
 CC pharmaceutical composition comprising an anticodon oligomer, and a
 CC pharmaceutical carrier; and increasing the sensitivity of a tumor cell to
 CC a chemotherapeutic agent. The anticodon oligomers have cytostatic
 CC activity. The oligomers may be used in gene therapy to treat cancer. The
 CC method is also useful for increasing the sensitivity of a tumor cell to a
 CC chemotherapeutic agent. The types of treatable cancer include non-
 CC Hodgkin's lymphoma, prostate cancer, breast cancer, gastro-intestinal
 CC cancer, or colon cancer. The anticodon oligomers are useful for inhibiting
 CC growth of cancer cells or killing tumor cells. This polynucleotide
 CC sequence represents a bcl-2 oligodeoxynucleotide of the invention.
 XX Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 83.3%; Score 15; DB 14; Length 17;
 Best Local Similarity 93.3%; Pred. No. 4e+02;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGAGGTCGCGACGCG 15
 DB 15 AGAGGTCGCGACGCG 1
 RESULT 46
 ADZ84115/c
 ID ADZ84115 standard; DNA; 17 BP.
 XX
 AC ADZ84115;
 XX
 DT 14-JUL-2005 (first entry)
 XX
 DE Human bcl-2 antisense oligonucleotide, SEQ ID NO:25.
 XX
 KW Drug delivery; antisense therapy; antisense oligonucleotide;
 KW cell proliferation; cancer; tumor; neoplasm; cytostatic; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6887906-B1.
 XX
 PD 03-MAY-2005.
 XX
 PF 01-JUL-1998; 98US-00108673.
 XX
 PR 01-JUL-1997; 97US-00866829.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Teng C, Hardee G;
 XX
 DR WPI; 2005-321255/33.
 XX
 PT Composition useful for enhancing the transport of nucleic acids at
 PT various sites in the alimentary canal, comprising a modified nucleic acid
 PT and capric acid and lauric acid or their salts.
 XX
 PS Example 2; SEQ ID NO 25; 65pp; English.
 XX

CC The invention relates to a composition comprising a nucleic acid with a
 CC modified nucleobase or a modified sugar residue, and capric acid and
 CC lauric acid or pharmaceutically acceptable salts thereof. The modified
 CC nucleic acid used in the composition of the invention is especially an
 CC antisense oligonucleotide which decreases the expression of a cellular
 CC adhesion protein or the rate of cellular proliferation, and preferably
 CC contains a 5-methyl-cytosine base or a 2'-methoxyethoxy (2'-MOE) sugar
 CC modification. Depending on the molecular target of the antisense
 CC oligonucleotide present in the composition, the compositions can be used
 CC for the treatment of cancers and tumors, Alzheimer's disease, beta-
 CC thalassemia, parasite infections and viral (including retroviral) in-
 CC fections. The fatty acids capric and lauric acid (and their
 CC pharmaceutically acceptable salts) serve as penetration enhancers which
 CC facilitate the transport of the therapeutic nucleic acid across mucous
 CC membranes such as those of the alimentary canal, thereby increasing their
 CC alimentary bioavailability. The composition of the invention is therefore
 CC useful for the oral or rectal delivery of therapeutic nucleic acids such
 CC as antisense oligonucleotides which to date have required parenteral
 CC administration. The compositions therefore reduce the complications
 CC (e.g. the need for sterile procedures and patient hospitalization) and
 CC the concomitant expense associated with intravenous and other traumatic
 CC means of administering therapeutic nucleic acids. Sequences ADZ84098-
 CC ADZ84140 and ADZ84221 represent antisense oligonucleotides that modulate
 CC cellular proliferation which may be used in compositions of the invention
 CC for the treatment of tumors.
 XX Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 83.3%; Score 15; DB 14; Length 17;
 Best Local Similarity 93.3%; Pred. No. 4e+02;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGAGGTCGCGACGCG 15
 DB 15 AGAGGTCGCGACGCG 1
 RESULT 47
 ADM36038/c
 ID ADM36038 standard; DNA; 18 BP.
 XX
 AC ADM36038;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Immunostimulatory CpG/dU DNA oligonucleotide #41.
 XX
 KW ss; immunostimulatory; deoxyinosine; deoxyuridine; antigenic;
 KW immune system deficiency; autoimmune disorder;
 KW systemic lupus erythematosus; SLE; myasthenia gravis;
 KW immunodeficiency disorder; AIDS; malignant tumor; gastric cancer;
 KW skin cancer; leukaemia; lymphoma; infectious disease; dermatological;
 KW immunosuppressive; antiinflammatory; antibacterial; virucide;
 KW antiparasitic; cytostatic; antirheumatic; antitubercitic; neuroprotective;
 KW antimicrobial; antiallergic; immunopharmacological.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT 1. 18
 FT modified_base /tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= Any n represents deoxyuridine or
 FT deoxyinosine"
 XX
 PN WO2003047602-A1.
 XX
 PD 12-JUN-2003.
 XX
 PF 05-DEC-2002; 2002WO-EP013791.
 XX
 PR 07-DEC-2001; 2001AT-00001924.
 XX

PA (INTE-) INTERCELL BIOMEDIZINISCHE FORSCHUNGS.
 XX
 XX Schmidt W, Schellack C, Eyed A, Lingnan K;
 XX
 XX WPI; 2003-569024/53.
 DR
 XX
 XX
 PT Use of an immunostimulatory oligodeoxynucleic acid molecule in the
 PT preparation of pharmaceutical composition for treating e.g. systemic
 PT lupus erythematosus, sepsis or viral infections.
 XX
 XX
 PS Example 14; Page 111; 139pp; English.
 XX
 XX This invention relates to a novel use of immunostimulatory
 CC oligodeoxynucleic acid molecules (ODNs) that contain deoxyinosine (di) or
 CC deoxyuridine (du). Specifically, it refers to ODN molecules that encode
 CC antigenic proteins, yet do not induce the systemic production of pro-
 CC inflammatory cytokines such as TNF-alpha and interleukin-6 (IL-6), thus
 CC reducing the induction of potential harmful side effects. The present
 CC invention describes compositions that are useful for preparing a
 CC pharmaceutical composition that can activate dendritic cells, B cells,
 CC natural killer cells and hence treat an immune system deficiency.
 CC Furthermore, they can be used to treat various diseases including
 CC autoimmune disorders such as systemic lupus erythematosus (SLE) and
 CC myasthenia gravis, immunodeficiency disorders such as AIDS, malignant
 CC tumours that cause gastric and skin cancer as well as leukaemia and
 CC lymphoma, and various infectious diseases for example from bacteria,
 CC viruses and protozoa. Accordingly, such compositions exhibit
 CC dermatological, immunosuppressive, antiinflammatory, antibacterial,
 CC virucide, antiparasitic, cytostatic, antirheumatic, antiarthritic,
 CC neuroprotective, antitubercular and antiallergic activities. These
 CC oligodeoxynucleotides have immunopharmacological activity and induce a
 CC synergistic antigen specific immune response of an immunopotentiating
 CC cytokine. This oligonucleotide sequence is an immunostimulatory di/du
 CC containing ODN taken from table 1 of the invention.
 XX
 SQ Sequence 18 BP; 2 A; 8 C; 1 G; 4 T; 0 U; 3 Other;
 Query Match 83.3%; Score 15; DB 11; Length 18;
 Best Local Similarity 72.2%; Pred. No. 4e+02;
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 AGAGGCGCGACGCGGUA 18
 Db 18 AGAGGCTGCGANGNGTA 1
 RESULT 48
 ADM35932/C
 ID ADM35932 standard; DNA; 18 BP.
 XX
 AC ADM35932;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 XX DNA oligo #3 useful for induction of natural killer lytic activity.
 DE
 XX
 XX as; immunostimulatory; deoxyinosine; deoxyuridine; antigenic;
 KW immune system deficiency; autoimmune disorder;
 KW systemic lupus erythematosus; SLE; myasthenia gravis;
 KW immunodeficiency disorder; AIDS; malignant tumour; gastric cancer;
 KW skin cancer; leukaemia; lymphoma; infectious disease; dermatological;
 KW immunosuppressive; antiinflammatory; antibacterial; virucide;
 KW antiparasitic; cytostatic; antirheumatic; antiarthritic; neuroprotective;
 KW antitubercular; antiallergic; immunopharmacological.
 XX
 OS Synthetic.
 XX
 EH Key Location/Qualifiers
 FT modified_base 1..18
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= OTHER= Any n represents deoxyuridine or
 FT deoxyinosine.

XX
 PN WO2003047602-A1.
 XX
 XX 12-JUN-2003.
 PD
 XX
 XX 05-DEC-2002; 2002WO-EP013791.
 PF
 XX 07-DEC-2001; 2001AT-00001924.
 PR
 XX
 XX (INTE-) INTERCELL BIOMEDIZINISCHE FORSCHUNGS.
 PA
 XX
 XX Schmidt W, Schellack C, Eyed A, Lingnan K;
 XX
 XX WPI; 2003-569024/53.
 DR
 XX
 XX
 PT Use of an immunostimulatory oligodeoxynucleic acid molecule in the
 PT preparation of pharmaceutical composition for treating e.g. systemic
 PT lupus erythematosus, sepsis or viral infections.
 XX
 XX
 PS Example 14; Page 107; 139pp; English.
 XX
 XX This invention relates to a novel use of immunostimulatory
 CC oligodeoxynucleic acid molecules (ODNs) that contain deoxyinosine (di) or
 CC deoxyuridine (du). Specifically, it refers to ODN molecules that encode
 CC antigenic proteins, yet do not induce the systemic production of pro-
 CC inflammatory cytokines such as TNF-alpha and interleukin-6 (IL-6), thus
 CC reducing the induction of potential harmful side effects. The present
 CC invention describes compositions that are useful for preparing a
 CC pharmaceutical composition that can activate dendritic cells, B cells,
 CC natural killer cells and hence treat an immune system deficiency.
 CC Furthermore, they can be used to treat various diseases including
 CC autoimmune disorders such as systemic lupus erythematosus (SLE) and
 CC myasthenia gravis, immunodeficiency disorders such as AIDS, malignant
 CC tumours that cause gastric and skin cancer as well as leukaemia and
 CC lymphoma, and various infectious diseases for example from bacteria,
 CC viruses and protozoa. Accordingly, such compositions exhibit
 CC dermatological, immunosuppressive, antiinflammatory, antibacterial,
 CC virucide, antiparasitic, cytostatic, antirheumatic, antiarthritic,
 CC neuroprotective, antitubercular and antiallergic activities. These
 CC oligodeoxynucleotides have immunopharmacological activity and induce a
 CC synergistic antigen specific immune response of an immunopotentiating
 CC cytokine. This oligonucleotide sequence is an immunostimulatory di/du
 CC containing ODN of the invention.
 XX
 SQ Sequence 18 BP; 2 A; 8 C; 1 G; 4 T; 0 U; 3 Other;
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 Db 18 AGAGGCTGCGANGNGTA 1
 RESULT 49
 ADQ17851
 ID ADQ17851 standard; DNA; 337 BP.
 XX
 AC ADQ17851;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 668.
 DE
 XX
 XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
 KW ds.
 KW
 XX
 OS Homo sapiens.
 XX
 XX WO2004048938-A2.
 PN
 XX 10-JUN-2004.
 PD

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XX 26-NOV-2003; 2003MO-US038193.
PR
XX
XX 26-NOV-2002; 2002US-0429739P.
PR
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
PA
XX
XX Aziz N, Ginsburg WM, Zlotnick A;
PI
XX
XX WPI; 2004-441208/41.
DR
XX
XX
XX Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
XX
XX Example 2; SEQ ID NO 668; 210bp; English.
PS
XX
XX The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
XX
XX Sequence 337 BP; 55 A; 98 C; 107 G; 77 T; 0 U; 0 Other;
SQ
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Best Local Similarity 93.3%; Pred. No. 4.3e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 128 GAGGGTCCGACGCGG 142

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DR WPI; 2001-514838/56.
DR
XX P-PSDB; AAO12046.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX
XX Claim 1; SEQ ID NO 12037; 1399bp + Sequence Listing; English.
XX
XX
XX The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pat_sequences
XX
XX
XX Sequence 381 BP; 87 A; 91 C; 108 G; 95 T; 0 U; 0 Other;
SQ
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Best Local Similarity 93.3%; Pred. No. 4.3e+02;
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DB 20 GAGGGTCCGACGCGG 34

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AC
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XX 06-NOV-2001 (first entry)
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XX Human polynucleotide SEQ ID NO 12037.
DB
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XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukemia;
XX nervous system disorders; arthritis; inflammation; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200164835-A2.
PN
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XX 07-SEP-2001.
PD
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XX 26-FEB-2001; 2001MO-US004927.
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XX 28-FEB-2000; 2000US-00515126.
PR
XX 18-MAY-2000; 2000US-00577409.
XX
XX (HYSE-) HYSEQ INC.
PA
XX
XX Tang YT, Liu C, Drmanac RT;
PI
XX

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C 123	11.4	81.4	19	10	US-11-101-244-729727	Sequence 729727, A	C 196	11.4	81.4	422	6	US-09-925-065A-392823	Sequence 392823, A
C 124	11.4	81.4	19	10	US-11-101-244-924735	Sequence 924735, A	C 197	11.4	81.4	423	7	US-10-932-182A-2697	Sequence 2697, Ap
C 125	11.4	81.4	19	10	US-11-101-244-1137219	Sequence 1137219, A	C 198	11.4	81.4	423	7	US-10-932-182A-2697	Sequence 2697, Ap
C 126	11.4	81.4	19	10	US-11-101-244-1250575	Sequence 1250575, A	C 199	11.4	81.4	427	6	US-09-925-065A-207157	Sequence 207157, A
C 127	11.4	81.4	19	10	US-11-101-244-1270527	Sequence 1270527, A	C 200	11.4	81.4	442	6	US-09-925-065A-472173	Sequence 472173, A
C 128	11.4	81.4	19	10	US-11-101-244-1342155	Sequence 1342155, A	C 201	11.4	81.4	446	6	US-09-925-065A-470329	Sequence 470329, A
C 129	11.4	81.4	19	11	US-11-083-784-84431	Sequence 84431, A	C 202	11.4	81.4	486	6	US-09-925-065A-740815	Sequence 740815, A
C 130	11.4	81.4	19	11	US-11-083-784-84521	Sequence 84521, A	C 203	11.4	81.4	488	6	US-09-925-065A-489817	Sequence 489817, A
C 131	11.4	81.4	19	11	US-11-083-784-336099	Sequence 336099, A	C 204	11.4	81.4	503	6	US-09-925-065A-208087	Sequence 208087, A
C 132	11.4	81.4	19	11	US-11-083-784-341997	Sequence 341997, A	C 205	11.4	81.4	503	6	US-09-925-065A-208088	Sequence 208088, A
C 133	11.4	81.4	19	11	US-11-083-784-348963	Sequence 348963, A	C 206	11.4	81.4	504	6	US-09-925-065A-355321	Sequence 355321, A
C 134	11.4	81.4	19	11	US-11-083-784-560794	Sequence 560794, A	C 207	11.4	81.4	506	6	US-09-925-065A-624825	Sequence 624825, A
C 135	11.4	81.4	19	11	US-11-083-784-647858	Sequence 647858, A	C 208	11.4	81.4	511	6	US-09-925-065A-760089	Sequence 760089, A
C 136	11.4	81.4	19	11	US-11-083-784-729727	Sequence 729727, A	C 209	11.4	81.4	523	6	US-09-925-065A-558558	Sequence 558558, A
C 137	11.4	81.4	19	11	US-11-083-784-924735	Sequence 924735, A	C 210	11.4	81.4	524	12	US-11-128-061-1216	Sequence 1216, Ap
C 138	11.4	81.4	19	11	US-11-083-784-1137219	Sequence 1137219, A	C 211	11.4	81.4	524	12	US-11-128-061-1216	Sequence 1216, Ap
C 139	11.4	81.4	19	11	US-11-083-784-1250575	Sequence 1250575, A	C 212	11.4	81.4	524	12	US-11-128-061-1216	Sequence 1216, Ap
C 140	11.4	81.4	19	11	US-11-083-784-1270527	Sequence 1270527, A	C 213	11.4	81.4	524	12	US-11-128-049-4858	Sequence 4858, Ap
C 141	11.4	81.4	20	7	US-11-083-784-1342155	Sequence 1342155, A	C 214	11.4	81.4	533	6	US-09-925-065A-392822	Sequence 392822, A
C 142	11.4	81.4	20	7	US-10-831-286A-22449	Sequence 22449, A	C 215	11.4	81.4	533	6	US-09-925-065A-392824	Sequence 392824, A
C 143	11.4	81.4	20	12	US-10-831-286A-22896	Sequence 22896, A	C 216	11.4	81.4	537	6	US-09-925-065A-593536	Sequence 593536, A
C 144	11.4	81.4	20	12	US-11-226-943-7	Sequence 7, Appl	C 217	11.4	81.4	542	9	US-11-116-881A-616	Sequence 616, App
C 145	11.4	81.4	20	12	US-11-226-943-78	Sequence 78, Appl	C 218	11.4	81.4	545	6	US-09-925-065A-42076	Sequence 42076, A
C 146	11.4	81.4	21	8	US-10-310-914A-53884	Sequence 53884, A	C 219	11.4	81.4	545	6	US-09-925-065A-939369	Sequence 939369, A
C 147	11.4	81.4	24	8	US-10-310-914A-883471	Sequence 883471, A	C 220	11.4	81.4	548	6	US-09-925-065A-12538	Sequence 12538, A
C 148	11.4	81.4	25	7	US-10-932-182A-28325	Sequence 28325, A	C 221	11.4	81.4	548	6	US-09-925-065A-42462	Sequence 42462, A
C 149	11.4	81.4	25	7	US-10-932-182A-68934	Sequence 68934, A	C 222	11.4	81.4	551	6	US-09-925-065A-768235	Sequence 768235, A
C 150	11.4	81.4	25	7	US-10-932-182A-68937	Sequence 68937, A	C 223	11.4	81.4	551	6	US-09-925-065A-790930	Sequence 790930, A
C 151	11.4	81.4	25	7	US-10-932-182A-68938	Sequence 68938, A	C 224	11.4	81.4	551	6	US-09-925-065A-790930	Sequence 790930, A
C 152	11.4	81.4	25	7	US-10-932-182A-68939	Sequence 68939, A	C 225	11.4	81.4	553	6	US-09-925-065A-552124	Sequence 552124, A
C 153	11.4	81.4	25	7	US-10-932-182A-68939	Sequence 68939, A	C 226	11.4	81.4	553	6	US-09-925-065A-153267	Sequence 153267, A
C 154	11.4	81.4	25	7	US-10-932-182A-90577	Sequence 90577, A	C 227	11.4	81.4	555	6	US-09-925-065A-789150	Sequence 789150, A
C 155	11.4	81.4	25	7	US-10-932-182A-115957	Sequence 115957, A	C 228	11.4	81.4	555	6	US-09-925-065A-789151	Sequence 789151, A
C 156	11.4	81.4	25	7	US-10-932-182A-28325	Sequence 28325, A	C 229	11.4	81.4	559	6	US-09-925-065A-263542	Sequence 263542, A
C 157	11.4	81.4	25	7	US-10-932-182A-68934	Sequence 68934, A	C 230	11.4	81.4	561	6	US-09-925-065A-119415	Sequence 119415, A
C 158	11.4	81.4	25	7	US-10-932-182A-68937	Sequence 68937, A	C 231	11.4	81.4	561	6	US-09-925-065A-119415	Sequence 119415, A
C 159	11.4	81.4	25	7	US-10-932-182A-68938	Sequence 68938, A	C 232	11.4	81.4	565	6	US-09-925-065A-149751	Sequence 149751, A
C 160	11.4	81.4	25	7	US-10-932-182A-68939	Sequence 68939, A	C 233	11.4	81.4	565	6	US-09-925-065A-149752	Sequence 149752, A
C 161	11.4	81.4	25	7	US-10-932-182A-90577	Sequence 90577, A	C 234	11.4	81.4	565	6	US-09-925-065A-291745	Sequence 291745, A
C 162	11.4	81.4	25	7	US-10-932-182A-115957	Sequence 115957, A	C 235	11.4	81.4	565	6	US-09-925-065A-355603	Sequence 355603, A
C 163	11.4	81.4	25	7	US-10-933-982-39124	Sequence 39124, A	C 236	11.4	81.4	566	6	US-09-925-065A-355604	Sequence 355604, A
C 164	11.4	81.4	25	7	US-10-933-982-62646	Sequence 62646, A	C 237	11.4	81.4	566	6	US-09-925-065A-271433	Sequence 271433, A
C 165	11.4	81.4	25	7	US-10-933-982-62646	Sequence 62646, A	C 238	11.4	81.4	566	6	US-09-925-065A-271433	Sequence 271433, A
C 166	11.4	81.4	25	7	US-10-933-982-101441	Sequence 101441, A	C 239	11.4	81.4	568	6	US-09-925-065A-271434	Sequence 271434, A

C 240	11.4	81.4	568	6	US-09-925-065A-421457	Sequence 421457,	C 313	11.4	81.4	653	6	US-09-925-065A-840013	Sequence 840013,
C 241	11.4	81.4	569	6	US-09-925-065A-490760	Sequence 490760,	C 314	11.4	81.4	660	6	US-09-925-065A-354747	Sequence 354747,
C 242	11.4	81.4	573	6	US-09-925-065A-402205	Sequence 402205,	C 315	11.4	81.4	660	6	US-09-925-065A-354748	Sequence 354748,
C 243	11.4	81.4	573	6	US-09-925-065A-412582	Sequence 412582,	C 316	11.4	81.4	660	6	US-09-925-065A-906681	Sequence 906681,
C 244	11.4	81.4	576	6	US-09-925-065A-412583	Sequence 412583,	C 317	11.4	81.4	668	12	US-11-136-527-1493	Sequence 1493, Ap
C 245	11.4	81.4	576	6	US-09-925-065A-106712	Sequence 106712,	C 318	11.4	81.4	683	6	US-09-925-065A-908737	Sequence 908737,
C 246	11.4	81.4	580	6	US-09-925-065A-144982	Sequence 144982,	C 319	11.4	81.4	708	6	US-09-925-065A-847600	Sequence 847600,
C 247	11.4	81.4	580	6	US-09-925-065A-148748	Sequence 148748,	C 320	11.4	81.4	708	6	US-09-925-065A-847601	Sequence 847601,
C 248	11.4	81.4	581	6	US-09-925-065A-419877	Sequence 419877,	C 321	11.4	81.4	732	7	US-10-932-182A-2479	Sequence 2479, Ap
C 249	11.4	81.4	581	6	US-09-925-065A-419878	Sequence 419878,	C 322	11.4	81.4	732	7	US-10-932-182A-2479	Sequence 2479, Ap
C 250	11.4	81.4	581	6	US-09-925-065A-419879	Sequence 419879,	C 323	11.4	81.4	750	7	US-10-932-182A-4661	Sequence 4661, Ap
C 251	11.4	81.4	582	6	US-09-925-065A-477973	Sequence 477973,	C 324	11.4	81.4	750	7	US-10-932-182A-4661	Sequence 4661, Ap
C 252	11.4	81.4	583	6	US-09-925-065A-116860	Sequence 116860,	C 325	11.4	81.4	756	7	US-10-510-959-2	Sequence 2, Appl1
C 253	11.4	81.4	583	6	US-09-925-065A-116861	Sequence 116861,	C 326	11.4	81.4	759	8	US-10-750-623-50114	Sequence 50114, A
C 254	11.4	81.4	583	6	US-09-925-065A-116862	Sequence 116862,	C 327	11.4	81.4	759	8	US-10-750-623-50114	Sequence 50114, A
C 255	11.4	81.4	583	6	US-09-925-065A-116863	Sequence 116863,	C 328	11.4	81.4	783	8	US-10-467-657-599	Sequence 599, App
C 256	11.4	81.4	584	6	US-09-925-065A-168782	Sequence 168782,	C 329	11.4	81.4	793	8	US-10-750-185-59353	Sequence 59353, A
C 257	11.4	81.4	587	6	US-09-925-065A-529457	Sequence 529457,	C 330	11.4	81.4	793	8	US-10-750-623-59353	Sequence 59353, A
C 258	11.4	81.4	587	6	US-09-925-065A-529458	Sequence 529458,	C 331	11.4	81.4	825	8	US-10-467-657-2241	Sequence 2241, Ap
C 259	11.4	81.4	587	6	US-09-925-065A-529459	Sequence 529459,	C 332	11.4	81.4	832	6	US-09-925-065A-679848	Sequence 679848,
C 260	11.4	81.4	588	6	US-09-925-065A-477972	Sequence 477972,	C 333	11.4	81.4	834	8	US-10-750-185-49368	Sequence 49368, A
C 261	11.4	81.4	589	6	US-09-925-065A-291182	Sequence 291182,	C 334	11.4	81.4	834	8	US-10-750-623-49368	Sequence 49368, A
C 262	11.4	81.4	589	6	US-09-925-065A-537680	Sequence 537680,	C 335	11.4	81.4	856	9	US-11-096-568A-4928	Sequence 4928, Ap
C 263	11.4	81.4	591	6	US-09-925-065A-538282	Sequence 538282,	C 336	11.4	81.4	886	9	US-11-096-568A-20682	Sequence 20682, A
C 264	11.4	81.4	591	6	US-09-925-065A-538283	Sequence 538283,	C 337	11.4	81.4	891	7	US-10-932-182A-2025	Sequence 2025, Ap
C 265	11.4	81.4	591	6	US-09-925-065A-538284	Sequence 538284,	C 338	11.4	81.4	891	7	US-10-932-182A-2025	Sequence 2025, Ap
C 266	11.4	81.4	595	6	US-09-925-065A-556162	Sequence 556162,	C 339	11.4	81.4	916	7	US-09-925-065A-42170	Sequence 42170, A
C 267	11.4	81.4	596	6	US-09-925-065A-126154	Sequence 126154,	C 340	11.4	81.4	969	7	US-10-932-182A-2129	Sequence 2129, Ap
C 268	11.4	81.4	600	6	US-09-925-065A-168975	Sequence 168975,	C 341	11.4	81.4	969	7	US-10-932-182A-2129	Sequence 2129, Ap
C 269	11.4	81.4	600	8	US-10-750-185-235	Sequence 235, App	C 342	11.4	81.4	994	12	US-11-024-959-183	Sequence 183, App
C 270	11.4	81.4	600	8	US-10-750-185-1663	Sequence 1663, Ap	C 343	11.4	81.4	1014	7	US-10-921-793-53	Sequence 53, Appl1
C 271	11.4	81.4	600	8	US-10-750-623-225	Sequence 225, App	C 344	11.4	81.4	1014	7	US-10-931-198-53	Sequence 53, Appl1
C 272	11.4	81.4	600	8	US-10-750-623-1663	Sequence 1663, App	C 345	11.4	81.4	1026	7	US-10-932-182A-1112	Sequence 1112, Ap
C 273	11.4	81.4	600	12	US-11-136-527-5589	Sequence 5589, Ap	C 346	11.4	81.4	1026	7	US-10-932-182A-1112	Sequence 1112, Ap
C 274	11.4	81.4	603	6	US-09-925-065A-468902	Sequence 468902,	C 347	11.4	81.4	1030	8	US-10-775-169-343	Sequence 343, App
C 275	11.4	81.4	603	6	US-09-925-065A-468903	Sequence 468903,	C 348	11.4	81.4	1040	6	US-09-925-065A-78540	Sequence 78540, A
C 276	11.4	81.4	603	6	US-09-925-065A-468904	Sequence 468904,	C 349	11.4	81.4	1093	6	US-09-925-065A-80603	Sequence 80603, A
C 277	11.4	81.4	603	6	US-09-925-065A-468905	Sequence 468905,	C 350	11.4	81.4	1093	6	US-09-925-065A-80603	Sequence 80603, A
C 278	11.4	81.4	605	6	US-09-925-065A-470416	Sequence 470416,	C 351	11.4	81.4	1107	7	US-10-932-182A-75407	Sequence 75407, A
C 279	11.4	81.4	608	12	US-11-112-908-490	Sequence 490, App	C 352	11.4	81.4	1107	7	US-10-932-182A-75407	Sequence 75407, A
C 280	11.4	81.4	609	8	US-10-467-657-7495	Sequence 7495, Ap	C 353	11.4	81.4	1116	6	US-09-925-065A-699915	Sequence 699915,
C 281	11.4	81.4	611	6	US-09-925-065A-718946	Sequence 718946,	C 354	11.4	81.4	1128	6	US-10-793-626-1171	Sequence 1171, Ap
C 282	11.4	81.4	611	6	US-09-925-065A-718947	Sequence 718947,	C 355	11.4	81.4	1138	6	US-09-925-065A-692849	Sequence 692849,
C 283	11.4	81.4	611	6	US-09-925-065A-718948	Sequence 718948,	C 356	11.4	81.4	1138	6	US-09-925-065A-93708	Sequence 93708, A
C 284	11.4	81.4	611	6	US-09-925-065A-718949	Sequence 718949,	C 357	11.4	81.4	1175	6	US-09-925-065A-93708	Sequence 93708, A
C 285	11.4	81.4	611	6	US-09-925-065A-824936	Sequence 824936,	C 358	11.4	81.4	1175	6	US-09-925-065A-93709	Sequence 93709, A
C 286	11.4	81.4	612	6	US-09-925-065A-137044	Sequence 137044,	C 359	11.4	81.4	1177	6	US-09-925-065A-43709	Sequence 43709, Ap
C 287	11.4	81.4	612	6	US-09-925-065A-137045	Sequence 137045,	C 360	11.4	81.4	1182	7	US-10-932-182A-76041	Sequence 76041, A
C 288	11.4	81.4	614	6	US-09-925-065A-523513	Sequence 523513,	C 361	11.4	81.4	1182	7	US-10-932-182A-76041	Sequence 76041, A
C 289	11.4	81.4	616	6	US-09-925-065A-461824	Sequence 461824,	C 362	11.4	81.4	1182	12	US-11-144-236-7	Sequence 7, Appl1
C 290	11.4	81.4	616	6	US-09-925-065A-461825	Sequence 461825,	C 363	11.4	81.4	1196	8	US-10-750-185-58400	Sequence 58400, A
C 291	11.4	81.4	618	6	US-09-925-065A-938880	Sequence 938880,	C 364	11.4	81.4	1235	8	US-10-750-623-58400	Sequence 58400, A
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C 293	11.4	81.4	621	6	US-09-925-065A-525353	Sequence 525353,	C 366	11.4	81.4	1252	9	US-11-096-568A-7048	Sequence 7048, Ap
C 294	11.4	81.4	621	6	US-09-925-065A-820790	Sequence 820790,	C 367	11.4	81.4	1290	8	US-10-750-185-40140	Sequence 40140, A
C 295	11.4	81.4	622	6	US-09-925-065A-213345	Sequence 213345,	C 368	11.4	81.4	1290	8	US-10-750-623-40140	Sequence 40140, A
C 296	11.4	81.4	622	6	US-09-925-065A-421458	Sequence 421458,	C 369	11.4	81.4	1306	8	US-10-750-185-34631	Sequence 34631, A
C 297	11.4	81.4	622	6	US-09-925-065A-886865	Sequence 886865,	C 370	11.4	81.4	1306	8	US-10-750-623-34631	Sequence 34631, A
C 298	11.4	81.4	623	6	US-09-925-065A-54104	Sequence 54104, A	C 371	11.4	81.4	1329	9	US-10-932-182A-75773	Sequence 75773, A
C 299	11.4	81.4	624	6	US-09-925-065A-409851	Sequence 409851, A	C 372	11.4	81.4	1329	9	US-10-932-182A-75773	Sequence 75773, A
C 300	11.4	81.4	632	6	US-09-925-065A-460178	Sequence 460178,	C 373	11.4	81.4	1348	9	US-11-096-568A-21697	Sequence 21697, A
C 301	11.4	81.4	632	6	US-09-925-065A-469646	Sequence 469646,	C 374	11.4	81.4	1353	8	US-10-750-185-60402	Sequence 60402, A
C 302	11.4	81.4	632	6	US-09-925-065A-687225	Sequence 687225,	C 375	11.4	81.4	1353	8	US-10-750-623-60402	Sequence 60402, A
C 303	11.4	81.4	632	6	US-09-925-065A-903405	Sequence 903405,	C 376	11.4	81.4	1356	8	US-10-510-876-3	Sequence 3, Appl1
C 304	11.4	81.4	635	6	US-09-925-065A-488298	Sequence 488298,	C 377	11.4	81.4	1372	8	US-10-750-185-44630	Sequence 44630, A
C 305	11.4	81.4	636	6	US-09-925-065A-284166	Sequence 284166,	C 378	11.4	81.4	1372	8	US-10-750-623-44630	Sequence 44630, A
C 306	11.4	81.4	636	6	US-09-925-065A-284167	Sequence 284167,	C 379	11.4	81.4	1386	8	US-10-750-185-61595	Sequence 61595, A
C 307	11.4	81.4	640	6	US-09-925-065A-908935	Sequence 908935,	C 380	11.4	81.4	1386	8	US-10-750-623-61595	Sequence 61595, A
C 308	11.4	81.4	644	6	US-09-925-065A-131661	Sequence 131661,	C 381	11.4	81.4	1391	9	US-11-096-568A-10024	Sequence 10024, A
C 309	11.4	81.4	644	6	US-09-925-065A-131662	Sequence 131662,	C 382	11.4	81.4	1396	8	US-10-750-185-30337	Sequence 30337, A
C 310	11.4	81.4	644	6	US-09-925-065A-131663	Sequence 131663,	C 383	11.4	81.4	1396	8	US-10-750-623-30337	Sequence 30337, A
C 311	11.4	81.4	645	6	US-09-925-065A-753018	Sequence 753018,	C 384	11.4	81.4	1399	5	US-09-978-360A-395	Sequence 395, App
C 312	11.4	81.4	645	6	US-09-925-065A-824428	Sequence 824428,	C 385	11.4	81.4	1430	8	US-10-750-185-61160	Sequence 61160, A

532	11	78.6	22	8	US-10-453-372-1326	Sequence 1326, Ap	c 605	11	78.6	454	6	US-09-925-065A-161559	Sequence 161559,
533	11	78.6	23	8	US-10-310-914A-883522	Sequence 883522, Ap	c 606	11	78.6	456	6	US-09-925-065A-456544	Sequence 456544,
534	11	78.6	23	8	US-10-310-914A-1262763	Sequence 1262763,	c 607	11	78.6	470	6	US-09-925-065A-293778	Sequence 293778,
535	11	78.6	24	8	US-10-310-914A-657805	Sequence 657805,	c 608	11	78.6	471	6	US-09-925-065A-223240	Sequence 223240,
536	11	78.6	24	8	US-10-310-914A-1351031	Sequence 1351031,	c 609	11	78.6	472	8	US-10-750-185-35119	Sequence 35119, A
537	11	78.6	25	7	US-10-932-182A-12922	Sequence 12922, A	c 610	11	78.6	473	6	US-09-925-065A-231134	Sequence 231134,
538	11	78.6	25	7	US-10-932-182A-149601	Sequence 149601, A	c 611	11	78.6	476	6	US-09-925-065A-765073	Sequence 765073,
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541	11	78.6	25	7	US-10-933-982-45415	Sequence 45415, A	c 614	11	78.6	478	6	US-09-925-065A-239591	Sequence 239591,
542	11	78.6	25	7	US-10-933-982-60683	Sequence 60683, A	c 615	11	78.6	481	6	US-09-925-065A-345104	Sequence 345104,
543	11	78.6	25	7	US-10-933-982-150739	Sequence 150739,	c 616	11	78.6	481	6	US-09-925-065A-345104	Sequence 345104,
544	11	78.6	25	7	US-10-933-982-194520	Sequence 194520,	c 617	11	78.6	481	6	US-09-925-065A-345105	Sequence 345105,
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548	11	78.6	25	12	US-11-121-849-163441	Sequence 163441,	c 621	11	78.6	491	6	US-09-925-065A-293897	Sequence 293897,
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552	11	78.6	25	12	US-11-121-849-386995	Sequence 386995,	c 625	11	78.6	494	6	US-09-925-065A-487017	Sequence 487017,
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561	11	78.6	25	9	US-11-204-311-674	Sequence 674, App	c 634	11	78.6	505	6	US-09-925-065A-843337	Sequence 843337,
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563	11	78.6	50	12	US-11-175-859-56213	Sequence 56213, A	c 636	11	78.6	507	6	US-09-925-065A-829964	Sequence 829964,
564	11	78.6	50	12	US-11-175-859-57260	Sequence 57260, A	c 637	11	78.6	509	6	US-09-925-065A-407146	Sequence 407146,
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566	11	78.6	195	12	US-11-124-367A-3040	Sequence 3040, Ap	c 639	11	78.6	509	6	US-09-925-065A-843337	Sequence 843337,
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574	11	78.6	201	12	US-11-124-367A-3050	Sequence 3050, Ap	c 647	11	78.6	521	12	US-11-128-061-621	Sequence 621, App
575	11	78.6	201	12	US-11-124-367A-3082	Sequence 3082, Ap	c 648	11	78.6	521	12	US-11-128-049-621	Sequence 621, App
576	11	78.6	201	12	US-11-124-367A-3126	Sequence 3126, Ap	c 649	11	78.6	521	12	US-11-128-049-621	Sequence 621, App
577	11	78.6	201	12	US-11-124-367A-5732	Sequence 5732, Ap	c 650	11	78.6	521	12	US-11-128-049-621	Sequence 621, App
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583	11	78.6	201	12	US-11-124-367A-21067	Sequence 21067, A	c 656	11	78.6	531	6	US-09-925-065A-554859	Sequence 554859,
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586	11	78.6	300	12	US-11-234-786-281	Sequence 281, App	c 659	11	78.6	546	12	US-11-074-176-217	Sequence 217, App
587	11	78.6	330	6	US-09-925-065A-454519	Sequence 454519,	c 660	11	78.6	546	6	US-09-925-065A-578020	Sequence 578020,
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589	11	78.6	363	7	US-10-993-543-9	Sequence 9, App11	c 662	11	78.6	551	6	US-09-925-065A-446881	Sequence 446881,
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719	11	78.6	598	6	US-09-925-065A-454516	Sequence 454516,	792	11	78.6	705	8	US-10-453-372-421	Sequence 421, App
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732	11	78.6	600	8	US-10-750-623-20461	Sequence 20461, A	805	11	78.6	864	6	US-09-925-065A-56818	Sequence 56818, A
733	11	78.6	600	12	US-11-136-527-4624	Sequence 4624, Ap	806	11	78.6	864	6	US-09-925-065A-56819	Sequence 56819, A
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ALIGNMENTS

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RESULT 1
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; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30493
; LENGTH: 542
; TYPE: DNA
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US-09-925-065A-30493

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; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
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US-10-932-182A-162449

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; Publication No. US20060046253A1
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; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
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; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO

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; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82453
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-10-932-182A-82453

Query Match          92.9%; Score 13; DB 7; Length 1017;
Best Local Similarity 76.9%; Pred. No. 92;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACUGCAACUCG 14
        |||:|||||:|
Db      477 GTACTGCAACTCG 465

RESULT 5
US-10-932-182A-82453/c
; Sequence 82453, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82453
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-10-932-182A-82453

Query Match          92.9%; Score 13; DB 7; Length 1017;
Best Local Similarity 76.9%; Pred. No. 92;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACUGCAACUCG 14
        |||:|||||:|
Db      477 GTACTGCAACTCG 465

RESULT 6
US-10-932-182A-1393/c
; Sequence 1393, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1393
; LENGTH: 2055
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-10-932-182A-1393
```

```

Query Match          92.9%; Score 13; DB 7; Length 2055;
Best Local Similarity 76.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACUGCAACUCG 14
        |||:|||||:|
Db      1095 GTACTGCAACTCG 1083

RESULT 7
US-10-932-182A-1393/c
; Sequence 1393, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1393
; LENGTH: 2055
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-10-932-182A-1393

Query Match          92.9%; Score 13; DB 7; Length 2055;
Best Local Similarity 76.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACUGCAACUCG 14
        |||:|||||:|
Db      1095 GTACTGCAACTCG 1083

RESULT 8
US-11-136-527-2658
; Sequence 2658, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2658
; LENGTH: 3002
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURES:
; NAME/KEY: misc feature
; LOCATION: (2885)..(2885)
; OTHER INFORMATION: n is a, c, g, or t
; US-11-136-527-2658

Query Match          92.9%; Score 13; DB 12; Length 3002;
Best Local Similarity 76.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACUGCAACUCG 14
        |||:|||||:|
Db      1472 GTACTGCAACTCG 1484
```

```

RESULT 9
US-11-124-367A-5111
; Sequence 5111, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5111
; LENGTH: 12514
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-5111

```

```

Query Match          92.9%; Score 13; DB 12; Length 12514;
Best Local Similarity 76.9%; Pred. No. 1.5e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 GUACUGCAACUC 14
||:|||||:|
Db      6306 GTACTGCAACTCG 6318

```

```

RESULT 10
US-10-995-561-16849
; Sequence 16849, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16849
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-16849

```

```

Query Match          90.0%; Score 12.6; DB 8; Length 201;
Best Local Similarity 76.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CGUACUGCAACUC 13
||:|||||:|
Db      99 CGYACTGCAACTC 111

```

```

RESULT 11
US-10-995-561-66965/c
; Sequence 66965, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

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```

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66965
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-66965

```

```

Query Match          90.0%; Score 12.6; DB 8; Length 201;
Best Local Similarity 76.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CGUACUGCAACUC 13
||:|||||:|
Db      103 CGYACTGCAACTC 91

```

```

RESULT 12
US-10-995-561-13387/c
; Sequence 13387, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13387
; LENGTH: 29871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(29871)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13387

```

```

Query Match          90.0%; Score 12.6; DB 8; Length 29871;
Best Local Similarity 76.9%; Pred. No. 3.5e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CGUACUGCAACUC 13
||:|||||:|
Db      14198 CGYACTGCAACTC 14186

```

```

RESULT 13
US-10-995-561-13204
; Sequence 13204, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13204
; LENGTH: 321019
; TYPE: DNA
; ORGANISM: Homo sapiens

```


FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(321019)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13204

Query Match 90.0%; Score 12.6; DB 8; Length 321019;
Best Local Similarity 76.9%; Pred. No. 5.5e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13
||:|:|:|:|:|:|:
DB 16112 CGTACTCGCACTC 16124

RESULT 14
US-11-101-244-868490/c
Sequence 868490, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmoon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 868490
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-868490

Query Match 88.6%; Score 12.4; DB 10; Length 19;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 14
||:|:|:|:|:|:|:
DB 18 CGTACTCGCACTCG 5

RESULT 15
US-11-083-784-868490/c
Sequence 868490, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmoon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary
SEQ ID NO 868490
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-868490

Query Match 88.6%; Score 12.4; DB 11; Length 19;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 14
||:|:|:|:|:|:|:
DB 18 CGTACTCGCACTCG 5

RESULT 16
US-10-933-982-90062/c
Sequence 90062, Application US/10933982
Publication No. US20060051769A1
GENERAL INFORMATION:
APPLICANT: Barts, Jennifer
TITLE OF INVENTION: Methods of Genetic Analysis of E. coli
FILE REFERENCE: 3700
CURRENT APPLICATION NUMBER: US/10/933,982
CURRENT FILING DATE: 2004-09-03
NUMBER OF SEQ ID NOS: 224976
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 90062
LENGTH: 25
TYPE: DNA
ORGANISM: E. coli
US-10-933-982-90062

Query Match 88.6%; Score 12.4; DB 7; Length 25;
Best Local Similarity 78.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 14
||:|:|:|:|:|:|:
DB 23 CGTACTCGCAACACG 10

RESULT 17
US-09-925-065A-138336
Sequence 138336, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 138336
LENGTH: 499
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-138336

Query Match 88.6%; Score 12.4; DB 6; Length 499;

Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUG 14
|:|:|:|:|:|:|:
Db 247 CTTACTGCAACTCG 260

RESULT 18

US-11-096-568A-11706/c
; Sequence 11706, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; PRIOR FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 11706
; LENGTH: 575
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(575)
; OTHER INFORMATION: Ceres Seq. ID no. 13656404
US-11-096-568A-11706

Query Match 88.6%; Score 12.4; DB 9; Length 575;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUG 14
|:|:|:|:|:|:|:
Db 558 CGTTCTGCAACTCG 545

RESULT 19

US-10-750-185-2691
; Sequence 2691, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2691
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-2691

Query Match 88.6%; Score 12.4; DB 8; Length 600;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUG 14
|:|:|:|:|:|:|:
Db 31 CGTCTGCAACTCG 44

RESULT 20

US-10-750-623-2691
; Sequence 2691, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2691
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-623-2691

Query Match 88.6%; Score 12.4; DB 8; Length 600;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUG 14
|:|:|:|:|:|:|:
Db 31 CGTCTGCAACTCG 44

RESULT 21

US-11-096-568A-20227
; Sequence 20227, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; PRIOR FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20227
; LENGTH: 847
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(847)
; OTHER INFORMATION: Ceres Seq. ID no. 12379704
US-11-096-568A-20227

Query Match 88.6%; Score 12.4; DB 9; Length 847;
Best Local Similarity 78.6%; Pred. No. 2.3e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUG 14
|:|:|:|:|:|:|:
Db 511 CGTACGCAACTCG 524

RESULT 22

US-10-467-657-4195/c
; Sequence 4195, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA

APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 4195
LENGTH: 1080
TYPE: DNA
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4195

Query Match 88.6%; Score 12.4; DB 8; Length 1080;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUCG 14
||:|||||:
DB 763 CGTCCTGCAACTCG 750

RESULT 23
US-10-750-185-56170/c
Sequence 56170, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 56170
LENGTH: 1223
TYPE: DNA
ORGANISM: Bovine 19866880790313
US-10-750-185-56170

Query Match 88.6%; Score 12.4; DB 8; Length 1223;
Best Local Similarity 78.6%; Pred. No. 2.5e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUCG 14
||:|||||:
DB 765 CGTACGCAACTCG 772

RESULT 24
US-10-750-623-56170/c
Sequence 56170, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen

APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 56170
LENGTH: 1223
TYPE: DNA
ORGANISM: Bovine 19866880790313
US-10-750-623-56170

Query Match 88.6%; Score 12.4; DB 8; Length 1223;
Best Local Similarity 78.6%; Pred. No. 2.5e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUCG 14
||:|||||:
DB 785 CGTACGCAACTCG 772

RESULT 25
US-11-096-568A-19170
Sequence 19170, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 19170
LENGTH: 1733
TYPE: DNA
ORGANISM: Zea mays subsp. mays
FEATURES:
NAME/KEY: misc feature
LOCATION: (1)_(1733)
OTHER INFORMATION: Ceres Seq. ID no. 12369271
US-11-096-568A-19170

Query Match 88.6%; Score 12.4; DB 9; Length 1733;
Best Local Similarity 78.6%; Pred. No. 2.7e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUCG 14
||:|||||:
DB 1054 CGTACGCAACTCG 1067

RESULT 26
US-10-504-034B-1/c
Sequence 1, Application US/10504034B
Publication No. US20060040343A1
GENERAL INFORMATION:
APPLICANT: Van Der Geize, Robert
APPLICANT: Van Der Weijden, Peter
APPLICANT: Hesseels, Gerda
APPLICANT: Dijkhuizen, Lubbert
TITLE OF INVENTION: Microbial delta-1-dehydrogenation of steroids
FILE REFERENCE: 2002.716US
CURRENT APPLICATION NUMBER: US/10/504,034B
CURRENT FILING DATE: 2004-08-05
PRIOR APPLICATION NUMBER: PCT/EP03/50025
PRIOR FILING DATE: 2003-02-19
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn ver. 3.3
SEQ ID NO 1

LENGTH: 1770
TYPE: DNA
ORGANISM: Rhodococcus erythropolis SQ1
US-10-504-034B-1

Query Match 88.6%; Score 12.4; DB 7; Length 1770;
Best Local Similarity 78.6%; Pred. No. 2.7e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14
||:|||||
Db 1354 CTTACTGCAACTCG 1341

RESULT 27
US-10-750-185-29862/c
Sequence 29862, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
PRIOR FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29862
LENGTH: 3250
TYPE: DNA
ORGANISM: Bovine 1986680972249
US-10-750-185-29862

Query Match 88.6%; Score 12.4; DB 8; Length 3250;
Best Local Similarity 71.4%; Pred. No. 3.1e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14
||:|||||
Db 335 CTTACTGCAACTCG 322

RESULT 28
US-10-750-623-29862/c
Sequence 29862, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
PRIOR FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29862
LENGTH: 3250
TYPE: DNA
ORGANISM: Bovine 1986680972249

US-10-750-623-29862

Query Match 88.6%; Score 12.4; DB 8; Length 3250;
Best Local Similarity 71.4%; Pred. No. 3.1e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14
||:|||||
Db 335 CTTACTGCAACTCG 322

RESULT 29
US-10-750-185-29967
Sequence 29967, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
PRIOR FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29967
LENGTH: 3661
TYPE: DNA
ORGANISM: Bovine 1986680504081
US-10-750-185-29967

Query Match 88.6%; Score 12.4; DB 8; Length 3661;
Best Local Similarity 71.4%; Pred. No. 3.2e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14
||:|||||
Db 1322 CGTGCTGCAACTCG 1335

RESULT 30
US-10-750-623-29967
Sequence 29967, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
PRIOR FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29967
LENGTH: 3661
TYPE: DNA
ORGANISM: Bovine 1986680504081
US-10-750-623-29967

Query Match 88.6%; Score 12.4; DB 8; Length 3661;

Best Local Similarity 71.4%; Pred. No. 3.2e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCACTCG 14
Db 1322 CGTGTGCAACTCG 1335

RESULT 31

US-11-082-154A-18/c
; Sequence 18, Application US/11082154A
; Publication No. US20060024820A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan

TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS

FILE REFERENCE: 17084-022003 (420C)

CURRENT APPLICATION NUMBER: US/11/082,154A

PRIOR FILING DATE: 2005-03-15

PRIOR APPLICATION NUMBER: 60/294,758

PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: 60/366,891

PRIOR FILING DATE: 2002-03-21

PRIOR APPLICATION NUMBER: US 10/161,403

PRIOR FILING DATE: 2002-05-30

NUMBER OF SEQ ID NOS: 129

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 18

LENGTH: 22118

TYPE: DNA

ORGANISM: Mus musculus

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: GenBank X82564

DATEBASE ENTRY DATE: 1996-04-09

US-11-082-154A-18

Query Match 88.6%; Score 12.4; DB 12; Length 22118;
Best Local Similarity 78.6%; Pred. No. 4.6e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCACTCG 14
Db 3661 CGTGTGCAACTCG 3648

RESULT 32

US-11-101-244-1009794/c

; Sequence 1009794, Application US/11101244

; Publication No. US20050246794A1

; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 1349905

CURRENT APPLICATION NUMBER: US/11/101,244

PRIOR FILING DATE: 2005-04-07

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 1009794

LENGTH: 19

TYPE: RNA

ORGANISM: Homo sapiens

US-11-101-244-1009794

Query Match 85.7%; Score 12; DB 10; Length 19;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCACTCG 12
Db 18 GTACTGCAACTC 7

RESULT 33

US-11-101-244-1239747/c

; Sequence 1239747, Application US/11101244

; Publication No. US20050246794A1

; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 1349905

CURRENT APPLICATION NUMBER: US/11/101,244

PRIOR FILING DATE: 2005-04-07

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 1239747

LENGTH: 19

TYPE: RNA

ORGANISM: Homo sapiens

US-11-101-244-1239747

Query Match 85.7%; Score 12; DB 10; Length 19;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GUACUGCACTCG 13
Db 18 GTACTGCAACTC 7

RESULT 34

US-11-083-784-1009794/c

; Sequence 1009794, Application US/11083784

; Publication No. US20050246794A1

; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 1349905

CURRENT APPLICATION NUMBER: US/11/083,784

PRIOR FILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: US/10/714,333

PRIOR FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 1009794

SEQ ID NO 1009794
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-083-784-1009794

Query Match 85.7%; Score 12; DB 11; Length 19;
 Best Local Similarity 75.0%; Pred. No. 2e+02;
 Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACU 12
 ||:|||||:
 Db 18 GCTACTGCAACT 7

RESULT 35
 US-11-083-784-1239747/c
 Sequence 1239747, Application US/11083784
 Publication No. US20050245475A1
 GENERAL INFORMATION:
 APPLICANT: Dharmacon, Inc.
 APPLICANT: Khvorova, Anastasia
 APPLICANT: Reynolds, Angela
 APPLICANT: Leake, Devin
 APPLICANT: Marshall, William
 APPLICANT: Scaringe, Stephen
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 FILE REFERENCE: 13499US
 CURRENT APPLICATION NUMBER: US/11/083,784
 CURRENT FILING DATE: 2005-03-18
 PRIOR APPLICATION NUMBER: US/10/714,333
 PRIOR FILING DATE: 2003-11-14
 PRIOR APPLICATION NUMBER: 60/502,050
 PRIOR FILING DATE: 2003-09-10
 PRIOR APPLICATION NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 1591911
 SOFTWARE: Proprietary
 SEQ ID NO 1239747
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-083-784-1239747

Query Match 85.7%; Score 12; DB 11; Length 19;
 Best Local Similarity 75.0%; Pred. No. 2e+02;
 Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACUC 13
 |:|||||:
 Db 18 GTACTGCAACTC 7

RESULT 36
 US-10-310-914A-573268
 Sequence 573268, Application US/10110914A
 Publication No. US2006003322A1
 GENERAL INFORMATION:
 APPLICANT: Bentwich, Isaac
 APPLICANT: Shiller, Kiyazaki
 TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 TITLE OF INVENTION: uses thereof
 FILE REFERENCE: 06087.0200.CPUS01
 CURRENT APPLICATION NUMBER: US/10/310,914A
 CURRENT FILING DATE: 2002-12-06
 NUMBER OF SEQ ID NOS: 1388402
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 573268
 LENGTH: 20
 TYPE: RNA
 ORGANISM: Human
 US-10-310-914A-573268

Query Match 85.7%; Score 12; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACUC 13
 |||||||:
 Db 6 GUACUGCAACUC 17

RESULT 37
 US-10-521-162-30
 Sequence 30, Application US/10521162
 Publication No. US20050287529A1
 GENERAL INFORMATION:
 APPLICANT: Brandt, Kevin S.
 TITLE OF INVENTION: FLEA AND TICK OCTOPAMINE RECEPTOR NUCLEIC ACID MOLECULES,
 TITLE OF INVENTION: PROTEINS AND USES THEREOF
 FILE REFERENCE: FC-11-PCT
 CURRENT APPLICATION NUMBER: US/10/521,162
 CURRENT FILING DATE: 2005-01-13
 PRIOR APPLICATION NUMBER: 60/319,402
 PRIOR FILING DATE: 2003-07-17
 PRIOR APPLICATION NUMBER: 60/426,601
 PRIOR FILING DATE: 2003-11-15
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 30
 LENGTH: 102
 TYPE: DNA
 ORGANISM: Rhipicephalus sanguineus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(102)
 US-10-521-162-30

Query Match 85.7%; Score 12; DB 8; Length 102;
 Best Local Similarity 75.0%; Pred. No. 2.9e+02;
 Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 UACUGCAACUC 14
 ||:|||||:
 Db 76 TACTGCAACTCG 87

RESULT 38
 US-10-521-162-32/c
 Sequence 32, Application US/10521162
 Publication No. US20050287529A1
 GENERAL INFORMATION:
 APPLICANT: Brandt, Kevin S.
 TITLE OF INVENTION: FLEA AND TICK OCTOPAMINE RECEPTOR NUCLEIC ACID MOLECULES,
 TITLE OF INVENTION: PROTEINS AND USES THEREOF
 FILE REFERENCE: FC-11-PCT
 CURRENT APPLICATION NUMBER: US/10/521,162
 CURRENT FILING DATE: 2005-01-13
 PRIOR APPLICATION NUMBER: 60/319,402
 PRIOR FILING DATE: 2003-07-17
 PRIOR APPLICATION NUMBER: 60/426,601
 PRIOR FILING DATE: 2003-11-15
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 32
 LENGTH: 102
 TYPE: DNA
 ORGANISM: Rhipicephalus sanguineus
 US-10-521-162-32

Query Match 85.7%; Score 12; DB 8; Length 102;
 Best Local Similarity 75.0%; Pred. No. 2.9e+02;
 Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 UACUGCAACUC 14
 ||:|||||:
 Db 76 TACTGCAACTCG 87

Db 27 TACTGCACTCG 16

RESULT 39

US-10-995-561-81304/c
; Sequence 81304, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81304
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-81304

Query Match 85.7%; Score 12; DB 8; Length 201;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GUACUGCAATC 13

Db 125 GTACTGCACTC 114

RESULT 40

US-10-995-561-81478/c
; Sequence 81478, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81478
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-81478

Query Match 85.7%; Score 12; DB 8; Length 201;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GUACUGCAATC 13

Db 128 GTACTGCACTC 117

RESULT 41

US-10-932-182A-637/c
; Sequence 637, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043

CURRENT APPLICATION NUMBER: US/10/932,182A

CURRENT FILING DATE: 2004-09-02

NUMBER OF SEQ ID NOS: 197023

SOFTWARE: Patentin version 3.3

SEQ ID NO 637

LENGTH: 444

TYPE: DNA

ORGANISM: Saccharomyces pastorianus

US-10-932-182A-637

Query Match 85.7%; Score 12; DB 7; Length 444;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GUACUGCAATC 13

Db 285 GTACTGCACTC 274

RESULT 42

US-10-932-182A-637/c
; Sequence 637, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 637
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-637

Query Match 85.7%; Score 12; DB 7; Length 444;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GUACUGCAATC 13

Db 285 GTACTGCACTC 274

RESULT 43

US-09-925-065A-746961/c
; Sequence 746961, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 746961
/ LENGTH: 445
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-746961

Query Match 85.7%; Score 12; DB 6; Length 445;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GUACGCAACUC 13
Db 292 GTACTGCAACTC 281

RESULT 44
US-10-521-162-33
/ Sequence 33, Application US/10521162
/ Publication No. US20050287529A1
/ GENERAL INFORMATION:

/ APPLICANT: Brandt, Kevin S.
/ TITLE OF INVENTION: FLEA AND TICK OCTOPAMINE RECEPTOR NUCLEIC ACID MOLECULES,
/ FILE REFERENCE: FC-11-PCT
/ CURRENT APPLICATION NUMBER: US/10/521,162
/ PRIOR FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: 60/319,402
/ PRIOR FILING DATE: 2003-07-17
/ PRIOR APPLICATION NUMBER: 60/426,601
/ PRIOR FILING DATE: 2003-11-15
/ NUMBER OF SEQ ID NOS: 50
/ SOFTWARE: PatentIn version 3.2

SEQ ID NO 33

LENGTH: 499
TYPE: DNA
ORGANISM: Rhinipicephalus sanguineus

FEATURE:
NAME/KEY: CDS
LOCATION: (3)..(278)

FEATURE:
NAME/KEY: misc_feature
LOCATION: (8)..(8)

OTHER INFORMATION: n = unknown
OTHER INFORMATION: Xaa at location 2 = Tyr
US-10-521-162-33

Query Match 85.7%; Score 12; DB 8; Length 499;
Best Local Similarity 75.0%; Pred. No. 4e+02;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 UACUGCAACUCG 14
Db 99 TACTGCAACTCG 110

RESULT 45
US-10-521-162-35/c

/ Sequence 35, Application US/10521162
/ Publication No. US20050287529A1
/ GENERAL INFORMATION:

/ APPLICANT: Brandt, Kevin S.
/ TITLE OF INVENTION: FLEA AND TICK OCTOPAMINE RECEPTOR NUCLEIC ACID MOLECULES,
/ FILE REFERENCE: FC-11-PCT
/ CURRENT APPLICATION NUMBER: US/10/521,162
/ PRIOR FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: 60/319,402
/ PRIOR FILING DATE: 2003-07-17
/ PRIOR APPLICATION NUMBER: 60/426,601
/ PRIOR FILING DATE: 2003-11-15
/ NUMBER OF SEQ ID NOS: 50
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 35

/ LENGTH: 499
/ TYPE: DNA
/ ORGANISM: Rhinipicephalus sanguineus
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (492)..(492)
/ OTHER INFORMATION: n = unknown
US-10-521-162-35

Query Match 85.7%; Score 12; DB 8; Length 499;
Best Local Similarity 75.0%; Pred. No. 4e+02;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 UACUGCAACUCG 14
Db 401 TACTGCAACTCG 390

RESULT 46
US-09-925-065A-313926/c
/ Sequence 313926, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:

/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ PRIOR FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 313926
/ LENGTH: 542
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-313926

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Best Local Similarity 75.0%; Pred. No. 4.1e+02;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GUACGCAACUC 13
Db 22 GTACTGCAACTC 11

RESULT 47
US-09-925-065A-53948

/ Sequence 53948, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:

/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ PRIOR FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30

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OM nucleic - nucleic search, using sw model1

Run on: March 18, 2006, 18:35:47 ; Search time 2096.77 Seconds
(without alignments)
55.214 Million cell updates/sec

Title: US-10-800-926-2

Perfect score: 14

Sequence: 14

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

19587084

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications NA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	14	100.0	1981	US-10-369-493-28056	Sequence 28056, A
5	14	100.0	1986	US-10-282-122A-12964	Sequence 12964, A
6	14	100.0	2080	US-10-369-493-30810	Sequence 30810, A
7	14	100.0	2460	US-10-282-122A-33109	Sequence 33109, A
8	14	100.0	6024	US-10-437-963-61758	Sequence 61758, A
9	14	100.0	6808	US-10-437-963-87284	Sequence 87284, A
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11	13	92.9	196	US-10-437-963-5526	Sequence 5526, A
12	13	92.9	472	US-10-425-115-6477	Sequence 4677, A
13	13	92.9	600	US-10-972-079-46310	Sequence 46310, A
14	13	92.9	653	US-10-425-115-16169	Sequence 16169, A
15	13	92.9	838	US-10-437-963-98896	Sequence 98896, A
16	13	92.9	1042	US-10-437-963-84553	Sequence 84553, A
17	13	92.9	1239	US-10-156-761-4883	Sequence 4883, A
18	13	92.9	1306	US-10-369-493-29486	Sequence 29486, A
19	13	92.9	1359	US-10-450-763-8883	Sequence 8883, A
20	13	92.9	1473	US-10-957-828-11	Sequence 11, Appl1
21	13	92.9	1647	US-09-815-242-6126	Sequence 6126, A
22	13	92.9	1647	US-10-282-122A-20432	Sequence 20432, A
23	13	92.9	1720	US-09-801-042-1	Sequence 1, Appl1

24	13	92.9	1732	US-10-450-763-28629	Sequence 28629, A
25	13	92.9	1919	US-10-450-763-25885	Sequence 25885, A
26	13	92.9	1945	US-09-864-761-4533	Sequence 4533, A
27	13	92.9	2133	US-10-450-763-23995	Sequence 23995, A
28	13	92.9	2559	US-10-156-761-2636	Sequence 2636, A
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49	12.4	88.6	331	US-10-424-599-138244	Sequence 138244, A
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52	12.4	88.6	371	US-10-425-115-40014	Sequence 40014, A
53	12.4	88.6	387	US-10-424-599-59801	Sequence 59801, A
54	12.4	88.6	389	US-10-425-115-181715	Sequence 181715, A
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56	12.4	88.6	446	US-09-860-432-20	Sequence 20, Appl1
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58	12.4	88.6	478	US-10-424-599-120244	Sequence 120244, A
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63	12.4	88.6	503	US-10-425-115-94418	Sequence 94418, A
64	12.4	88.6	515	US-10-425-115-12601	Sequence 12601, A
65	12.4	88.6	521	US-10-425-115-156043	Sequence 156043, A
66	12.4	88.6	558	US-09-815-242-5946	Sequence 5946, A
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69	12.4	88.6	570	US-10-363-345A-32709	Sequence 32709, A
70	12.4	88.6	570	US-10-363-345A-33710	Sequence 33710, A
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75	12.4	88.6	582	US-10-425-115-145338	Sequence 145338, A
76	12.4	88.6	594	US-10-363-345A-1517	Sequence 1517, A
77	12.4	88.6	594	US-10-363-345A-1518	Sequence 1518, A
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82	12.4	88.6	630	US-10-437-963-23809	Sequence 23809, A
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85	12.4	88.6	711	US-10-156-761-5594	Sequence 5594, A
86	12.4	88.6	712	US-10-437-963-109	Sequence 109, A
87	12.4	88.6	712	US-10-767-701-11773	Sequence 11773, A
88	12.4	88.6	733	US-10-450-763-1417	Sequence 1417, A
89	12.4	88.6	819	US-10-437-963-40318	Sequence 40318, A
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93	12.4	88.6	855	US-10-425-115-83584	Sequence 83584, A
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96	12.4	88.6	889	US-10-398-221-1272	Sequence 1272, A

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C 98	12.4	88.6	915	6	US-10-369-493-38130	Sequence 38130, A	171	12.4	88.6	2066	8	US-10-425-115-16562	Sequence 16562, A
C 99	12.4	88.6	915	6	US-10-369-493-38451	Sequence 38451, A	172	12.4	88.6	2062	8	US-10-425-115-16562	Sequence 16562, A
C 100	12.4	88.6	915	6	US-10-369-493-38931	Sequence 38931, A	173	12.4	88.6	2132	7	US-10-437-963-56684	Sequence 56684, A
C 101	12.4	88.6	927	6	US-10-369-493-39316	Sequence 39316, A	174	12.4	88.6	2253	3	US-09-765-231A-6	Sequence 6, Appl1
C 102	12.4	88.6	960	8	US-10-425-115-18223	Sequence 18223, A	175	12.4	88.6	2302	5	US-10-106-698-2091	Sequence 2091, Ap
C 103	12.4	88.6	960	10	US-11-097-143-9890	Sequence 9890, Ap	176	12.4	88.6	2308	6	US-10-786-148-74	Sequence 74, Appl1
C 104	12.4	88.6	1028	10	US-11-097-143-35978	Sequence 35978, A	177	12.4	88.6	2406	6	US-10-777-131A-32	Sequence 32, Appl1
C 105	12.4	88.6	1032	6	US-10-084-846A-47	Sequence 47, Appl1	178	12.4	88.6	2406	6	US-10-777-131A-32	Sequence 32, Appl1
C 106	12.4	88.6	1035	6	US-10-107-431-82	Sequence 82, Appl1	179	12.4	88.6	2409	3	US-09-855-604-618	Sequence 618, App
C 107	12.4	88.6	1065	9	US-10-450-763-14128	Sequence 14128, A	180	12.4	88.6	2409	3	US-09-855-604-618	Sequence 618, App
C 108	12.4	88.6	1092	8	US-10-414-588-7	Sequence 7, Appl1	181	12.4	88.6	2448	9	US-10-756-149-3651	Sequence 3651, App
C 109	12.4	88.6	1137	6	US-10-156-761-3714	Sequence 3714, Ap	182	12.4	88.6	2451	3	US-09-855-604-620	Sequence 620, App
C 110	12.4	88.6	1144	8	US-10-216-817-20	Sequence 20, Appl1	183	12.4	88.6	2451	3	US-09-855-604-620	Sequence 620, App
C 111	12.4	88.6	1152	7	US-10-777-131A-20	Sequence 20, Appl1	184	12.4	88.6	2451	3	US-10-037-270-272	Sequence 272, App
C 112	12.4	88.6	1152	7	US-10-282-122A-28882	Sequence 28882, A	185	12.4	88.6	2495	6	US-10-117-722-272	Sequence 272, App
C 113	12.4	88.6	1182	7	US-10-437-963-20085	Sequence 20085, A	186	12.4	88.6	2495	6	US-10-122-851-272	Sequence 272, App
C 114	12.4	88.6	1185	3	US-09-815-242-7909	Sequence 7909, Ap	187	12.4	88.6	2502	9	US-10-450-763-18340	Sequence 18340, A
C 115	12.4	88.6	1185	7	US-10-282-122A-30463	Sequence 30463, A	188	12.4	88.6	2508	7	US-10-282-122A-33100	Sequence 33100, A
C 116	12.4	88.6	1195	9	US-10-495-300-29	Sequence 29, Appl1	189	12.4	88.6	2553	6	US-10-369-493-37353	Sequence 37353, A
C 117	12.4	88.6	1206	3	US-09-996-008B-1	Sequence 1, Appl1	190	12.4	88.6	2556	7	US-10-398-221-3606	Sequence 3606, Ap
C 118	12.4	88.6	1206	9	US-10-491-958-3	Sequence 3, Appl1	191	12.4	88.6	2571	7	US-10-282-122A-23256	Sequence 23256, A
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C 122	12.4	88.6	1264	9	US-10-491-958-2	Sequence 2, Appl1	195	12.4	88.6	2645	9	US-10-840-060-193	Sequence 193, App
C 123	12.4	88.6	1266	6	US-10-156-761-4878	Sequence 4878, Ap	196	12.4	88.6	2645	10	US-11-097-143-5480	Sequence 5480, Ap
C 124	12.4	88.6	1278	7	US-10-425-114-33084	Sequence 33084, A	197	12.4	88.6	2697	7	US-10-437-963-48159	Sequence 48159, A
C 125	12.4	88.6	1285	7	US-10-425-114-3185	Sequence 3185, Ap	198	12.4	88.6	2721	6	US-10-369-493-44876	Sequence 44876, A
C 126	12.4	88.6	1287	3	US-09-815-242-7768	Sequence 7768, Ap	199	12.4	88.6	2757	7	US-10-437-963-53102	Sequence 53102, A
C 127	12.4	88.6	1287	9	US-10-282-122A-30181	Sequence 30181, Ap	200	12.4	88.6	2806	8	US-10-216-817-22	Sequence 22, Appl1
C 128	12.4	88.6	1287	9	US-10-953-901-292	Sequence 292, App	201	12.4	88.6	2806	8	US-10-777-131A-22	Sequence 22, Appl1
C 129	12.4	88.6	1290	9	US-10-437-963-44218	Sequence 44218, A	202	12.4	88.6	2852	10	US-11-097-143-18682	Sequence 18682, A
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C 134	12.4	88.6	1326	7	US-10-424-559-11531	Sequence 11531, A	207	12.4	88.6	3348	10	US-11-097-143-9889	Sequence 9889, Ap
C 135	12.4	88.6	1349	7	US-10-425-114-4160	Sequence 4160, Ap	208	12.4	88.6	3398	10	US-11-097-143-1887	Sequence 6187, Ap
C 136	12.4	88.6	1363	7	US-10-425-114-17575	Sequence 17575, A	209	12.4	88.6	3468	9	US-10-450-763-30051	Sequence 30051, A
C 137	12.4	88.6	1363	7	US-10-425-114-40125	Sequence 40125, A	210	12.4	88.6	3472	10	US-11-097-143-18680	Sequence 8680, Ap
C 138	12.4	88.6	1365	6	US-10-369-493-40125	Sequence 40125, A	211	12.4	88.6	3507	10	US-11-097-143-17789	Sequence 17789, A
C 139	12.4	88.6	1374	7	US-10-425-114-6260	Sequence 6260, Ap	212	12.4	88.6	3710	10	US-11-097-143-17030	Sequence 17030, A
C 140	12.4	88.6	1397	7	US-10-282-122A-12951	Sequence 12951, A	213	12.4	88.6	3773	10	US-11-097-143-8063	Sequence 8063, Ap
C 141	12.4	88.6	1397	7	US-10-425-114-22792	Sequence 22792, A	214	12.4	88.6	3812	10	US-10-450-763-29192	Sequence 29192, A
C 142	12.4	88.6	1406	7	US-10-424-559-122464	Sequence 122464, A	215	12.4	88.6	3846	8	US-10-425-115-69524	Sequence 69524, A
C 143	12.4	88.6	1411	7	US-10-425-114-24493	Sequence 24493, A	216	12.4	88.6	3939	7	US-10-168-582-17	Sequence 17, Appl1
C 144	12.4	88.6	1443	7	US-10-424-559-139711	Sequence 139711, A	217	12.4	88.6	4029	7	US-10-282-122A-38904	Sequence 38904, A
C 145	12.4	88.6	1489	7	US-10-437-963-22814	Sequence 22814, A	218	12.4	88.6	4143	3	US-09-815-242-9945	Sequence 9945, Ap
C 146	12.4	88.6	1498	7	US-10-425-114-3307	Sequence 3307, Ap	219	12.4	88.6	4251	9	US-10-450-763-25459	Sequence 25459, A
C 147	12.4	88.6	1541	7	US-10-425-114-4160	Sequence 4160, Ap	220	12.4	88.6	4285	5	US-10-128-714-343	Sequence 343, App
C 148	12.4	88.6	1557	9	US-10-760-493-66	Sequence 760, Appl	221	12.4	88.6	4357	5	US-10-259-194A-185	Sequence 185, App
C 149	12.4	88.6	1572	3	US-09-815-242-7820	Sequence 7820, Ap	222	12.4	88.6	4651	5	US-10-128-714-5343	Sequence 5343, Ap
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C 153	12.4	88.6	1584	6	US-10-425-115-47186	Sequence 47186, A	226	12.4	88.6	5188	7	US-11-097-143-13993	Sequence 13993, A
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C 156	12.4	88.6	1623	8	US-10-425-115-18597	Sequence 18597, A	229	12.4	88.6	6465	7	US-10-282-122A-30511	Sequence 30511, A
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C 159	12.4	88.6	1645	6	US-10-369-493-36141	Sequence 36141, A	232	12.4	88.6	7365	10	US-11-097-143-15166	Sequence 15166, A
C 160	12.4	88.6	1690	9	US-10-956-157-4898	Sequence 4898, Ap	233	12.4	88.6	8544	10	US-11-097-143-17972	Sequence 17972, Ap
C 161	12.4	88.6	1703	7	US-10-437-963-54978	Sequence 54978, Ap	234	12.4	88.6	8802	10	US-11-097-143-17788	Sequence 17788, A
C 162	12.4	88.6	1707	7	US-10-282-122A-13869	Sequence 13869, A	235	12.4	88.6	10387	3	US-09-754-468-15	Sequence 15, Appl1
C 163	12.4	88.6	1743	7	US-10-282-122A-24153	Sequence 24153, A	236	12.4	88.6	11204	9	US-10-893-671-30	Sequence 30, Appl1
C 164	12.4	88.6	1795	7	US-10-424-559-130899	Sequence 130899, A	237	12.4	88.6	14283	10	US-11-097-143-5479	Sequence 5479, Appl1
C 165	12.4	88.6	1823	8	US-10-425-115-147697	Sequence 147697, A	238	12.4	88.6	15042	10	US-11-097-143-36010	Sequence 36010, A
C 166	12.4	88.6	1878	7	US-10-437-963-41189	Sequence 41189, A	239	12.4	88.6	15711	10	US-11-097-143-33609	Sequence 3609, A
C 167	12.4	88.6	1926	9	US-10-450-763-15831	Sequence 15831, A	240	12.4	88.6	16499	10	US-11-097-143-17029	Sequence 17029, A
C 168	12.4	88.6	1938	7	US-10-424-559-34488	Sequence 34488, A	241	12.4	88.6	22118	3	US-09-799-462A-16	Sequence 16, Appl1
C 169	12.4	88.6	1954	8	US-10-425-115-117144	Sequence 117144, A	242	12.4	88.6	22118	3	US-09-815-981-5	Sequence 5, Appl1

C 243	12.4	88.6	22118	3	US-09-836-911A-16	Sequence 16, Appl	C 316	12	85.7	476	5	US-10-040-862-3499	Sequence 3499, Ap
C 244	12.4	88.6	22118	3	US-09-815-979-5	Sequence 5, Appl	C 317	12	85.7	476	6	US-10-057-4758-3499	Sequence 3499, Ap
C 245	12.4	88.6	22118	5	US-10-125-767-16	Sequence 16, Appl	C 318	12	85.7	476	6	US-10-154-8848-3499	Sequence 3499, Ap
C 246	12.4	88.6	22118	5	US-10-151-081-16	Sequence 16, Appl	C 319	12	85.7	476	8	US-10-764-324-3499	Sequence 3499, Ap
C 247	12.4	88.6	22118	5	US-10-287-313-16	Sequence 16, Appl	C 320	12	85.7	477	7	US-10-424-599-43792	Sequence 43792, A
C 248	12.4	88.6	22118	5	US-10-219-694-16	Sequence 16, Appl	C 321	12	85.7	477	7	US-10-642-277-30	Sequence 30, Appl
C 249	12.4	88.6	22118	5	US-10-235-119-5	Sequence 5, Appl	C 322	12	85.7	481	8	US-10-647-625A-143	Sequence 143, App
C 250	12.4	88.6	22118	6	US-10-161-403-18	Sequence 18, Appl	C 323	12	85.7	488	7	US-10-260-238-2687	Sequence 2687, Ap
C 251	12.4	88.6	22118	6	US-10-086-745-5	Sequence 5, Appl	C 324	12	85.7	501	5	US-09-796-692-5809	Sequence 5809, Ap
C 252	12.4	88.6	22118	6	US-10-428-653-5	Sequence 5, Appl	C 325	12	85.7	501	5	US-10-040-862-5809	Sequence 5809, Ap
C 253	12.4	88.6	22118	7	US-10-808-689-16	Sequence 16, Appl	C 326	12	85.7	501	6	US-10-057-4758-5809	Sequence 5809, Ap
C 254	12.4	88.6	22118	9	US-10-976-394-5	Sequence 5, Appl	C 327	12	85.7	501	6	US-10-154-8848-5809	Sequence 5809, Ap
C 255	12.4	88.6	22118	9	US-10-151-078A-16	Sequence 16, Appl	C 328	12	85.7	501	8	US-10-764-324-5809	Sequence 5809, Ap
C 256	12.4	88.6	22118	10	US-11-006-076-18	Sequence 18, Appl	C 329	12	85.7	539	7	US-09-918-995-29429	Sequence 29429, A
C 257	12.4	88.6	22432	10	US-11-097-143-4756	Sequence 4756, Ap	C 330	12	85.7	539	7	US-10-152-119A-485	Sequence 485, App
C 258	12.4	88.6	45055	6	US-10-107-431-277	Sequence 277, App	C 331	12	85.7	542	4	US-09-925-065A-313926	Sequence 313926, A
C 259	12.4	88.6	59816	6	US-10-084-846A-1	Sequence 1, Appl	C 332	12	85.7	544	3	US-09-918-995-26616	Sequence 26616, A
C 260	12.4	88.6	59816	6	US-10-084-846A-2	Sequence 2, Appl	C 333	12	85.7	546	4	US-09-925-065A-53948	Sequence 53948, A
C 261	12.4	88.6	60872	9	US-10-915-740A-17	Sequence 17, Appl	C 334	12	85.7	554	4	US-09-925-065A-940341	Sequence 940341, A
C 262	12.4	88.6	64482	7	US-10-323-696-151	Sequence 151, App	C 335	12	85.7	557	4	US-09-925-065A-940300	Sequence 940300, A
C 263	12.4	88.6	164051	9	US-10-760-493-18	Sequence 18, Appl	C 336	12	85.7	558	4	US-09-925-065A-922392	Sequence 922392, A
C 264	12.4	88.6	326002	9	US-10-461-862-56	Sequence 56, Appl	C 337	12	85.7	566	4	US-10-756-149-4554	Sequence 4554, Ap
C 265	12.4	88.6	561515	8	US-10-741-601-5682	Sequence 56, Appl	C 338	12	85.7	573	4	US-09-925-065A-831424	Sequence 831424, A
C 266	12.4	88.6	561515	8	US-10-741-600-17730	Sequence 17730, A	C 339	12	85.7	574	7	US-10-767-701-27715	Sequence 27715, A
C 267	12.4	88.6	713059	6	US-10-027-632-174581	Sequence 174581, A	C 340	12	85.7	582	4	US-09-925-065A-563409	Sequence 563409, A
C 268	12.4	88.6	2242716	9	US-10-915-740A-1068	Sequence 1068, Ap	C 341	12	85.7	582	4	US-09-925-065A-865611	Sequence 862611, A
C 270	12.4	88.6	2256646	7	US-10-470-565-1	Sequence 1, Appl	C 342	12	85.7	584	4	US-09-925-065A-484572	Sequence 484572, A
C 271	12.4	88.6	2256646	7	US-10-470-565-1	Sequence 1, Appl	C 343	12	85.7	584	4	US-09-925-065A-484572	Sequence 484572, A
C 272	12.4	88.6	2940917	5	US-10-027-632-174763	Sequence 174763, A	C 344	12	85.7	594	4	US-09-925-065A-415302	Sequence 415302, A
C 273	12.4	88.6	2940917	6	US-10-027-632-174763	Sequence 174763, A	C 345	12	85.7	595	4	US-09-925-065A-747987	Sequence 747987, A
C 274	12.4	88.7	2940917	6	US-10-027-632-174763	Sequence 174763, A	C 346	12	85.7	600	9	US-10-972-079-18197	Sequence 18197, A
C 275	12.4	88.7	2940917	6	US-10-027-632-174763	Sequence 174763, A	C 347	12	85.7	600	9	US-10-972-079-18197	Sequence 18197, A
C 276	12.4	88.7	2940917	6	US-10-027-632-174763	Sequence 174763, A	C 348	12	85.7	601	5	US-10-027-632-116332	Sequence 116332, A
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C 537	12	85.7	3828	7	US-10-211-462-39	Sequence 29, Appl	610	11.4	81.4	20	3	US-09-873-873-7	Sequence 7, Appl
C 538	12	85.7	4089	7	US-10-437-963-56240	Sequence 56240, A	611	11.4	81.4	20	3	US-09-873-873-18	Sequence 18, Appl
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C 540	12	85.7	4121	6	US-10-325-878-4	Sequence 4, Appl1	613	11.4	81.4	20	3	US-09-916-956A-18	Sequence 18, Appl1
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C 542	12	85.7	4128	7	US-10-437-963-28616	Sequence 28616, A	615	11.4	81.4	20	3	US-09-997-914-18	Sequence 18, Appl1
C 543	12	85.7	4181	8	US-10-425-115-106917	Sequence 106917, A	616	11.4	81.4	20	6	US-10-365-645-18	Sequence 7, Appl1
C 544	12	85.7	4203	7	US-10-437-963-56192	Sequence 56192, A	617	11.4	81.4	20	6	US-10-365-645-7	Sequence 7, Appl1
C 545	12	85.7	4290	10	US-11-097-143-31753	Sequence 31753, A	618	11.4	81.4	20	7	US-10-612-163-7	Sequence 7, Appl1
C 546	12	85.7	4323	7	US-10-437-963-87253	Sequence 87253, A	619	11.4	81.4	20	7	US-10-612-163-18	Sequence 18, Appl1
C 547	12	85.7	4369	6	US-11-097-143-3384	Sequence 2384, Ap	620	11.4	81.4	20	7	US-10-739-482-7	Sequence 7, Appl1
C 548	12	85.7	4369	6	US-10-108-260A-1401	Sequence 1401, Ap	621	11.4	81.4	20	7	US-10-739-482-18	Sequence 18, Appl1
C 549	12	85.7	4405	7	US-10-437-963-9786	Sequence 9786, Ap	622	11.4	81.4	20	7	US-10-817-182-7	Sequence 7, Appl1
C 550	12	85.7	4455	7	US-10-437-963-87217	Sequence 87217, A	623	11.4	81.4	20	7	US-10-817-182-18	Sequence 18, Appl1
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C 552	12	85.7	4513	10	US-11-097-143-39436	Sequence 39436, A	625	11.4	81.4	25	5	US-09-940-185-4648	Sequence 4648, Ap
C 553	12	85.7	4562	8	US-10-775-920-121	Sequence 121, App	626	11.4	81.4	25	5	US-10-215-112-5836	Sequence 5836, Ap
C 554	12	85.7	4562	8	US-10-775-920-123	Sequence 123, App	627	11.4	81.4	25	7	US-10-719-956-142027	Sequence 142027,
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C 556	12	85.7	4860	7	US-10-437-963-12409	Sequence 12409, A	629	11.4	81.4	25	7	US-10-719-956-270637	Sequence 270637,
C 557	12	85.7	4900	5	US-10-270-333-142	Sequence 142, App	630	11.4	81.4	25	7	US-10-719-956-425273	Sequence 425273,
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C 563	12	85.7	7040	10	US-11-097-143-31759	Sequence 2383, Ap	636	11.4	81.4	25	7	US-10-719-956-637939	Sequence 637939,
C 564	12	85.7	7176	10	US-11-097-143-31759	Sequence 31759, A	637	11.4	81.4	25	8	US-10-719-900-11471	Sequence 11471, A
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C 567	12	85.7	9577	10	US-11-097-143-9904	Sequence 9904, Ap	640	11.4	81.4	25	8	US-10-719-900-127237	Sequence 127237,
C 568	12	85.7	9870	6	US-10-115-831-118	Sequence 118, App	641	11.4	81.4	25	8	US-10-719-900-27669	Sequence 27669,
C 569	12	85.7	10486	10	US-11-097-143-7438	Sequence 7438, Ap	642	11.4	81.4	25	8	US-10-719-900-402953	Sequence 402953,
C 570	12	85.7	13227	10	US-11-097-143-23788	Sequence 23788, A	643	11.4	81.4	25	8	US-10-719-900-580171	Sequence 580171,
C 571	12	85.7	15762	10	US-11-097-143-7615	Sequence 7615, Ap	644	11.4	81.4	25	8	US-10-719-900-580171	Sequence 580171,
C 572	12	85.7	17379	3	US-09-764-860-861	Sequence 861, App	645	11.4	81.4	25	8	US-10-719-900-752648	Sequence 752648,
C 573	12	85.7	17379	3	US-10-212-872-861	Sequence 861, App	646	11.4	81.4	25	8	US-10-719-900-752648	Sequence 752648,
C 574	12	85.7	17379	6	US-10-212-872-861	Sequence 861, App	647	11.4	81.4	25	8	US-10-719-900-773677	Sequence 773677,
C 575	12	85.7	21570	6	US-09-754-468-37	Sequence 37, Appl	648	11.4	81.4	25	8	US-10-719-900-807162	Sequence 807162,
C 576	12	85.7	24081	6	US-10-132-134-13	Sequence 13, Appl	649	11.4	81.4	25	8	US-10-719-900-836594	Sequence 836594,
C 577	12	85.7	26190	6	US-10-242-355-693	Sequence 693, App	650	11.4	81.4	25	8	US-10-719-900-856543	Sequence 856543,
C 578	12	85.7	30553	8	US-10-741-600-17577	Sequence 17577, A	651	11.4	81.4	25	8	US-10-719-900-856543	Sequence 856543,
C 579	12	85.7	52101	6	US-10-132-134-1	Sequence 1, Appl1	652	11.4	81.4	25	8	US-10-719-900-861184	Sequence 861184,
C 580	12	85.7	72409	7	US-10-737-318-80	Sequence 80, Appl	653	11.4	81.4	25	9	US-10-809-189-6531	Sequence 6531, Ap
C 581	12	85.7	84409	7	US-10-741-601-5696	Sequence 5696, Ap	654	11.4	81.4	25	9	US-10-809-189-87490	Sequence 87490, A
C 582	12	85.7	84409	8	US-10-741-601-17771	Sequence 17771, A	655	11.4	81.4	25	9	US-10-809-189-87490	Sequence 87490, A
C 583	12	85.7	113486	5	US-10-417-375-18	Sequence 18, Appl	656	11.4	81.4	25	9	US-10-809-189-109332	Sequence 109332,
C 584	12	85.7	115284	5	US-10-087-192-673	Sequence 673, App	657	11.4	81.4	25	9	US-10-809-189-109332	Sequence 109332,
C 585	12	85.7	122673	9	US-10-737-082-33	Sequence 33, Appl	658	11.4	81.4	25	9	US-10-809-189-109334	Sequence 109334,
C 586	12	85.7	122673	9	US-10-765-790-33	Sequence 33, Appl	659	11.4	81.4	25	9	US-10-843-527-48826	Sequence 48826, A
C 587	12	85.7	143899	3	US-09-972-546-15	Sequence 15, Appl	660	11.4	81.4	25	9	US-10-843-527-48826	Sequence 48826, A
C 588	12	85.7	143899	8	US-10-735-256-15	Sequence 15, Appl	661	11.4	81.4	25	9	US-10-843-527-48826	Sequence 48826, A
C 589	12	85.7	150275	9	US-10-981-277-55	Sequence 55, App	662	11.4	81.4	25	9	US-10-843-527-48826	Sequence 48826, A
C 590	12	85.7	168325	5	US-10-087-192-955	Sequence 95, App	663	11.4	81.4	25	9	US-10-843-527-183565	Sequence 183565,
C 591	12	85.7	193074	5	US-10-981-277-43	Sequence 43, Appl	664	11.4	81.4	25	9	US-10-843-527-187887	Sequence 187887,
C 592	12	85.7	230101	8	US-10-719-993-6829	Sequence 6829, Ap	665	11.4	81.4	25	10	US-11-036-317-75935	Sequence 75935, A
C 593	12	85.7	235070	5	US-10-087-192-1990	Sequence 1990, Ap	666	11.4	81.4	25	10	US-11-036-317-128858	Sequence 128858,
C 594	12	85.7	301692	6	US-10-428-487-11	Sequence 11, Appl	667	11.4	81.4	25	10	US-11-036-317-128858	Sequence 128858,
C 595	12	85.7	310268	7	US-10-367-094-195	Sequence 195, App	668	11.4	81.4	25	10	US-11-036-317-610162	Sequence 610162,
C 596	12	85.7	653122	5	US-10-087-192-226	Sequence 226, App	669	11.4	81.4	25	10	US-11-036-317-610162	Sequence 610162,
C 597	12	85.7	1223197	5	US-10-027-632-179264	Sequence 179264, Sequence 179264, A	670	11.4	81.4	25	10	US-11-036-317-403094	Sequence 403094,
C 598	12	85.7	1223197	6	US-10-027-632-179264	Sequence 179264, A	671	11.4	81.4	25	10	US-11-036-317-403094	Sequence 403094,
C 599	12	85.7	2731748	7	US-10-297-465A-1	Sequence 1, Appl1	672	11.4	81.4	25	10	US-11-036-317-497540	Sequence 497540,
C 600	11.6	82.9	552	5	US-10-027-632-146814	Sequence 146814, A	673	11.4	81.4	25	10	US-11-036-317-497541	Sequence 497541,
C 601	11.6	82.9	552	5	US-10-027-632-146815	Sequence 146815, A	674	11.4	81.4	25	10	US-11-036-317-497541	Sequence 497541,
C 602	11.6	82.9	552	6	US-10-027-632-146814	Sequence 146814, A	675	11.4	81.4	25	10	US-11-036-317-610162	Sequence 610162,
C 603	11.6	82.9	552	6	US-10-027-632-146815	Sequence 146815, A	676	11.4	81.4	25	10	US-11-036-317-610162	Sequence 610162,
C 604	11.6	82.9	600	9	US-10-972-079-10987	Sequence 10987, A	677	11.4	81.4	25	10	US-11-036-317-681377	Sequence 681377,
C 605	11.6	82.9	600	9	US-10-972-079-11511	Sequence 11511, A	678	11.4	81.4	25	10	US-11-036-317-681377	Sequence 681377,
C 606	11.6	82.9	600	9	US-10-972-079-11512	Sequence 11512, A	679	11.4	81.4	25	10	US-11-036-317-723463	Sequence 723463,
C 607	11.6	82.9	600	9	US-10-972-079-11513	Sequence 11513, A	680	11.4	81.4	25	10	US-11-036-317-799819	Sequence 799819,
												US-11-036-317-825620	Sequence 825620,

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663	11.4	81.4	25	10	US-11-060-756-156141	Sequence 156141,	756	11.4	81.4	300	8	US-10-425-115-118130	Sequence 118130,
C 664	11.4	81.4	25	10	US-11-060-756-217029	Sequence 217029,	C 757	11.4	81.4	305	3	US-09-728-445-32	Sequence 32, App1
665	11.4	81.4	25	10	US-11-060-756-227686	Sequence 227686,	C 758	11.4	81.4	305	9	US-10-964-549-93	Sequence 32, App1
666	11.4	81.4	25	10	US-11-060-756-237269	Sequence 237269,	C 759	11.4	81.4	307	8	US-10-425-115-121120	Sequence 121120,
667	11.4	81.4	25	10	US-11-060-756-248267	Sequence 248267,	760	11.4	81.4	310	3	US-09-796-692-6500	Sequence 6500, Ap
C 668	11.4	81.4	50	3	US-09-389-782-29	Sequence 29, App1	761	11.4	81.4	310	3	US-10-040-862-6500	Sequence 6500, Ap
C 669	11.4	81.4	60	3	US-09-908-975-10521	Sequence 10521, A	762	11.4	81.4	310	6	US-10-057-475B-6500	Sequence 6500, Ap
C 670	11.4	81.4	60	3	US-09-908-975-15073	Sequence 15073, A	763	11.4	81.4	310	6	US-10-154-884B-6500	Sequence 6500, Ap
C 671	11.4	81.4	60	3	US-09-908-975-22492	Sequence 22492, A	764	11.4	81.4	310	7	US-10-242-535A-52001	Sequence 52001, A
C 672	11.4	81.4	60	5	US-10-021-723A-55	Sequence 55, App1	765	11.4	81.4	310	7	US-10-085-783A-52001	Sequence 52001, A
C 673	11.4	81.4	65	3	US-09-908-975-11225	Sequence 1225, Ap	766	11.4	81.4	310	8	US-10-764-324-6500	Sequence 6500, Ap
C 674	11.4	81.4	67	5	US-10-021-723A-30	Sequence 30, App1	767	11.4	81.4	316	8	US-10-425-115-2445	Sequence 2445, Ap
C 675	11.4	81.4	110	3	US-09-844-653-35	Sequence 35, App1	C 768	11.4	81.4	316	3	US-09-783-590-2380	Sequence 2380, Ap
C 676	11.4	81.4	117	8	US-10-425-115-65825	Sequence 65825, A	769	11.4	81.4	316	7	US-10-437-963-23225	Sequence 23225, A
C 677	11.4	81.4	117	8	US-09-783-590-8202	Sequence 8202, Ap	C 770	11.4	81.4	320	7	US-10-242-535A-4436	Sequence 4436, Ap
C 678	11.4	81.4	139	8	US-10-425-115-5003	Sequence 5003, Ap	C 771	11.4	81.4	320	7	US-10-085-783A-4436	Sequence 4436, Ap
C 679	11.4	81.4	147	6	US-10-084-846A-23	Sequence 23, App1	C 772	11.4	81.4	321	3	US-09-062-113-99	Sequence 99, App1
C 680	11.4	81.4	156	3	US-09-923-876-1642	Sequence 1642, Ap	C 773	11.4	81.4	321	6	US-10-232-658-99	Sequence 99, App1
C 681	11.4	81.4	156	3	US-09-923-876-1642	Sequence 1642, Ap	C 774	11.4	81.4	321	7	US-10-663-244-82	Sequence 82, App1
C 682	11.4	81.4	159	3	US-09-864-761-31331	Sequence 31331, A	C 775	11.4	81.4	321	7	US-10-785-109-99	Sequence 99, App1
C 683	11.4	81.4	162	3	US-09-864-761-22190	Sequence 22190, A	C 776	11.4	81.4	321	7	US-10-785-114-99	Sequence 99, App1
C 684	11.4	81.4	165	8	US-10-425-115-8054	Sequence 8054, Ap	C 777	11.4	81.4	321	8	US-10-929-958-99	Sequence 99, App1
C 685	11.4	81.4	165	8	US-10-425-115-162709	Sequence 162709, A	C 778	11.4	81.4	321	8	US-10-929-748-99	Sequence 99, App1
C 686	11.4	81.4	173	3	US-09-864-761-26899	Sequence 26899, A	C 779	11.4	81.4	321	9	US-10-979-303-99	Sequence 99, App1
C 687	11.4	81.4	175	7	US-10-424-559-72699	Sequence 72699, A	C 780	11.4	81.4	321	9	US-10-979-654-99	Sequence 99, App1
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C 689	11.4	81.4	180	6	US-10-395-740-13	Sequence 13, App1	C 782	11.4	81.4	324	7	US-10-424-559-142496	Sequence 142496, A
C 690	11.4	81.4	180	7	US-10-437-963-94631	Sequence 94631, A	C 783	11.4	81.4	324	7	US-10-437-963-17072	Sequence 17072, A
C 691	11.4	81.4	189	7	US-10-282-122A-13298	Sequence 13298, A	784	11.4	81.4	324	3	US-09-918-995-29929	Sequence 29929, A
C 692	11.4	81.4	190	7	US-10-437-963-94533	Sequence 94533, A	C 785	11.4	81.4	348	8	US-10-425-115-33057	Sequence 33057, A
C 693	11.4	81.4	191	3	US-09-864-761-24983	Sequence 24983, A	786	11.4	81.4	352	6	US-10-029-386-26611	Sequence 26611, A
C 694	11.4	81.4	191	8	US-10-425-115-125439	Sequence 125439, A	787	11.4	81.4	354	7	US-10-424-559-120746	Sequence 120746, A
C 695	11.4	81.4	195	5	US-10-106-698-2331	Sequence 2331, Ap	788	11.4	81.4	354	7	US-10-437-963-37632	Sequence 37632, A
C 696	11.4	81.4	198	3	US-09-864-408A-3381	Sequence 3381, Ap	789	11.4	81.4	358	8	US-09-770-791-582	Sequence 582, App
C 697	11.4	81.4	198	6	US-10-029-386-18252	Sequence 18252, A	C 790	11.4	81.4	369	8	US-10-425-115-83408	Sequence 83408, A
C 698	11.4	81.4	201	7	US-10-741-601-18990	Sequence 18990, A	791	11.4	81.4	373	7	US-10-424-559-124569	Sequence 124569
C 699	11.4	81.4	201	8	US-10-719-993-9101	Sequence 9101, Ap	C 792	11.4	81.4	378	6	US-10-395-740-7	Sequence 7, App1
C 700	11.4	81.4	201	8	US-10-741-600-21912	Sequence 21912, A	C 793	11.4	81.4	381	3	US-09-918-995-34114	Sequence 34114, A
C 701	11.4	81.4	201	8	US-10-741-600-50717	Sequence 50717, A	794	11.4	81.4	383	7	US-10-424-559-60571	Sequence 60521, A
C 702	11.4	81.4	203	3	US-09-923-876-1846	Sequence 1846, Ap	795	11.4	81.4	385	3	US-10-424-559-93866	Sequence 93866, A
C 703	11.4	81.4	203	3	US-09-923-876-1846	Sequence 1846, Ap	C 796	11.4	81.4	388	3	US-09-918-995-6867	Sequence 6867, Ap
C 704	11.4	81.4	209	7	US-10-425-115-160936	Sequence 65475, A	797	11.4	81.4	392	8	US-10-425-115-155397	Sequence 155397, A
C 705	11.4	81.4	211	8	US-10-425-115-160936	Sequence 160936, A	C 798	11.4	81.4	395	8	US-10-425-115-122879	Sequence 122879, A
C 706	11.4	81.4	216	9	US-10-756-149-1508	Sequence 1508, Ap	C 799	11.4	81.4	396	7	US-10-424-559-131073	Sequence 131073, A
C 707	11.4	81.4	221	8	US-10-674-124A-19480	Sequence 19480, A	800	11.4	81.4	397	8	US-10-425-115-116176	Sequence 116176, A
C 708	11.4	81.4	221	8	US-10-437-963-52698	Sequence 52698, A	C 801	11.4	81.4	398	3	US-09-960-352-1749	Sequence 1749, Ap
C 709	11.4	81.4	222	7	US-10-437-963-52698	Sequence 52698, A	C 802	11.4	81.4	398	3	US-10-485-508B-6	Sequence 6, App1
C 710	11.4	81.4	224	8	US-10-425-115-22979	Sequence 22979, A	C 803	11.4	81.4	402	8	US-10-425-115-115151	Sequence 115151, A
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C 713	11.4	81.4	237	9	US-10-450-763-7640	Sequence 7640, Ap	C 806	11.4	81.4	405	6	US-10-029-386-16555	Sequence 16525, A
C 714	11.4	81.4	238	8	US-10-425-115-3093	Sequence 3093, Ap	C 807	11.4	81.4	405	7	US-10-282-122A-6507	Sequence 6507, Ap
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C 716	11.4	81.4	244	3	US-10-437-963-27310	Sequence 27310, A	C 809	11.4	81.4	405	9	US-10-779-543-12743	Sequence 12743, A
C 717	11.4	81.4	250	6	US-10-238-075-77	Sequence 77, App1	C 810	11.4	81.4	406	3	US-09-918-995-36397	Sequence 36397, A
C 718	11.4	81.4	252	3	US-09-783-590-6711	Sequence 6711, Ap	811	11.4	81.4	406	8	US-10-425-115-33573	Sequence 33593, A
C 719	11.4	81.4	262	7	US-10-437-963-41790	Sequence 41790, A	C 812	11.4	81.4	408	3	US-09-960-352-2750	Sequence 2654, Ap
C 720	11.4	81.4	263	8	US-10-425-115-22937	Sequence 22937, A	C 813	11.4	81.4	412	3	US-09-960-352-2750	Sequence 2750, App
C 721	11.4	81.4	264	3	US-09-738-626-1658	Sequence 1658, Ap	814	11.4	81.4	413	7	US-10-469-285-812	Sequence 812, App
C 722	11.4	81.4	264	8	US-10-425-115-105548	Sequence 105548, A	C 815	11.4	81.4	414	7	US-10-242-535A-26405	Sequence 26405, A
C 723	11.4	81.4	266	3	US-09-987-899-5286	Sequence 5286, Ap	C 816	11.4	81.4	414	7	US-10-085-783A-26405	Sequence 26405, A
C 724	11.4	81.4	279	3	US-09-294-093B-4114	Sequence 4114, Ap	817	11.4	81.4	415	3	US-09-724-569-11	Sequence 7, App1
C 725	11.4	81.4	284	8	US-10-425-115-162584	Sequence 162584, A	818	11.4	81.4	415	8	US-10-425-115-10986	Sequence 30986, A
C 726	11.4	81.4	284	8	US-10-425-115-162584	Sequence 162584, A	C 819	11.4	81.4	417	3	US-09-983-965-5753	Sequence 5753, Ap
C 727	11.4	81.4	290	8	US-09-736-457-832	Sequence 832, App	C 820	11.4	81.4	417	4	US-09-925-065A-483092	Sequence 483092, A
C 728	11.4	81.4	291	3	US-09-902-941-832	Sequence 832, App	C 821	11.4	81.4	419	7	US-10-437-963-23609	Sequence 23609, A
C 729	11.4	81.4	291	3	US-09-849-626-832	Sequence 832, App	C 822	11.4	81.4	420	8	US-10-357-930-16283	Sequence 16283, A
C 730	11.4	81.4	291	5	US-10-017-754-832	Sequence 832, App	C 823	11.4	81.4	421	3	US-09-867-550-1849	Sequence 1849, Ap
C 731	11.4	81.4	291	5	US-10-113-872-832	Sequence 832, App	C 824	11.4	81.4	421	9	US-10-424-559-48144	Sequence 48144, A
C 732	11.4	81.4	291	6	US-10-283-017-832	Sequence 832, App	825	11.4	81.4	421	9	US-10-424-559-48144	Sequence 12255, A
C 733	11.4	81.4	293	3	US-09-987-899-5824	Sequence 5824, Ap	C 826	11.4	81.4	422	4	US-09-925-065A-392821	Sequence 392821, A
C 734	11.4	81.4	293	8	US-10-425-115-181462	Sequence 181462, A							

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830	11.4	81.4	422	6	US-10-027-632-140713	Sequence 140713,	C 903	11.4	81.4	473	7	US-10-424-599-926	Sequence 926, App
831	11.4	81.4	422	6	US-10-027-632-140713	Sequence 140713,	C 904	11.4	81.4	476	5	US-10-027-632-94159	Sequence 94159, A
832	11.4	81.4	422	6	US-09-925-065A-207157	Sequence 207157,	C 905	11.4	81.4	476	6	US-10-027-632-94159	Sequence 94159, A
833	11.4	81.4	429	3	US-09-960-352-1407	Sequence 1407,	C 906	11.4	81.4	476	6	US-10-424-599-24036	Sequence 24036, A
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836	11.4	81.4	431	7	US-10-085-763A-5420	Sequence 5420, Ap	C 909	11.4	81.4	480	7	US-10-085-763A-2211	Sequence 2211, Ap
837	11.4	81.4	431	8	US-10-425-115-52209	Sequence 52209, A	C 910	11.4	81.4	483	3	US-09-918-995-970	Sequence 970, App
C 838	11.4	81.4	432	3	US-09-062-113-98	Sequence 98, Appl	C 911	11.4	81.4	486	4	US-09-925-065A-740815	Sequence 740815,
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C 840	11.4	81.4	432	6	US-10-233-858-98	Sequence 98, Appl	C 913	11.4	81.4	480	3	US-09-918-995-20602	Sequence 20602, A
C 841	11.4	81.4	432	7	US-10-785-109-98	Sequence 98, Appl	C 914	11.4	81.4	480	3	US-10-425-114-25294	Sequence 25294, A
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C 849	11.4	81.4	433	6	US-10-027-632-288751	Sequence 288751,	C 922	11.4	81.4	501	3	US-09-864-761-8249	Sequence 8249, Ap
C 850	11.4	81.4	435	7	US-10-424-599-59884	Sequence 59884, A	C 923	11.4	81.4	503	4	US-10-450-763-27439	Sequence 27439, A
C 851	11.4	81.4	435	8	US-10-425-115-135104	Sequence 135104,	C 924	11.4	81.4	503	4	US-09-925-065A-208087	Sequence 208087,
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C 866	11.4	81.4	446	3	US-09-918-995-1383	Sequence 1383, Ap	C 939	11.4	81.4	511	7	US-10-242-535A-16421	Sequence 16421, A
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C 882	11.4	81.4	458	6	US-10-357-886-25	Sequence 25, Appl	C 955	11.4	81.4	523	5	US-10-027-632-278377	Sequence 278377,
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C 999 11.4 81.4 552 7 US-10-424-599-59319 Sequence 59319, A
1000 11.4 81.4 552 7 US-10-767-701-25051 Sequence 25051, A

ALIGNMENTS

RESULT 1
US-10-800-926-2
Sequence 2, Application US/10800926
Publication No. US20050032731A1
GENERAL INFORMATION:
APPLICANT: MARSHALL, WILLIAM E.
TITLE OF INVENTION: OLIGONUCLEOTIDES ALERT THE IMMUNE SYSTEM OF ANIMALS
TITLE OF INVENTION: TO THE IMMUNITY OF MICROBIAL INFECTION
FILE REFERENCE: P01936US06
CURRENT APPLICATION NUMBER: US/10/800,926
PRIOR FILING DATE: 2004-03-15
PRIOR APPLICATION NUMBER: 09/883,550
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 09/193,653
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 08/739,264
PRIOR FILING DATE: 1996-10-29
PRIOR APPLICATION NUMBER: 08/517,016
PRIOR FILING DATE: 1995-08-18
PRIOR APPLICATION NUMBER: 08/376,175
PRIOR FILING DATE: 1995-01-20
PRIOR APPLICATION NUMBER: 08/059,745
PRIOR FILING DATE: 1993-05-11
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 2
LENGTH: 14
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-800-926-2

Query Match 100.0%; Score 14; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGUACUGCACTCG 14
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Db 1 CGUACUGCACTCG 14
RESULT 2
US-09-925-065A-30493/C
Sequence 30493, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/253,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30493
LENGTH: 542
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-30493

Query Match 100.0%; Score 14; DB 4; Length 542;
Best Local Similarity 78.6%; Pred. No. 4e+02;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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Db 423 CGTACTGCACTCG 410

RESULT 3
US-10-369-493-36408
Sequence 36408, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 36408
LENGTH: 1786
TYPE: DNA
ORGANISM: Aspergillus nidulans
US-10-369-493-36408

Query Match 100.0%; Score 14; DB 6; Length 1786;
Best Local Similarity 78.6%; Pred. No. 4.2e+02;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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Db 128 CGTACTGCACTCG 141

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RESULT 4
US-10-369-493-28056/c
; Sequence 28056, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 28056
; LENGTH: 1981
; TYPE: DNA
; ORGANISM: Burkholderia fungorum
US-10-369-493-28056

Query Match      100.0%; Score 14; DB 6; Length 1981;
Best Local Similarity 78.6%; Pred. No. 4.2e+02;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Cy      1 CGUACUGCACTCG 14
Db      1510 CGTACTGCACTCG 1497

RESULT 5
US-10-282-122A-12964/c
; Sequence 12964, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
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;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 12964
;; LENGTH: 1986
;; TYPE: DNA
;; ORGANISM: Burkholderia fungorum
US-10-282-122A-12964

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Best Local Similarity 78.6%; Pred. No. 4.2e+02;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Cy      1 CGUACUGCACTCG 14
Db      1510 CGTACTGCACTCG 1497

RESULT 6
US-10-369-493-30810/c
; Sequence 30810, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 30810
; LENGTH: 2080
; TYPE: DNA
; ORGANISM: Burkholderia cepacia
US-10-369-493-30810

Query Match      100.0%; Score 14; DB 6; Length 2080;
Best Local Similarity 78.6%; Pred. No. 4.2e+02;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Cy      1 CGUACUGCACTCG 14
Db      1510 CGTACTGCACTCG 1497

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US-10-282-122A-33109/c
; Sequence 33109, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 33109
LENGTH: 2460
TYPE: DNA
ORGANISM: Pseudomonas syringae
US-10-282-122A-33109

Query Match 100.0%; Score 14; DB 7; Length 2460;
Best Local Similarity 78.6%; Pred. No. 4.2e+02;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACTCG 14
DB 1408 CGTACTGCAACTCG 1395

RESULT 8
US-10-437-963-61758/C
Sequence 61758, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 61758
LENGTH: 6024
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_6315C.1
US-10-437-963-61758

Query Match 100.0%; Score 14; DB 7; Length 6024;
Best Local Similarity 78.6%; Pred. No. 4.3e+02;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACTCG 14
DB 3493 CGTACTGCAACTCG 3480

RESULT 9
US-10-437-963-87284/C
Sequence 87284, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 87284
LENGTH: 6808
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)...(6808)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_86244C.1
US-10-437-963-87284

Query Match 100.0%; Score 14; DB 7; Length 6808;
Best Local Similarity 78.6%; Pred. No. 4.4e+02;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACTCG 14
DB 3715 CGTACTGCAACTCG 3702

RESULT 10
US-09-908-975-23753
Sequence 23753, Application US/09908975
Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Ilat
APPLICANT: FAIGLER, Simcha
TITLE OF INVENTION: Oligonucleotide Library for Detecting RNA Transcripts and Splice
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23753
LENGTH: 65
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
OTHER INFORMATION: Mus musculus
US-09-908-975-23753

Query Match 92.9%; Score 13; DB 3; Length 65;
Best Local Similarity 76.9%; Pred. No. 1.5e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 250 GTACTGCACTCG 238

```

RESULT 13
US-10-972-079-46310/c
: Sequence 46310, Application US/10972079
: Publication No. US20050153317A1
: GENERAL INFORMATION:
: APPLICANT: MMI GENOMICS, INC.
: APPLICANT: DENISE, Sue K.
: APPLICANT: ROSENFELD, David
: APPLICANT: KERR, Richard
: APPLICANT: BATES, Stephen
: APPLICANT: HOLM, Tom
: TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEED
: TITLE OF INVENTION: LIVESOCK
: FILE REFERENCE: MM1110-2
: CURRENT APPLICATION NUMBER: US/10/972,079
: CURRENT FILING DATE: 2004-10-22
: PRIOR APPLICATION NUMBER: US 60/514,333
: PRIOR FILING DATE: 2003-10-24
: NUMBER OF SEQ ID NOS: 96631
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 46310
: LENGTH: 600
: TYPE: DNA
: ORGANISM: Chicken 19866894287168_1
US-10-972-079-46310

```

Query Match	92.9%	Score 13	DB 9	Length 600
Best Local Similarity	76.9%	Pred. No. 1.6e+03		
Matches	10	Conservative	3	Mismatches 0
				Indels 0
				Gaps 0
QY	1	CGGACUGGCAACUC	13	
		: : : : : :		
DB	261	CGGACUGGCAACUC	249	

```

RESULT 14
US-10-425-115-161649/c
Sequence 161649, Application US/10425115
Publication NO. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OR INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425.115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 161649
LENGTH: 653
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1) ..(653)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: MWT4577_79000C.1
US-10-425-115-161649

```

	Query Match	92.98%	Score 13	DB 8	Length 653	
	Best Local Similarity	76.98%	Pred. No.	1.6e+03		
	Matches	10	Conservative	3	Mismatches	0
					Gaps	0
OY	1	CGUACUCGCAACTC	13			
		:: :: :: :: :				
D6	428	CGTACTGTGCAACTC	416			

RESULT 15

US-10-437-963-98896
; Sequence 98896, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Mu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bardazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221) B
; CURRENT APPLICATION NUMBER: US/10/437,963
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 98896
; LENGTH: 838
; TYPE: DNA
; ORGANISM: *Oryza sativa*
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_96760C.1
US-10-437-963-98896

Query Match 92.9%; Score 13; DB 7; Length 838;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;

Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GUACUGCAACUCG 14
||:|||||:
Db 649 GTACTGCAACTCG 661

RESULT 16

US-10-437-963-84553/c
; Sequence 84553, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Mu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bardazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221) B
; CURRENT APPLICATION NUMBER: US/10/437,963
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 84553
; LENGTH: 1042
; TYPE: DNA
; ORGANISM: *Oryza sativa*
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_83779C.1
US-10-437-963-84553

Query Match 92.9%; Score 13; DB 7; Length 1042;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;

Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUC 13
||:|||||:
Db 1019 GTACTGCAACTC 1007

RESULT 17

US-10-156-761-4883
; Sequence 4883, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4883
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: *Streptomyces avermitilis*
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1239)
US-10-156-761-4883

Query Match 92.9%; Score 13; DB 6; Length 1239;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;

Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GUACUGCAACUCG 14
||:|||||:
Db 1176 GTACTGCAACTCG 1188

RESULT 18

US-10-369-493-29486
; Sequence 29486, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052) B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 29486
; LENGTH: 1306
; TYPE: DNA
; ORGANISM: *Caenorhabditis elegans*
US-10-369-493-29486

Query Match 92.9%; Score 13; DB 6; Length 1306;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;

Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUC 13
||:|||||:
Db 701 GTACTGCAACTC 713

```
RESULT 19
US-10-450-763-8883
; Sequence 8883, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 8883
; LENGTH: 1359
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (142)..(699)
; OTHER INFORMATION: 72% homologous to Escherichia coli Rhd protein, accession
; US-10-450-763-8883

Query Match          92.9%; Score 13; DB 9; Length 1359;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACGCAACUCG 14
DB      1204 GTACTGCAACTCG 1216

RESULT 20
US-10-957-828-11/c
; Sequence 11, Application US/10957828
; Publication No. US20050221453A1
; GENERAL INFORMATION:
; APPLICANT: TAKAGI, HIROSHI
; APPLICANT: NAKAMORI, SHIGERU
; APPLICANT: YAMAGUCHI, AKIHITO
; APPLICANT: NISHINO, KUNIHICO
; TITLE OF INVENTION: L-CYSTEINE PRODUCING MICROORGANISM AND METHOD FOR PRODUCING
; FILE REFERENCE: 259781USO
; CURRENT APPLICATION NUMBER: US/10/957,828
; CURRENT FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: JP 2004-103652
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 1473
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1473)
; US-10-957-828-11

Query Match          92.9%; Score 13; DB 9; Length 1473;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACGCAACUCG 14
DB      1359 GTACTGCAACTCG 1347
```

```
RESULT 21
US-09-815-242-6126/c
; Sequence 6126, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Wall, Daniel
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6126
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1647)
; US-09-815-242-6126

Query Match          92.9%; Score 13; DB 3; Length 1647;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACGCAACUCG 14
DB      1533 GTACTGCAACTCG 1521

RESULT 22
US-10-282-122A-20432/c
; Sequence 20432, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
```

```

CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20432
LENGTH: 1647
TYPE: DNA
ORGANISM: Escherichia coli
US-10-283-122A-20432
```

```

Query Match          92.9%; Score 13; DB 7; Length 1647;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      2 GUACUGCACTCG 14
        ||:||:||:||:
Db      1533 GTACTGCACTCG 1521
```

```

RESULT 23
US-09-801-042-1/c
Sequence 1, Application US/09801042
Patent No. US20020127678A1
GENERAL INFORMATION:
APPLICANT: RIEPING, MECHTHILD
APPLICANT: THIERBACH, GEORG
APPLICANT: VAN DER REST, MICHEL, EDUARD
APPLICANT: MOLNAR, DOUME
TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE
FILE REFERENCE: MAS/21123/280410
CURRENT APPLICATION NUMBER: US/09/801,042
CURRENT FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/229,329
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: DE 100 34 833.5
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: DE 101 03874.7
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1720
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (7)..(1593)
OTHER INFORMATION: mqo gene
US-09-801-042-1
```

```

Query Match          92.9%; Score 13; DB 3; Length 1720;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      2 GUACUGCACTCG 14
        ||:||:||:||:
Db      1482 GTACTGCACTCG 1470
```

```

RESULT 24
US-10-450-763-28629/c
Sequence 28629, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 28629
LENGTH: 1732
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (1005)..(343)
OTHER INFORMATION: 94% homologous to Escherichia coli K12 putative flagellin
OTHER INFORMATION: structural protein, accession number AB000144, Smith-Waterman Score=
US-10-450-763-28629
```

```

Query Match          92.9%; Score 13; DB 9; Length 1732;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      2 GUACUGCACTCG 14
        ||:||:||:||:
Db      1683 GTACTGCACTCG 1671
```

```

RESULT 25
US-10-450-763-25885/c
Sequence 25885, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 25885
LENGTH: 1919
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (1005)..(343)
OTHER INFORMATION: 94% homologous to Escherichia coli K12 putative flagellin
OTHER INFORMATION: structural protein, accession number AB000144, Smith-Waterman Score=
US-10-450-763-25885
```


US-10-450-763-25885

Query Match 92.9%; Score 13; DB 9; Length 1919;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCACTCG 14
||:|||||:
DB 1683 GFACTGCACTCG 1671

RESULT 26

US-09-864-761-4533
; Sequence 4533, Application US/09864761
; Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: Aecm1ca-X-1

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Anomax Sequence Listing Engine vers. 1.1

SEQ ID NO 4533

LENGTH: 1945

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: MAP TO AL021808.1

OTHER INFORMATION: EXPRESSED IN HELI00, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
US-09-864-761-4533

Query Match 92.9%; Score 13; DB 3; Length 1945;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCACTCG 14
||:|||||:
DB 263 GFACTGCACTCG 275

RESULT 27

US-10-450-763-23995/c

; Sequence 23995, Application US/10450763

; Publication No. US20050196754A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REFERENCE: 790CIP3/US

CURRENT FILING DATE: 2003-06-11

PRIOR APPLICATION NUMBER: PCT/US01/08631

PRIOR FILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: 09/540,217

PRIOR FILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: 09/649,167

PRIOR FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SOFTWARE: Custom

SEQ ID NO 23995

LENGTH: 2133

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: SIMILAR

LOCATION: (1)..(774)

OTHER INFORMATION: 90% homologous to Escherichia coli ATP-dependent helicase

OTHER INFORMATION: HTPA homolog, accession number D90780, Smith-Waterman Score=1183.

US-10-450-763-23995

Query Match 92.9%; Score 13; DB 9; Length 2133;
Best Local Similarity 76.9%; Pred. No. 1.7e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCACTCG 14
||:|||||:
DB 2019 GFACTGCACTCG 2007

RESULT 28

US-10-156-761-2636/c

; Sequence 2636, Application US/10156761

; Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIKAWA, HIROSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SAKAKI, YOSHIYUKI

APPLICANT: HATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-05-30

```
/ PRIOR APPLICATION NUMBER: JP 2001-272697
/ PRIOR FILING DATE: 2001-08-02
/ NUMBER OF SEQ ID NOS: 15109
/ SEQ ID NO 2636
/ LENGTH: 2559
/ TYPE: DNA
/ ORGANISM: Streptomyces avermitilis
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(2559)
US-10-156-761-2636

Query Match          92.9%; Score 13; DB 6; Length 2559;
Best Local Similarity 76.9%; Pred. No. 1.7e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACUGCAACTCG 14
DB      669 GTACTGCAACTCG 657

RESULT 29
US-10-450-763-25886/C
/ Sequence 25886, Application US/10450763
/ Publication No. US20050196754A1
/ GENERAL INFORMATION:
/ APPLICANT: HySeq, Inc
/ TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
/ FILE REFERENCE: 790CIP3/US
/ CURRENT APPLICATION NUMBER: US/10/450,763
/ PRIOR FILING DATE: 2003-06-11
/ PRIOR APPLICATION NUMBER: PCT/US01/08631
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: 09/540,217
/ PRIOR FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: 09/649,167
/ PRIOR FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 60736
/ SOFTWARE: Custom
/ SEQ ID NO 25886
/ LENGTH: 3222
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIMILAR
/ LOCATION: (1)..(774)
/ OTHER INFORMATION: 90% homologous to Escherichia coli ATP-dependent helicase
US-10-450-763-25886

Query Match          92.9%; Score 13; DB 9; Length 3222;
Best Local Similarity 76.9%; Pred. No. 1.7e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACUGCAACTCG 14
DB      2019 GTACTGCAACTCG 2007

RESULT 30
US-10-057-475B-10475/C
/ Sequence 10475, Application US/10057475B
/ Publication No. US20040002068A1
/ GENERAL INFORMATION:
/ APPLICANT: Gaiger, Alexander
/ APPLICANT: Algate, Paul A.
/ APPLICANT: Mannion, Jane
/ APPLICANT: Clapper, Jonathan David
/ APPLICANT: Wang, Aljun
/ APPLICANT: Ordonez, Nadia
/ APPLICANT: Carter, Lauren
/ APPLICANT: McNeill, Patricia Dianne
/ APPLICANT: Corixa Corporation
```

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/ TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
/ FILE REFERENCE: 014058-014402US
/ CURRENT APPLICATION NUMBER: US/10/057,475B
/ PRIOR FILING DATE: 2002-01-22
/ PRIOR APPLICATION NUMBER: US 60/186,126
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: US 60/190,479
/ PRIOR FILING DATE: 2000-03-17
/ PRIOR APPLICATION NUMBER: US 60/200,545
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 60/200,303
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,779
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,999
/ PRIOR FILING DATE: 2000-05-01
/ PRIOR APPLICATION NUMBER: US 60/202,084
/ PRIOR FILING DATE: 2000-05-04
/ PRIOR APPLICATION NUMBER: US 60/206,201
/ PRIOR FILING DATE: 2000-05-22
/ PRIOR APPLICATION NUMBER: US 60/218,950
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 60/222,903
/ PRIOR FILING DATE: 2000-08-03
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 10979
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 10475
/ LENGTH: 51657
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)..(51657)
/ OTHER INFORMATION: n = G, A, C or T
US-10-057-475B-10475

Query Match          92.9%; Score 13; DB 6; Length 51657;
Best Local Similarity 76.9%; Pred. No. 1.8e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGUACUGCACTC 13
DB      44702 GTACTGCAACTC 44690

RESULT 31
US-10-154-884B-10475/C
/ Sequence 10475, Application US/10154884B
/ Publication No. US20040005561A1
/ GENERAL INFORMATION:
/ APPLICANT: Gaiger, Alexander
/ APPLICANT: Algate, Paul A.
/ APPLICANT: Mannion, Jane
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Corixa Corporation
/ TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
/ TITLE OF INVENTION: Hematological Malignancies
/ FILE REFERENCE: 014058-013521US
/ CURRENT APPLICATION NUMBER: US/10/154,884B
/ PRIOR FILING DATE: 2002-05-23
/ PRIOR APPLICATION NUMBER: US 60/186,126
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: US 60/190,479
/ PRIOR FILING DATE: 2000-03-17
/ PRIOR APPLICATION NUMBER: US 60/200,545
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 60/200,303
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,779
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,999
```

PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 11290
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10475
LENGTH: 51657
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(51657)
OTHER INFORMATION: n = g, a, c or t
US-10-154-884B-10475

Query Match 92.9%; Score 13; DB 6; Length 51657;
Best Local Similarity 76.9%; Pred. No. 1.8e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGUACUGCAACUC 13
Db 44702 CGTACTGCAACTC 44690

RESULT 32
US-10-331-053-61/c
Sequence 61, Application US/10331053
Publication No. US20040197778A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 529452001100
CURRENT APPLICATION NUMBER: US/10/331,053
CURRENT FILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 61
LENGTH: 83493
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(83493)
OTHER INFORMATION: n = A,T,C or G
US-10-331-053-61

Query Match 92.9%; Score 13; DB 8; Length 83493;
Best Local Similarity 76.9%; Pred. No. 1.8e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGUACUGCAACUC 13
Db 36317 CGTACTGCAACTC 36305

RESULT 33
US-10-398-221-9/c
Sequence 9, Application US/10398221
Publication No. US20040018514A1
GENERAL INFORMATION:
APPLICANT: KUNST, Frederick
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REFERENCE: 344 702 - US
CURRENT APPLICATION NUMBER: US/10/398,221

CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: FR 00/12 697
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 684707
TYPE: DNA
ORGANISM: Listeria innocua
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(end)
OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u
US-10-398-221-9

Query Match 92.9%; Score 13; DB 7; Length 684707;
Best Local Similarity 76.9%; Pred. No. 1.8e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGUACUGCAACUC 13
Db 646081 CGTACTGCAACTC 646069

RESULT 34
US-10-398-221-2058
Sequence 2058, Application US/10398221
Publication No. US20040018514A1
GENERAL INFORMATION:
APPLICANT: KUNST, Frederick
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REFERENCE: 344 702 - US
CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: FR 00/12 697
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2058
LENGTH: 3011208
TYPE: DNA
ORGANISM: Listeria innocua
US-10-398-221-2058

Query Match 92.9%; Score 13; DB 7; Length 3011208;
Best Local Similarity 76.9%; Pred. No. 1.4e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGUACUGCAACUC 13
Db 2634732 CGTACTGCAACTC 2634744

RESULT 35
US-10-156-761-1
Sequence 1, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMDURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHITAKA
APPLICANT: HATTORI, MASAHISA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761

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; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match          92.9%; Score 13; DB 6; Length 9025608;
Best Local Similarity 76.9%; Pred. No. 8.2e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACUGCAACUCG 14
Db      3248037 GTAGTCGCACTCG 3248049

RESULT 36
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match          92.9%; Score 13; DB 6; Length 9025608;
Best Local Similarity 76.9%; Pred. No. 8.2e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACUGCAACUCG 14
Db      5955055 GTAGTCGCACTCG 5955043

RESULT 37
US-10-843-527-74019
; Sequence 74019, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus

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; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 74019
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-74019

Query Match          88.6%; Score 12.4; DB 9; Length 25;
Best Local Similarity 78.6%; Pred. No. 3.3e+03;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGUACUGCAACUCG 14
Db      6 CGTACCGCAACTCG 19

RESULT 38
US-10-843-527-74993
; Sequence 74993, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 74993
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-74993

Query Match          88.6%; Score 12.4; DB 9; Length 25;
Best Local Similarity 71.4%; Pred. No. 3.3e+03;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGUACUGCAACUCG 14
Db      8 CGTACCGCAACTCG 21

RESULT 39
US-10-843-527-163184/c
; Sequence 163184, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 163184
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-163184

```

```
Query Match      88.6%; Score 12.4; DB 9; Length 25;
Best Local Similarity 71.4%; Pred. No. 3.3e+03;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy      1 CGUACUGCAACUCG 14
       ||:||:||:||:
Db      18 CGTACTGCAACTCG 5

RESULT 40
US-10-843-527-164158/c
; Sequence 164158, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Eric Schnell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; PRIOR FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 164158
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-164158

Query Match      88.6%; Score 12.4; DB 9; Length 25;
Best Local Similarity 78.6%; Pred. No. 3.3e+03;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy      1 CGUACUGCAACUCG 14
       ||:||:||:||:
Db      20 CGTACCGCAACTCG 7

RESULT 41
US-10-767-701-28070/c
; Sequence 28070, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 28070
; LENGTH: 110
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 7535295
US-10-767-701-28070

Query Match      88.6%; Score 12.4; DB 7; Length 110;
Best Local Similarity 71.4%; Pred. No. 3.4e+03;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy      1 CGUACUGCAACUCG 14
       ||:||:||:||:
Db      51 CGTACTGCAACTCG 38

RESULT 42
US-10-425-115-49773/c
; Sequence 49773, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 49773
; LENGTH: 219
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_145392C.1
US-10-425-115-49773

Query Match      88.6%; Score 12.4; DB 8; Length 219;
Best Local Similarity 78.6%; Pred. No. 3.5e+03;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy      1 CGUACUGCAACUCG 14
       ||:||:||:||:
Db      18 CGTACTGCAACTCG 5

RESULT 43
US-10-424-599-53399
; Sequence 53399, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 53399
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_19232C.1
US-10-424-599-53399

Query Match      88.6%; Score 12.4; DB 7; Length 229;
Best Local Similarity 71.4%; Pred. No. 3.5e+03;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy      1 CGUACUGCAACUCG 14
       ||:||:||:||:
Db      24 CATACTGCAACTCG 37

RESULT 44
US-10-424-599-133643
; Sequence 133643, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
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/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 133643
/ LENGTH: 258
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_91686C.1
US-10-424-599-133643

Query Match      88.6%; Score 12.4; DB 7; Length 258;
Best Local Similarity 71.4%; Pred. No. 3.5e+03;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGUACUGCAACUCG 14
        ||:|||||:|
DB      18 CGTCTGCAACTCG 31

RESULT 45
US-10-425-115-2980
/ Sequence 2980, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 2980
/ LENGTH: 285
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(285)
/ OTHER INFORMATION: unsure at all n locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_102715C.1
US-10-425-115-2980

Query Match      88.6%; Score 12.4; DB 8; Length 285;
Best Local Similarity 71.4%; Pred. No. 3.5e+03;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGUACUGCAACUCG 14
        ||:|||||:|
DB      101 CGTACTGCACTCG 114

RESULT 46
US-10-424-599-106360
/ Sequence 106360, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 106360
/ LENGTH: 308
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/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_6705C.1
US-10-424-599-106360

Query Match      88.6%; Score 12.4; DB 7; Length 308;
Best Local Similarity 71.4%; Pred. No. 3.5e+03;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGUACUGCAACUCG 14
        ||:|||||:|
DB      61 CGTACTGCACTCG 74

RESULT 47
US-10-425-115-86279
/ Sequence 86279, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 86279
/ LENGTH: 312
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_178697C.1
US-10-425-115-86279

Query Match      88.6%; Score 12.4; DB 8; Length 312;
Best Local Similarity 71.4%; Pred. No. 3.5e+03;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGUACUGCAACUCG 14
        ||:|||||:|
DB      228 CGTACTGCACTCG 241

RESULT 48
US-10-425-115-161997
/ Sequence 161997, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 161997
/ LENGTH: 322
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_79318C.1
US-10-425-115-161997

Query Match      88.6%; Score 12.4; DB 8; Length 322;
Best Local Similarity 78.6%; Pred. No. 3.6e+03;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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OY 1 CGUACUGCACTCG 14
 ||:|||||:
 DB 267 CGTACCGCACTCG 280

RESULT 49

US-10-424-599-68441/C
 ; Sequence 68441, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 68441
 ; LENGTH: 331
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_32815C.1
 US-10-424-599-68441

Query Match 88.6%; Score 12.4; DB 7; Length 331;
 Best Local Similarity 71.4%; Pred. No. 3.6e+03;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCACTCG 14
 ||:|||||:
 DB 192 CGTCTGCACTCG 179

RESULT 50

US-10-424-599-139244/C
 ; Sequence 139244, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 139244
 ; LENGTH: 343
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_96745C.1
 US-10-424-599-139244

Query Match 88.6%; Score 12.4; DB 7; Length 343;
 Best Local Similarity 71.4%; Pred. No. 3.6e+03;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCACTCG 14
 ||:|||||:
 DB 241 CGTCTGCACTCG 228

Search completed: March 19, 2006, 07:53:06
 Job time : 2134.77 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:35:23 ; Search time 53.5769 Seconds
(without alignments)
464.488 Million cell updates/sec

Title: US-10-800-926-2
Perfect score: 14
Sequence: 1 cguacgcaacug 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/1 COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5 COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B COMB.seq: *
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6: /cgn2_6/ptodata/1/ina/PTCUS COMB.seq: *
7: /cgn2_6/ptodata/1/ina/PP COMB.seq: *
8: /cgn2_6/ptodata/1/ina/RE COMB.seq: *
9: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	13	92.9	601	3	US-09-949-016-147054
C 2	13	92.9	1720	3	US-09-801-042-1
C 3	13	92.9	21372	3	US-09-949-016-16941
C 4	13	92.9	374159	3	US-09-949-016-15868
C 5	12.4	88.6	140	3	US-09-270-767-87123
C 6	12.4	88.6	323	3	US-09-513-999C-2299
C 7	12.4	88.6	349	3	US-08-303-861-15
C 8	12.4	88.6	339	3	US-09-621-976-681
C 9	12.4	88.6	435	3	US-09-252-991A-79
C 10	12.4	88.6	504	3	US-09-252-991A-1326
C 11	12.4	88.6	543	3	US-09-252-991A-233
C 12	12.4	88.6	543	3	US-09-252-991A-7705
C 13	12.4	88.6	597	3	US-09-270-767-5447
C 14	12.4	88.6	597	3	US-09-270-767-50729
C 15	12.4	88.6	669	3	US-09-252-991A-100
C 16	12.4	88.6	696	3	US-09-252-991A-9718
C 17	12.4	88.6	726	3	US-09-252-991A-14097
C 18	12.4	88.6	737	3	US-09-270-767-11527
C 19	12.4	88.6	756	3	US-09-252-991A-94
C 20	12.4	88.6	834	3	US-09-252-991A-6447
C 21	12.4	88.6	867	3	US-09-902-540-5805
C 22	12.4	88.6	930	3	US-09-252-991A-6103
C 23	12.4	88.6	1005	3	US-09-902-540-7341
C 24	12.4	88.6	1007	3	US-09-902-540-70

25	12.4	88.6	1017	3	US-09-107-532A-2165	Sequence 2165, Ap
C 26	12.4	88.6	1065	3	US-09-252-991A-90	Sequence 90, Appl
27	12.4	88.6	1104	3	US-09-489-039A-2883	Sequence 2883, Ap
C 28	12.4	88.6	1137	3	US-09-252-991A-6183	Sequence 6183, Ap
29	12.4	88.6	1152	3	US-09-252-991A-13050	Sequence 13050, A
C 30	12.4	88.6	1203	3	US-09-252-991A-7557	Sequence 7557, Ap
31	12.4	88.6	1203	3	US-09-252-991A-9574	Sequence 9574, Ap
C 32	12.4	88.6	1206	3	US-09-996-008B-1	Sequence 1, Appl
33	12.4	88.6	1233	3	US-09-252-991A-13225	Sequence 13225, A
C 34	12.4	88.6	1314	3	US-09-252-991A-7784	Sequence 7784, Ap
35	12.4	88.6	1359	3	US-09-489-039A-4444	Sequence 4444, Ap
C 36	12.4	88.6	1563	3	US-09-252-991A-12900	Sequence 12900, A
37	12.4	88.6	1629	3	US-09-252-991A-104	Sequence 104, App
C 38	12.4	88.6	1737	3	US-09-252-991A-252	Sequence 252, App
C 39	12.4	88.6	1737	3	US-09-252-991A-279	Sequence 279, App
C 40	12.4	88.6	1776	3	US-09-252-991A-12189	Sequence 12189, A
C 41	12.4	88.6	1800	3	US-09-252-991A-4152	Sequence 4152, Ap
C 42	12.4	88.6	1827	3	US-09-252-991A-1375	Sequence 1375, Ap
C 43	12.4	88.6	2262	3	US-09-252-991A-1416	Sequence 1416, Ap
C 44	12.4	88.6	2298	3	US-09-252-991A-12254	Sequence 12254, A
C 45	12.4	88.6	2346	3	US-09-252-991A-9536	Sequence 9536, Ap
46	12.4	88.6	2346	3	US-09-252-991A-13355	Sequence 13355, A
47	12.4	88.6	2370	3	US-09-489-039A-1363	Sequence 1363, Ap
C 48	12.4	88.6	2391	3	US-09-252-991A-1192	Sequence 1192, Ap
C 49	12.4	88.6	2472	3	US-09-252-991A-4456	Sequence 4456, Ap
C 50	12.4	88.6	2495	3	US-09-620-312D-272	Sequence 272, App
C 51	12.4	88.6	2632	3	US-09-489-039A-4584	Sequence 4584, Ap
C 52	12.4	88.6	2838	3	US-09-252-991A-14128	Sequence 14128, A
53	12.4	88.6	2847	2	US-08-087-007-2	Sequence 2, Appl1
54	12.4	88.6	2847	3	US-08-483-433-2	Sequence 2, Appl1
55	12.4	88.6	2847	3	US-09-566-254A-2	Sequence 2, Appl1
56	12.4	88.6	2847	6	PCT-US92-05920-2	Sequence 2, Appl1
C 57	12.4	88.6	2934	3	US-09-252-991A-84	Sequence 84, Appl
C 58	12.4	88.6	3897	3	US-09-252-991A-1008	Sequence 1008, A
C 59	12.4	88.6	6203	3	US-09-902-540-811	Sequence 811, App
C 60	12.4	88.6	22118	3	US-09-815-981A-5	Sequence 5, Appl1
C 61	12.4	88.6	72704	3	US-09-902-540-1273	Sequence 1273, Ap
C 62	12.4	88.6	108440	3	US-09-949-016-12065	Sequence 12065, A
C 63	12.4	88.6	108441	3	US-09-949-016-14990	Sequence 14090, A
64	12.4	88.6	4403765	3	US-09-103-840A-2	Sequence 2, Appl1
65	12.4	88.6	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
66	12	85.7	80	2	US-08-353-476-59	Sequence 59, Appl
67	12	85.7	423	3	US-09-248-796A-11879	Sequence 11879, A
C 68	12	85.7	523	3	US-09-802-540-5146	Sequence 5146, Ap
C 69	12	85.7	601	3	US-09-949-016-51279	Sequence 51279, A
C 70	12	85.7	601	3	US-09-949-016-89184	Sequence 89184, A
C 71	12	85.7	601	3	US-09-949-016-121311	Sequence 121311, A
C 72	12	85.7	601	3	US-09-949-016-121312	Sequence 121312, A
C 73	12	85.7	601	3	US-09-949-016-121313	Sequence 121313, A
C 74	12	85.7	601	3	US-09-949-016-121314	Sequence 121314, A
C 75	12	85.7	601	3	US-09-949-016-142961	Sequence 142961, A
76	12	85.7	601	3	US-09-949-016-142962	Sequence 142962, A
77	12	85.7	601	3	US-09-949-016-142963	Sequence 142963, A
C 78	12	85.7	703	3	US-09-533-559-6348	Sequence 6348, Ap
C 79	12	85.7	714	3	US-09-056-105-28	Sequence 28, Appl
C 80	12	85.7	812	3	US-09-270-767-4491	Sequence 4491, Ap
C 81	12	85.7	812	3	US-09-270-767-19773	Sequence 19773, A
C 82	12	85.7	819	3	US-09-248-796A-1668	Sequence 1668, Ap
C 83	12	85.7	864	3	US-09-328-352-1652	Sequence 1652, Ap
C 84	12	85.7	882	3	US-09-937-862B-59	Sequence 59, Appl
C 85	12	85.7	1047	3	US-09-921-017B-59	Sequence 59, Appl
C 86	12	85.7	1338	3	US-09-710-279-1233	Sequence 1233, Ap
C 87	12	85.7	1336	3	US-09-134-001E-1624	Sequence 1624, Ap
C 88	12	85.7	1368	3	US-09-453-702B-199	Sequence 199, App
C 89	12	85.7	1368	3	US-10-114-170-199	Sequence 199, App
C 90	12	85.7	1434	3	US-09-328-352-3639	Sequence 3639, Ap
C 91	12	85.7	1457	3	US-09-256-000-22	Sequence 22, Appl
C 92	12	85.7	1457	3	US-10-034-015A-22	Sequence 22, Appl
C 93	12	85.7	1457	3	US-10-083-620A-22	Sequence 22, Appl
C 94	12	85.7	1458	3	US-09-248-796A-6365	Sequence 6365, Ap
C 95	12	85.7	1537	3	US-09-620-312D-561	Sequence 561, App
C 96	12	85.7	1677	3	US-09-902-540-7773	Sequence 7773, Ap
97	12	85.7	1887	3	US-09-256-000-18	Sequence 18, Appl

98	12	85.7	1887	3	US-10-034-015A-18	Sequence 18, Appl	C 171	11.4	81.4	25	3	US-09-366-196G-109932	Sequence 109932,
99	12	85.7	1887	3	US-10-083-620A-18	Sequence 18, Appl	C 172	11.4	81.4	25	3	US-09-366-196G-109933	Sequence 109933,
100	12	85.7	1967	3	US-09-256-000-20	Sequence 20, Appl	C 173	11.4	81.4	25	3	US-09-396-196G-109934	Sequence 109934,
101	12	85.7	1967	3	US-10-034-015A-20	Sequence 20, Appl	C 174	11.4	81.4	30	6	US-07-661-378A-4	Sequence 4, Appl
102	12	85.7	1967	3	US-10-083-620A-20	Sequence 20, Appl	C 175	11.4	81.4	33	6	PCT-US94-09653A-6	Sequence 6, Appl
103	12	85.7	1989	3	US-09-949-016-5214	Sequence 5214, Ap	C 176	11.4	81.4	35	2	US-07-918-318-3	Sequence 3, Appl
104	12	85.7	1997	2	US-08-967-466-2	Sequence 2, Appl	C 177	11.4	81.4	134	3	US-09-270-767-169	Sequence 169,
105	12	85.7	1997	2	US-09-240-359-2	Sequence 2, Appl	C 178	11.4	81.4	134	3	US-09-270-767-169	Sequence 169,
106	12	85.7	1997	2	US-08-802-741-2	Sequence 2, Appl	C 179	11.4	81.4	160	3	US-09-270-767-169	Sequence 169,
107	12	85.7	2207	3	US-09-254-504-6	Sequence 6, Appl	C 180	11.4	81.4	168	6	PCT-US94-09653A-26	Sequence 26, Appl
108	12	85.7	2818	3	US-09-710-279-4012	Sequence 4012, Ap	C 181	11.4	81.4	171	6	PCT-US94-09653A-31	Sequence 31, Appl
109	12	85.7	3030	3	US-09-710-279-4001	Sequence 4001, Ap	C 182	11.4	81.4	171	6	PCT-US94-09653A-30	Sequence 30, Appl
110	12	85.7	3108	3	US-09-937-521-11	Sequence 11, Appl	C 183	11.4	81.4	183	6	US-09-134-000C-351	Sequence 351, Ap
111	12	85.7	3150	3	US-09-710-279-3893	Sequence 3893, Ap	C 184	11.4	81.4	195	3	US-09-540-236-371	Sequence 371, Appl
112	12	85.7	3348	3	US-09-799-451-302	Sequence 302, App	C 185	11.4	81.4	233	3	US-09-540-236-371	Sequence 371, Appl
113	12	85.7	3511	3	US-09-799-451-456	Sequence 456, App	C 186	11.4	81.4	231	3	US-09-702-705-832	Sequence 832, App
114	12	85.7	4121	3	US-09-604-978-4	Sequence 4, Appl	C 187	11.4	81.4	291	3	US-09-736-457-832	Sequence 832, App
115	12	85.7	4121	3	US-09-604-978-4	Sequence 4, Appl	C 188	11.4	81.4	291	3	US-09-614-1248-832	Sequence 832, App
116	12	85.7	4835	3	US-10-325-878-4	Sequence 4, Appl	C 189	11.4	81.4	291	3	US-09-614-1248-832	Sequence 832, App
117	12	85.7	4835	3	US-09-937-521-16	Sequence 16, Appl	C 190	11.4	81.4	291	3	US-09-614-1248-832	Sequence 832, App
118	12	85.7	6250	3	US-09-902-540-773	Sequence 773, App	C 191	11.4	81.4	291	3	US-09-614-1248-832	Sequence 832, App
119	12	85.7	14448	3	US-09-949-016-12108	Sequence 12108, A	C 192	11.4	81.4	291	3	US-09-614-1248-832	Sequence 832, App
120	12	85.7	18448	3	US-09-949-016-15345	Sequence 15345, A	C 193	11.4	81.4	292	3	US-09-614-1248-832	Sequence 832, App
121	12	85.7	22683	3	US-09-949-016-14054	Sequence 14054, A	C 194	11.4	81.4	308	3	US-09-313-294X-3894	Sequence 3894, Ap
122	12	85.7	22683	3	US-09-949-016-14055	Sequence 14055, A	C 195	11.4	81.4	321	3	US-09-313-294X-3894	Sequence 3894, Ap
123	12	85.7	22728	3	US-09-949-016-13774	Sequence 13774, A	C 196	11.4	81.4	321	3	US-09-313-294X-3894	Sequence 3894, Ap
124	12	85.7	29559	3	US-09-902-540-1254	Sequence 1254, Ap	C 197	11.4	81.4	321	3	US-09-313-294X-3894	Sequence 3894, Ap
125	12	85.7	31769	3	US-09-949-002-734	Sequence 734, App	C 198	11.4	81.4	405	3	US-09-711-164-224	Sequence 224, App
126	12	85.7	42898	3	US-09-949-016-12301	Sequence 12301, A	C 199	11.4	81.4	407	3	US-09-370-767-27503	Sequence 27503, A
127	12	85.7	42898	3	US-09-949-016-15904	Sequence 15904, A	C 200	11.4	81.4	432	3	US-10-332-858-98	Sequence 98, Appl
128	12	85.7	76321	3	US-09-949-002-578	Sequence 578, App	C 201	11.4	81.4	432	3	US-09-338-063A-98	Sequence 98, Appl
129	12	85.7	76321	3	US-09-949-002-803	Sequence 803, App	C 202	11.4	81.4	438	3	US-09-338-063A-98	Sequence 98, Appl
130	12	85.7	91232	3	US-09-949-002-607	Sequence 607, App	C 203	11.4	81.4	438	3	US-09-338-063A-98	Sequence 98, Appl
131	12	85.7	105733	3	US-09-949-016-13080	Sequence 13080, A	C 204	11.4	81.4	438	3	US-10-332-858-114	Sequence 114, Appl
132	12	85.7	121427	3	US-09-949-016-11950	Sequence 11950, A	C 205	11.4	81.4	438	3	US-09-338-063A-98	Sequence 98, Appl
133	12	85.7	121433	3	US-09-949-016-13230	Sequence 13230, A	C 206	11.4	81.4	438	3	US-09-338-063A-98	Sequence 98, Appl
134	12	85.7	125672	3	US-09-949-016-16956	Sequence 16956, A	C 207	11.4	81.4	438	3	US-09-338-063A-98	Sequence 98, Appl
135	12	85.7	141454	3	US-09-949-016-12055	Sequence 12055, A	C 208	11.4	81.4	438	3	US-09-338-063A-98	Sequence 98, Appl
136	12	85.7	141455	3	US-09-949-016-17190	Sequence 17190, A	C 209	11.4	81.4	438	3	US-09-338-063A-98	Sequence 98, Appl
137	12	85.7	14783	3	US-09-949-016-15127	Sequence 15127, A	C 210	11.4	81.4	438	3	US-09-338-063A-98	Sequence 98, Appl
138	12	85.7	23750	3	US-09-949-016-14273	Sequence 14273, A	C 211	11.4	81.4	438	3	US-09-338-063A-98	Sequence 98, Appl
139	12	85.7	26508	3	US-09-949-016-15779	Sequence 15779, A	C 212	11.4	81.4	438	3	US-09-338-063A-98	Sequence 98, Appl
140	12	85.7	42118	3	US-09-949-016-16297	Sequence 16297, A	C 213	11.4	81.4	438	3	US-09-338-063A-98	Sequence 98, Appl
141	12	85.7	81.4	20	US-08-754-490-7	Sequence 7, Appl	C 214	11.4	81.4	513	3	US-09-533-559-3845	Sequence 3845, Ap
142	11.4	81.4	81.4	20	US-08-754-490-18	Sequence 18, Appl	C 215	11.4	81.4	513	3	US-09-533-559-3845	Sequence 3845, Ap
143	11.4	81.4	81.4	20	US-08-923-505A-7	Sequence 7, Appl	C 216	11.4	81.4	513	3	US-09-533-559-3845	Sequence 3845, Ap
144	11.4	81.4	81.4	20	US-08-923-505A-18	Sequence 18, Appl	C 217	11.4	81.4	513	3	US-09-533-559-3845	Sequence 3845, Ap
145	11.4	81.4	81.4	20	US-08-923-505A-18	Sequence 18, Appl	C 218	11.4	81.4	513	3	US-09-533-559-3845	Sequence 3845, Ap
146	11.4	81.4	81.4	20	US-09-260-952A-18	Sequence 18, Appl	C 219	11.4	81.4	513	3	US-09-533-559-3845	Sequence 3845, Ap
147	11.4	81.4	81.4	20	US-09-253-341-7	Sequence 7, Appl	C 220	11.4	81.4	513	3	US-09-533-559-3845	Sequence 3845, Ap
148	11.4	81.4	81.4	20	US-09-253-341-18	Sequence 18, Appl	C 221	11.4	81.4	513	3	US-09-533-559-3845	Sequence 3845, Ap
149	11.4	81.4	81.4	20	US-09-253-341A-7	Sequence 7, Appl	C 222	11.4	81.4	513	3	US-09-533-559-3845	Sequence 3845, Ap
150	11.4	81.4	81.4	20	US-09-253-341A-18	Sequence 18, Appl	C 223	11.4	81.4	513	3	US-09-533-559-3845	Sequence 3845, Ap
151	11.4	81.4	81.4	20	US-09-261-040-7	Sequence 7, Appl	C 224	11.4	81.4	513	3	US-09-533-559-3845	Sequence 3845, Ap
152	11.4	81.4	81.4	20	US-09-261-040-18	Sequence 18, Appl	C 225	11.4	81.4	513	3	US-09-533-559-3845	Sequence 3845, Ap
153	11.4	81.4	81.4	20	US-09-916-956A-7	Sequence 7, Appl	C 226	11.4	81.4	513	3	US-09-949-016-50542	Sequence 50542, A
154	11.4	81.4	81.4	20	US-09-916-956A-18	Sequence 18, Appl	C 227	11.4	81.4	513	3	US-09-949-016-50542	Sequence 50542, A
155	11.4	81.4	81.4	20	US-09-873-873-7	Sequence 7, Appl	C 228	11.4	81.4	513	3	US-09-949-016-50542	Sequence 50542, A
156	11.4	81.4	81.4	20	US-09-873-873-18	Sequence 18, Appl	C 229	11.4	81.4	513	3	US-09-949-016-50542	Sequence 50542, A
157	11.4	81.4	81.4	20	US-09-997-914-7	Sequence 7, Appl	C 230	11.4	81.4	513	3	US-09-949-016-50542	Sequence 50542, A
158	11.4	81.4	81.4	20	US-09-997-914-18	Sequence 18, Appl	C 231	11.4	81.4	513	3	US-09-949-016-50542	Sequence 50542, A
159	11.4	81.4	81.4	20	US-09-636-746B-7	Sequence 7, Appl	C 232	11.4	81.4	513	3	US-09-949-016-50542	Sequence 50542, A
160	11.4	81.4	81.4	20	US-09-636-746B-18	Sequence 18, Appl	C 233	11.4	81.4	513	3	US-09-949-016-50542	Sequence 50542, A
161	11.4	81.4	81.4	20	US-10-365-645-7	Sequence 7, Appl	C 234	11.4	81.4	513	3	US-09-949-016-50542	Sequence 50542, A
162	11.4	81.4	81.4	20	US-10-365-645-18	Sequence 18, Appl	C 235	11.4	81.4	513	3	US-09-949-016-50542	Sequence 50542, A
163	11.4	81.4	81.4	20	US-10-817-182-7	Sequence 7, Appl	C 236	11.4	81.4	513	3	US-09-949-016-50542	Sequence 50542, A
164	11.4	81.4	81.4	20	US-10-817-182-18	Sequence 18, Appl	C 237	11.4	81.4	513	3	US-09-949-016-50542	Sequence 50542, A
165	11.4	81.4	81.4	20	US-10-672-163-7	Sequence 7, Appl	C 238	11.4	81.4	513	3	US-09-949-016-50542	Sequence 50542, A
166	11.4	81.4	81.4	20	US-10-672-163-18	Sequence 18, Appl	C 239	11.4	81.4	513	3	US-09-949-016-50542	Sequence 50542, A
167	11.4	81.4	81.4	25	US-08-737-607-3	Sequence 3, Appl	C 240	11.4	81.4	513	3	US-09-949-016-50542	Sequence 50542, A
168	11.4	81.4	81.4	25	US-09-366-196G-6531	Sequence 6531, Ap	C 241	11.4	81.4	513	3	US-09-949-016-50542	Sequence 50542, A
169	11.4	81.4	81.4	25	US-09-366-196G-87450	Sequence 87450, A	C 242	11.4	81.4	513	3	US-09-949-016-50542	Sequence 50542, A
170	11.4	81.4	81.4	25	US-09-366-196G-87491	Sequence 87491, A	C 243	11.4	81.4	513	3	US-09-949-016-50542	Sequence 50542, A

C 244	11.4	81.4	633	3	US-09-322-409-77	Sequence 77, Appl	C 317	11.4	81.4	1105	3	US-10-023-888-15	Sequence 15, Appl
C 245	11.4	81.4	633	3	US-09-322-409-79	Sequence 79, Appl	C 318	11.4	81.4	1107	3	US-09-614-921A-398	Sequence 398, Appl
C 246	11.4	81.4	633	3	US-09-451-527-77	Sequence 77, Appl	C 319	11.4	81.4	1113	3	US-09-252-921A-142	Sequence 342, Appl
C 247	11.4	81.4	633	3	US-09-451-527-79	Sequence 79, Appl	C 320	11.4	81.4	1123	3	US-09-502-540-9255	Sequence 9255, Appl
C 248	11.4	81.4	671	3	US-09-533-559-6036	Sequence 6036, Ap	C 321	11.4	81.4	1128	3	US-09-710-279-2171	Sequence 2171, Ap
C 249	11.4	81.4	709	3	US-09-270-767-10032	Sequence 10032, A	C 322	11.4	81.4	1150	3	US-09-931-401B-1	Sequence 1, Appl
C 250	11.4	81.4	717	3	US-09-252-991A-352	Sequence 352, Ap	C 323	11.4	81.4	1159	3	US-09-891-735-1	Sequence 1, Appl
C 251	11.4	81.4	726	3	US-09-338-352-3033	Sequence 3033, Ap	C 324	11.4	81.4	1169	3	US-09-270-767-14840	Sequence 14840, A
C 252	11.4	81.4	725	3	US-09-270-767-13913	Sequence 13913, A	C 325	11.4	81.4	1170	3	US-08-988-111-1	Sequence 1, Appl
C 253	11.4	81.4	762	3	US-09-543-681A-1624	Sequence 1624, Ap	C 326	11.4	81.4	1170	3	US-09-387-922-1	Sequence 1, Appl
C 254	11.4	81.4	766	3	US-09-270-767-1140	Sequence 1140, Ap	C 327	11.4	81.4	1177	3	US-09-949-016-1681	Sequence 1681, Ap
C 255	11.4	81.4	766	3	US-09-270-767-16422	Sequence 16422, A	C 328	11.4	81.4	1182	3	US-10-232-855-100	Sequence 100, Appl
C 256	11.4	81.4	777	3	US-09-252-991A-313	Sequence 313, A	C 329	11.4	81.4	1182	3	US-09-338-063A-100	Sequence 100, Appl
C 257	11.4	81.4	780	3	US-09-322-409-75	Sequence 75, Appl	C 330	11.4	81.4	1195	3	US-09-549-831-9	Sequence 9, Appl
C 258	11.4	81.4	780	3	US-09-322-409-76	Sequence 76, Appl	C 331	11.4	81.4	1200	3	US-10-232-856-94	Sequence 94, Appl
C 259	11.4	81.4	780	3	US-09-451-527-75	Sequence 76, Appl	C 332	11.4	81.4	1200	3	US-09-338-063A-94	Sequence 94, Appl
C 260	11.4	81.4	780	3	US-09-451-527-76	Sequence 76, Appl	C 333	11.4	81.4	1206	3	US-10-232-855-6	Sequence 6, Appl
C 261	11.4	81.4	788	3	US-09-142-623-10	Sequence 10, Appl	C 334	11.4	81.4	1206	3	US-10-232-855-83	Sequence 83, Appl
C 262	11.4	81.4	819	3	US-10-232-858-96	Sequence 96, Appl	C 335	11.4	81.4	1206	3	US-10-232-855-84	Sequence 84, Appl
C 263	11.4	81.4	819	3	US-09-338-063A-96	Sequence 96, Appl	C 336	11.4	81.4	1206	3	US-10-232-855-85	Sequence 85, Appl
C 264	11.4	81.4	849	3	US-09-252-991A-1357	Sequence 1357, Ap	C 337	11.4	81.4	1206	3	US-10-232-856-86	Sequence 86, Appl
C 265	11.4	81.4	861	3	US-09-489-039A-474	Sequence 474, Appl	C 338	11.4	81.4	1206	3	US-10-232-856-87	Sequence 87, Appl
C 266	11.4	81.4	867	3	US-09-902-540-3225	Sequence 3225, Ap	C 339	11.4	81.4	1206	3	US-09-338-063A-87	Sequence 87, Appl
C 267	11.4	81.4	879	2	US-08-158-682A-1	Sequence 1, Appl1	C 340	11.4	81.4	1206	3	US-09-338-063A-83	Sequence 83, Appl
C 268	11.4	81.4	879	2	US-08-015-203-1	Sequence 1, Appl1	C 341	11.4	81.4	1206	3	US-09-338-063A-84	Sequence 84, Appl
C 269	11.4	81.4	879	2	US-09-252-991A-13591	Sequence 13591, A	C 342	11.4	81.4	1206	3	US-09-338-063A-85	Sequence 85, Appl
C 270	11.4	81.4	885	3	US-09-322-409-72	Sequence 72, Appl	C 343	11.4	81.4	1206	3	US-09-338-063A-86	Sequence 86, Appl
C 271	11.4	81.4	885	3	US-09-322-409-74	Sequence 74, Appl	C 344	11.4	81.4	1206	3	US-09-338-063A-87	Sequence 87, Appl
C 272	11.4	81.4	885	3	US-09-451-527-72	Sequence 72, Appl	C 345	11.4	81.4	1224	3	US-09-134-001C-1078	Sequence 1078, Ap
C 273	11.4	81.4	885	3	US-09-451-527-74	Sequence 74, Appl	C 346	11.4	81.4	1224	3	US-09-489-039A-753	Sequence 753, Appl
C 274	11.4	81.4	886	3	US-08-134-231C-31	Sequence 31, Appl	C 347	11.4	81.4	1251	3	US-09-107-532A-1897	Sequence 1897, Ap
C 275	11.4	81.4	886	3	US-08-728-160-31	Sequence 31, Appl	C 348	11.4	81.4	1275	3	US-09-489-039A-566	Sequence 566, Appl
C 276	11.4	81.4	933	3	US-09-252-991A-326	Sequence 326, Appl	C 349	11.4	81.4	1307	3	US-09-270-767-12361	Sequence 12361, A
C 277	11.4	81.4	940	2	US-09-533-559-1571	Sequence 1571, Ap	C 350	11.4	81.4	1341	2	US-07-627-535G-6	Sequence 6, Appl1
C 278	11.4	81.4	954	2	US-08-343-443B-106	Sequence 106, Appl	C 351	11.4	81.4	1355	3	US-08-974-022-5	Sequence 5, Appl1
C 279	11.4	81.4	966	3	US-10-232-858-101	Sequence 101, Appl	C 352	11.4	81.4	1355	3	US-08-795-447A-5	Sequence 5, Appl1
C 280	11.4	81.4	966	3	US-09-338-063A-101	Sequence 101, Appl	C 353	11.4	81.4	1355	3	US-08-795-447A-5	Sequence 5, Appl1
C 281	11.4	81.4	981	3	US-10-232-858-92	Sequence 92, Appl	C 354	11.4	81.4	1355	3	US-08-974-166-5	Sequence 5, Appl1
C 282	11.4	81.4	981	3	US-09-338-063A-92	Sequence 92, Appl	C 355	11.4	81.4	1355	3	US-08-795-447A-5	Sequence 5, Appl1
C 283	11.4	81.4	984	3	US-10-232-858-93	Sequence 93, Appl	C 356	11.4	81.4	1355	3	US-08-706-945D-127	Sequence 127, Appl
C 284	11.4	81.4	984	3	US-09-338-063A-93	Sequence 93, Appl	C 357	11.4	81.4	1355	3	US-08-577-788C-5	Sequence 5, Appl1
C 285	11.4	81.4	987	3	US-09-489-039A-6045	Sequence 6045, Ap	C 358	11.4	81.4	1355	3	US-09-064-832-1	Sequence 1, Appl1
C 286	11.4	81.4	996	3	US-09-919-039-114	Sequence 114, Appl	C 359	11.4	81.4	1359	3	US-09-489-039A-559	Sequence 559, Appl
C 287	11.4	81.4	1014	3	US-09-248-796A-3864	Sequence 3864, Ap	C 360	11.4	81.4	1362	3	US-09-533-555-5689	Sequence 5689, Ap
C 288	11.4	81.4	1017	3	US-09-469-039A-3501	Sequence 3501, Ap	C 361	11.4	81.4	1377	3	US-09-252-991A-4240	Sequence 4240, Ap
C 289	11.4	81.4	1023	3	US-09-543-681A-796	Sequence 796, Appl	C 362	11.4	81.4	1392	3	US-09-247-155-144	Sequence 144, Appl
C 290	11.4	81.4	1024	3	US-09-949-016-5707	Sequence 5707, Ap	C 363	11.4	81.4	1399	3	US-09-902-540-8223	Sequence 8223, Ap
C 291	11.4	81.4	1042	3	US-09-949-016-4802	Sequence 4802, Ap	C 364	11.4	81.4	1407	3	US-09-903-190-144	Sequence 144, Appl
C 292	11.4	81.4	1050	3	US-09-230-132-3	Sequence 3, Appl1	C 365	11.4	81.4	1407	3	US-09-248-796A-3305	Sequence 3305, Ap
C 293	11.4	81.4	1054	3	US-08-956-171E-556	Sequence 556, Appl	C 366	11.4	81.4	1416	3	US-09-949-016-1951	Sequence 1951, Ap
C 294	11.4	81.4	1054	3	US-08-781-986A-556	Sequence 556, Appl	C 367	11.4	81.4	1422	3	US-09-352-991A-333	Sequence 333, Appl
C 295	11.4	81.4	1056	3	US-10-232-858-95	Sequence 95, Appl	C 368	11.4	81.4	1443	2	US-08-673-312-1	Sequence 1, Appl1
C 296	11.4	81.4	1056	3	US-09-338-063A-95	Sequence 95, Appl	C 369	11.4	81.4	1443	3	US-09-802-937A-2	Sequence 2, Appl1
C 297	11.4	81.4	1071	3	US-09-270-767-1061	Sequence 1061, Ap	C 370	11.4	81.4	1446	3	US-08-787-091-1	Sequence 1, Appl1
C 298	11.4	81.4	1071	3	US-09-270-767-16343	Sequence 16343, A	C 371	11.4	81.4	1454	2	US-08-657-392-1	Sequence 1, Appl1
C 299	11.4	81.4	1080	3	US-10-232-858-91	Sequence 91, Appl	C 372	11.4	81.4	1454	2	PCT-US94-02559-1	Sequence 1, Appl1
C 300	11.4	81.4	1080	3	US-09-338-063A-91	Sequence 91, Appl	C 373	11.4	81.4	1455	2	US-08-657-392-26	Sequence 26, Appl
C 301	11.4	81.4	1083	3	US-09-549-831-12	Sequence 12, Appl	C 374	11.4	81.4	1455	6	PCT-US94-02559-26	Sequence 26, Appl
C 302	11.4	81.4	1083	3	US-09-902-540-8475	Sequence 8475, Ap	C 375	11.4	81.4	1476	3	US-09-902-540-6246	Sequence 6246, Ap
C 303	11.4	81.4	1083	3	US-10-232-858-88	Sequence 88, Appl	C 376	11.4	81.4	1480	3	US-09-902-540-342	Sequence 342, Appl
C 304	11.4	81.4	1083	3	US-09-338-063A-88	Sequence 88, Appl	C 377	11.4	81.4	1480	3	US-09-578-154-6	Sequence 6, Appl1
C 305	11.4	81.4	1088	3	US-10-232-858-10	Sequence 10, Appl	C 378	11.4	81.4	1481	3	US-09-235-153-4	Sequence 4, Appl1
C 306	11.4	81.4	1089	3	US-09-338-063A-10	Sequence 10, Appl	C 379	11.4	81.4	1481	3	US-09-270-767-7175	Sequence 7175, Ap
C 307	11.4	81.4	1092	3	US-10-232-858-90	Sequence 90, Appl	C 380	11.4	81.4	1484	3	US-09-770-767-22457	Sequence 22457, A
C 308	11.4	81.4	1092	3	US-09-338-063A-90	Sequence 90, Appl	C 381	11.4	81.4	1484	3	US-08-968-563-1	Sequence 1, Appl1
C 309	11.4	81.4	1105	3	US-09-635-872A-17	Sequence 17, Appl	C 382	11.4	81.4	1484	3	US-08-968-563A-1	Sequence 1, Appl1
C 310	11.4	81.4	1105	3	US-09-636-077A-17	Sequence 17, Appl	C 383	11.4	81.4	1484	3	US-09-307-973A-6	Sequence 6, Appl1
C 311	11.4	81.4	1105	3	US-09-636-060C-17	Sequence 17, Appl	C 384	11.4	81.4	1484	3	US-09-308-207-1	Sequence 1, Appl1
C 312	11.4	81.4	1105	3	US-09-986-552-17	Sequence 17, Appl	C 385	11.4	81.4	1484	3	US-09-489-039A-2187	Sequence 2187, Ap
C 313	11.4	81.4	1105	3	US-09-636-596C-17	Sequence 17, Appl	C 386	11.4	81.4	1484	3	US-09-252-991A-1400	Sequence 1400, Ap
C 314	11.4	81.4	1105	3	US-10-023-894-15	Sequence 15, Appl	C 387	11.4	81.4	1484	3	US-08-487-429A-3	Sequence 3, Appl1
C 315	11.4	81.4	1105	3	US-10-306-686-17	Sequence 17, Appl	C 388	11.4	81.4	1716	6	PCT-US96-05330A-441	Sequence 541, Appl
C 316	11.4	81.4	1105	3	US-09-895-072-17	Sequence 17, Appl	C 389	11.4	81.4	1718	2	US-08-675-153-3	Sequence 3, Appl1

C 390	11.4	81.4	1718	2	US-08-841-252-3	Sequence 3, Appl1	463	11.4	81.4	3090	3	US-09-653-730-14	Sequence 14, Appl1
C 391	11.4	81.4	1718	2	US-08-881-571-3	Sequence 3, Appl1	464	11.4	81.4	3102	3	US-09-252-991A-440	Sequence 14, Appl1
C 392	11.4	81.4	1718	3	US-09-282-054-3	Sequence 3, Appl1	465	11.4	81.4	3105	3	US-08-542-635-1	Sequence 1, Appl1
C 393	11.4	81.4	1718	3	US-09-665-638-3	Sequence 3, Appl1	466	11.4	81.4	3108	3	US-09-710-279-3347	Sequence 3427, Ap
C 394	11.4	81.4	1737	3	US-09-252-991A-1205	Sequence 1205, Ap	467	11.4	81.4	3223	3	US-09-902-540-6416	Sequence 6416, Ap
C 395	11.4	81.4	1740	3	US-10-328-226A-16	Sequence 16, Appl	468	11.4	81.4	3275	3	US-09-902-540-435	Sequence 436, App
C 396	11.4	81.4	1794	3	US-09-012-515A-13	Sequence 13, Appl	469	11.4	81.4	3334	3	US-09-991-181-288	Sequence 288, App
C 397	11.4	81.4	1794	3	US-08-560-144A-13	Sequence 13, Appl	470	11.4	81.4	3334	3	US-09-990-444-288	Sequence 288, App
C 398	11.4	81.4	1794	3	US-09-012-504A-13	Sequence 13, Appl	471	11.4	81.4	3334	3	US-09-997-533-288	Sequence 288, App
C 399	11.4	81.4	1794	3	US-09-012-399A-13	Sequence 13, Appl	472	11.4	81.4	3334	3	US-09-992-598-288	Sequence 288, App
C 400	11.4	81.4	1794	6	PCT-US95-06722-13	Sequence 6, Appl	473	11.4	81.4	3389	3	US-10-104-047-842	Sequence 842, Appl
C 401	11.4	81.4	1815	2	US-08-606-288-6	Sequence 6, Appl	474	11.4	81.4	3411	3	US-09-002-285-77	Sequence 77, Appl
C 402	11.4	81.4	1815	3	US-09-347-483-6	Sequence 6, Appl1	475	11.4	81.4	3411	3	US-09-589-477-77	Sequence 77, Appl
C 403	11.4	81.4	1821	3	US-09-248-796A-173	Sequence 173, App	476	11.4	81.4	3411	3	US-10-099-285A-77	Sequence 77, Appl
C 404	11.4	81.4	1825	3	US-09-919-039-115	Sequence 115, App	C 477	11.4	81.4	3445	3	US-09-949-016-2556	Sequence 2556, Ap
C 405	11.4	81.4	1867	2	US-08-675-153-6	Sequence 6, Appl1	478	11.4	81.4	3468	3	US-09-001-982-9	Sequence 9, Appl1
C 406	11.4	81.4	1867	2	US-08-841-252-6	Sequence 6, Appl1	479	11.4	81.4	3468	3	US-09-668-650-9	Sequence 9, Appl1
C 407	11.4	81.4	1867	2	US-08-881-571-6	Sequence 6, Appl1	480	11.4	81.4	3471	3	US-09-002-285-71	Sequence 71, Appl
C 408	11.4	81.4	1867	3	US-09-282-054-6	Sequence 6, Appl1	481	11.4	81.4	3471	3	US-09-589-477-71	Sequence 71, Appl
C 409	11.4	81.4	1867	3	US-09-665-638-6	Sequence 6, Appl1	482	11.4	81.4	3471	3	US-10-099-285A-71	Sequence 71, Appl
C 410	11.4	81.4	1872	3	US-09-252-991A-4634	Sequence 4634, Ap	483	11.4	81.4	3567	2	US-07-828-788A-15	Sequence 15, Appl1
C 411	11.4	81.4	1896	3	US-09-732-615-7	Sequence 7, Appl1	484	11.4	81.4	3567	2	US-08-356-034-5	Sequence 5, Appl1
C 412	11.4	81.4	1896	3	US-10-273-051-7	Sequence 7, Appl1	485	11.4	81.4	3567	2	US-08-602-737-1	Sequence 1, Appl1
C 413	11.4	81.4	1905	3	US-09-142-623-2	Sequence 2, Appl1	486	11.4	81.4	3567	2	US-08-980-071-1	Sequence 1, Appl1
C 414	11.4	81.4	1907	3	US-08-771-986A-1	Sequence 1, Appl1	487	11.4	81.4	3567	2	US-08-980-071-3	Sequence 3, Appl1
C 415	11.4	81.4	1907	3	US-08-771-986A-3	Sequence 3, Appl1	488	11.4	81.4	3567	2	US-08-980-071-5	Sequence 5, Appl1
C 416	11.4	81.4	1907	3	US-08-769-802A-1	Sequence 1, Appl1	489	11.4	81.4	3567	2	US-08-980-071-7	Sequence 7, Appl1
C 417	11.4	81.4	1933	2									

536	11.4	81.4	3567	3	US-09-337-280-58	Sequence 58, Appl	609	11.4	81.4	5763	3	US-08-956-171E-505	Sequence 505, App
537	11.4	81.4	3567	3	US-09-337-280-60	Sequence 60, Appl	610	11.4	81.4	5763	3	US-08-781-986A-505	Sequence 505, App
538	11.4	81.4	3567	3	US-09-521-344-5	Sequence 5, Appl1	611	11.4	81.4	6091	3	US-09-221-017B-603	Sequence 803, App
539	11.4	81.4	3567	3	US-09-837-261A-5	Sequence 5, Appl1	612	11.4	81.4	6394	3	US-09-949-016-14380	Sequence 14380, A
540	11.4	81.4	3567	3	US-09-668-650-1	Sequence 1, Appl1	613	11.4	81.4	6676	3	US-09-252-991A-5283	Sequence 5283, Ap
541	11.4	81.4	3567	3	US-09-972-175-1	Sequence 1, Appl1	614	11.4	81.4	7513	3	US-09-902-540-892	Sequence 892, App
542	11.4	81.4	3567	3	US-09-972-175-5	Sequence 3, Appl1	615	11.4	81.4	9035	3	US-09-902-540-1084	Sequence 1084, Ap
543	11.4	81.4	3567	3	US-09-972-175-5	Sequence 5, Appl1	616	11.4	81.4	9454	3	US-09-949-016-12398	Sequence 12398, A
544	11.4	81.4	3567	3	US-09-972-175-7	Sequence 7, Appl1	617	11.4	81.4	9455	3	US-09-949-016-14650	Sequence 14650, A
545	11.4	81.4	3567	3	US-09-972-175-9	Sequence 9, Appl1	618	11.4	81.4	10190	3	US-10-232-885-105	Sequence 105, App
546	11.4	81.4	3567	3	US-09-972-175-11	Sequence 11, Appl1	619	11.4	81.4	10190	3	US-09-338-063A-105	Sequence 105, App
547	11.4	81.4	3567	3	US-09-972-175-58	Sequence 58, Appl1	620	11.4	81.4	10322	3	US-09-902-540-989	Sequence 989, App
548	11.4	81.4	3567	3	US-09-972-175-60	Sequence 60, Appl1	621	11.4	81.4	10480	3	US-09-732-615-13	Sequence 13, Appl
549	11.4	81.4	3567	3	US-10-200-522-1	Sequence 1, Appl1	622	11.4	81.4	10480	3	US-10-273-051-13	Sequence 13, Appl
550	11.4	81.4	3567	3	US-10-200-522-3	Sequence 3, Appl1	623	11.4	81.4	11268	3	US-09-434-840-5	Sequence 5, Appl1
551	11.4	81.4	3567	3	US-10-200-522-5	Sequence 5, Appl1	624	11.4	81.4	11271	3	US-08-956-171E-11	Sequence 11, Appl1
552	11.4	81.4	3567	3	US-10-200-522-7	Sequence 7, Appl1	625	11.4	81.4	11271	3	US-08-781-986A-11	Sequence 11, Appl1
553	11.4	81.4	3567	3	US-10-200-522-9	Sequence 9, Appl1	626	11.4	81.4	12145	3	US-08-968-563-19	Sequence 19, Appl1
554	11.4	81.4	3567	3	US-10-200-522-11	Sequence 11, Appl1	627	11.4	81.4	12145	3	US-08-969-689A-19	Sequence 19, Appl1
555	11.4	81.4	3567	3	US-10-200-522-58	Sequence 58, Appl1	628	11.4	81.4	12145	3	US-09-369-796-1	Sequence 1, Appl1
556	11.4	81.4	3567	3	US-10-200-522-60	Sequence 60, Appl1	629	11.4	81.4	12145	3	US-09-307-972A-10	Sequence 10, Appl1
557	11.4	81.4	3567	6	US-10-200-522-60	Sequence 15, Appl1	630	11.4	81.4	12145	3	US-09-641-652-1	Sequence 1, Appl1
558	11.4	81.4	3567	6	PCT-US92-11337-15	Sequence 15, Appl1	631	11.4	81.4	12145	3	US-09-641-652-1	Sequence 1, Appl1
559	11.4	81.4	3567	2	US-10-328-226A-17	Sequence 17, Appl1	632	11.4	81.4	12666	3	US-08-961-527-137	Sequence 137, App
560	11.4	81.4	3579	2	US-08-602-737-7	Sequence 7, Appl1	633	11.4	81.4	12695	3	US-09-949-016-16775	Sequence 16775, A
561	11.4	81.4	3579	3	US-08-754-490-29	Sequence 29, Appl1	634	11.4	81.4	13543	3	US-10-127-862-1	Sequence 1, Appl1
562	11.4	81.4	3579	3	US-08-922-505A-29	Sequence 29, Appl1	635	11.4	81.4	14330	3	US-09-949-016-14949	Sequence 14949, A
563	11.4	81.4	3579	3	US-09-001-982-7	Sequence 7, Appl1	636	11.4	81.4	15338	3	US-09-902-540-1121	Sequence 1121, Ap
564	11.4	81.4	3579	3	US-09-260-952A-29	Sequence 29, Appl1	637	11.4	81.4	15482	3	US-09-902-540-1067	Sequence 1067, Ap
565	11.4	81.4	3579	3	US-09-253-341-29	Sequence 29, Appl1	638	11.4	81.4	15483	3	US-09-949-016-17225	Sequence 17225, A
566	11.4	81.4	3579	3	US-09-253-331A-29	Sequence 29, Appl1	639	11.4	81.4	15689	3	US-09-902-540-1129	Sequence 1129, Ap
567	11.4	81.4	3579	3	US-09-251-040-29	Sequence 29, Appl1	640	11.4	81.4	17654	3	US-09-902-540-1161	Sequence 1161, Ap
568	11.4	81.4	3579	3	US-09-916-956A-29	Sequence 29, Appl1	641	11.4	81.4	17726	3	US-09-902-540-118	Sequence 118, Ap
569	11.4	81.4	3579	3	US-09-873-873-29	Sequence 29, Appl1	642	11.4	81.4	19637	3	US-09-949-016-16544	Sequence 16544, A
570	11.4	81.4	3579	3	US-09-997-914-29	Sequence 29, Appl1	643	11.4	81.4	21177	3	US-09-949-016-15479	Sequence 15479, A
571	11.4	81.4	3579	3	US-09-636-746B-29	Sequence 29, Appl1	644	11.4	81.4	21180	3	US-09-949-016-12395	Sequence 12395, A
572	11.4	81.4	3579	3	US-10-365-645-29	Sequence 29, Appl1	645	11.4	81.4	21180	3	US-09-949-016-12894	Sequence 12894, A
573	11.4	81.4	3579	3	US-09-668-650-7	Sequence 7, Appl1	646	11.4	81.4	23257	3	US-09-949-016-14300	Sequence 14300, A
574	11.4	81.4	3579	3	US-10-817-182-29	Sequence 29, Appl1	647	11.4	81.4	23257	3	US-09-949-016-14300	Sequence 14300, A
575	11.4	81.4	3579	3	US-10-672-163-39	Sequence 39, Appl1	648	11.4	81.4	24459	3	US-09-902-540-5004	Sequence 5004, Ap
576	11.4	81.4	3588	3	US-09-566-921-23	Sequence 23, Appl1	649	11.4	81.4	26050	3	US-09-949-016-17449	Sequence 17449, A
577	11.4	81.4	3722	3	US-09-221-017B-784	Sequence 784, App	650	11.4	81.4	29272	3	US-09-902-540-1217	Sequence 1217, Ap
578	11.4	81.4	3808	3	US-10-104-047-367	Sequence 367, App	651	11.4	81.4	30062	3	US-09-949-016-15866	Sequence 15866, A
579	11.4	81.4	3810	3	US-09-902-540-8379	Sequence 8379, App	652	11.4	81.4	31063	3	US-09-596-002-719	Sequence 719, App
580	11.4	81.4	3813	3	US-09-902-540-1085	Sequence 7085, App	653	11.4	81.4	32241	3	US-09-902-540-1247	Sequence 1247, Ap
581	11.4	81.4	3923	2	US-09-902-540-634	Sequence 634, App	654	11.4	81.4	33529	3	US-09-949-016-12865	Sequence 12865, A
582	11.4	81.4	3923	2	US-08-465-609-4	Sequence 4, Appl1	655	11.4	81.4	33529	3	US-09-949-016-17364	Sequence 17364, A
583	11.4	81.4	3923	3	US-09-176-320-7	Sequence 7, Appl1	656	11.4	81.4	35081	2	US-08-752-760A-1	Sequence 1, Appl1
584	11.4	81.4	3923	3	US-09-661-016-7	Sequence 7, Appl1	657	11.4	81.4	35100	3	US-08-923-137-1	Sequence 26, Appl1
585	11.4	81.4	4170	2	US-08-619-198-4	Sequence 4, Appl1	658	11.4	81.4	35254	3	US-08-923-137-1	Sequence 1, Appl1
586	11.4	81.4	4200	3	US-09-949-016-1124	Sequence 4124, Ap	659	11.4	81.4	36851	3	US-09-949-016-14674	Sequence 14674, A
587	11.4	81.4	4259	3	US-09-155-183-12	Sequence 12, Appl1	660	11.4	81.4	40465	3	US-09-949-016-12651	Sequence 12651, A
588	11.4	81.4	4259	3	US-09-733-383-12	Sequence 12, Appl1	661	11.4	81.4	43804	3	US-09-171-461-1	Sequence 1, Appl1
589	11.4	81.4	4269	3	US-09-540-336-1101	Sequence 1101, Ap	662	11.4	81.4	43804	3	US-09-970-711-1	Sequence 719, App
590	11.4	81.4	4284	2	US-09-252-991A-4006	Sequence 4006, Ap	663	11.4	81.4	45432	3	US-09-949-016-1719	Sequence 16539, A
591	11.4	81.4	4338	2	US-08-015-986A-1	Sequence 1, Appl1	664	11.4	81.4	45436	3	US-09-949-016-16539	Sequence 16518, A
592	11.4	81.4	4338	2	US-08-446-363-1	Sequence 1, Appl1	665	11.4	81.4	52496	3	US-09-949-016-16118	Sequence 16118, A
593	11.4	81.4	4354	3	US-09-802-937A-1	Sequence 1, Appl1	666	11.4	81.4	52496	3	US-09-949-016-16119	Sequence 16119, A
594	11.4	81.4	4359	3	US-09-328-352-1037	Sequence 1037, Ap	667	11.4	81.4	53260	3	US-09-949-016-1498	Sequence 14298, A
595	11.4	81.4	4704	3	US-09-252-991A-3906	Sequence 3906, Ap	668	11.4	81.4	55216	3	US-09-716-865-23	Sequence 23, Appl1
596	11.4	81.4	4788	3	US-09-584-586-7	Sequence 7, Appl1	669	11.4	81.4	59140	3	US-09-949-016-16623	Sequence 16023, A
597	11.4	81.4	4810	3	US-09-596-824-5	Sequence 5, Appl1	670	11.4	81.4	63760	3	US-09-949-016-14087	Sequence 14087, A
598	11.4	81.4	4810	3	US-09-885-329-5	Sequence 5, Appl1	671	11.4	81.4	63760	3	US-09-949-016-14088	Sequence 14088, A
599	11.4	81.4	5192	2	US-09-252-991A-5192	Sequence 5192, Ap	672	11.4	81.4	63760	3	US-09-949-016-13576	Sequence 13576, A
600	11.4	81.4	5192	2	US-08-619-198-8	Sequence 8, Appl1	673	11.4	81.4	67755	3	US-09-949-016-13703	Sequence 13703, A
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602	11.4	81.4	5268	3	US-09-830-751-9	Sequence 9, Appl1	675	11.4	81.4	84571	3	US-09-949-016-17420	Sequence 17420, A
603	11.4	81.4	5280	3	US-09-902-540-770	Sequence 770, App	676	11.4	81.4	99639	3	US-09-596-002-37	Sequence 37, Appl1
604	11.4	81.4	5391	3	US-08-811-519-2	Sequence 2, Appl1	677	11.4	81.4	125188	3	US-09-949-016-11380	Sequence 11380, A
605	11.4	81.4	5518	3	US-09-902-540-849	Sequence 849, App	678	11.4	81.4	133368	3	US-09-949-016-16564	Sequence 16564, A
606	11.4	81.4	5519	3	US-08-737-607-1	Sequence 1, Appl1	679	11.4	81.4	133368	3	US-09-949-016-12651	Sequence 12651, A
607	11.4	81.4	5610	3	US-09-262-537-57	Sequence 57, Appl1	680	11.4	81.4	134008	3	US-09-949-016-13841	Sequence 13841, A
608	11.4	81.4	5693	3	US-09-262-537-19	Sequence 19, Appl1	681	11.4	81.4	152582	3	US-09-949-016-12086	Sequence 12086, A

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C 684	11.4	81.4	174493	3	US-09-804-471A-3	Sequence 3, App1	C 757	11	78.6	301	3	US-09-679-426-281	Sequence 281, App
C 685	11.4	81.4	174493	3	US-10-238-709-3	Sequence 3, App1	C 758	11	78.6	301	3	US-09-759-143-281	Sequence 281, App
C 686	11.4	81.4	174493	3	US-10-724-594-3	Sequence 3, App1	C 759	11	78.6	301	3	US-09-651-236-281	Sequence 281, App
C 687	11.4	81.4	175236	3	US-09-949-016-14353	Sequence 14353, A	C 760	11	78.6	301	3	US-09-657-279-281	Sequence 281, App
C 688	11.4	81.4	187580	3	US-09-949-016-13266	Sequence 13266, A	C 761	11	78.6	301	3	US-10-012-896-281	Sequence 281, App
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C 691	11.4	81.4	198942	3	US-09-949-016-13209	Sequence 13209, A	C 764	11	78.6	302	3	US-09-966-608-1	Sequence 1, App1
C 692	11.4	81.4	200663	3	US-09-949-016-12559	Sequence 12559, A	C 765	11	78.6	306	3	US-09-252-991A-7727	Sequence 7727, App
C 693	11.4	81.4	203093	3	US-09-949-016-14445	Sequence 14445, A	C 766	11	78.6	319	3	US-09-513-999C-1442	Sequence 1442, App
C 694	11.4	81.4	227750	3	US-09-949-016-17175	Sequence 17175, A	C 767	11	78.6	324	3	US-09-489-039A-3825	Sequence 5825, App
C 695	11.4	81.4	245286	3	US-09-949-016-15497	Sequence 15497, A	C 768	11	78.6	326	3	US-09-489-039A-3825	Sequence 5825, App
C 696	11.4	81.4	246240	2	US-08-724-394A-20	Sequence 20, App1	C 769	11	78.6	336	3	US-09-270-767-72544	Sequence 72544, App
C 697	11.4	81.4	246240	2	US-08-724-394A-21	Sequence 21, App1	C 770	11	78.6	348	3	US-09-513-999C-1770	Sequence 1770, App
C 698	11.4	81.4	246240	2	US-08-724-394A-22	Sequence 22, App1	C 771	11	78.6	370	3	US-09-640-211A-1783	Sequence 1783, App
C 699	11.4	81.4	255679	3	US-09-949-016-17189	Sequence 17189, A	C 772	11	78.6	389	3	US-08-956-172E-4242	Sequence 4242, App
C 700	11.4	81.4	276687	3	US-09-949-016-13840	Sequence 13840, A	C 773	11	78.6	389	3	US-08-781-986A-4242	Sequence 4242, App
C 701	11.4	81.4	312474	3	US-09-949-016-17434	Sequence 17434, A	C 774	11	78.6	396	3	US-09-328-352-680	Sequence 680, App
C 702	11.4	81.4	312957	3	US-09-949-001-31	Sequence 31, App1	C 775	11	78.6	399	3	US-09-107-532A-936	Sequence 936, App
C 703	11.4	81.4	312957	3	US-09-949-001-34	Sequence 34, App1	C 776	11	78.6	404	3	US-09-270-767-30960	Sequence 30960, A
C 704	11.4	81.4	331814	3	US-09-949-016-12008	Sequence 12008, A	C 777	11	78.6	420	2	US-08-528-057-4	Sequence 4, App1
C 705	11.4	81.4	331814	3	US-09-949-016-17056	Sequence 17056, A	C 778	11	78.6	425	3	US-08-956-172E-3792	Sequence 3792, App
C 706	11.4	81.4	536165	3	US-09-214-808-1	Sequence 1, App1	C 779	11	78.6	425	3	US-08-781-986A-3792	Sequence 3792, App
C 707	11.4	81.4	636591	3	US-09-949-016-11808	Sequence 11808, A	C 780	11	78.6	432	3	US-09-513-999C-87	Sequence 87, App1
C 708	11.4	81.4	636591	3	US-09-949-016-13388	Sequence 13388, A	C 781	11	78.6	433	3	US-08-956-172E-3850	Sequence 3850, App
C 709	11.4	81.4	640681	3	US-09-790-988-1	Sequence 1, App1	C 782	11	78.6	433	3	US-08-781-986A-3850	Sequence 3850, App
C 710	11.4	81.4	1230025	3	US-09-198-452A-1	Sequence 1, App1	C 783	11	78.6	468	3	US-09-712-363-9	Sequence 9, App1
C 711	11.4	81.4	1230230	3	US-09-438-185A-1	Sequence 1, App1	C 784	11	78.6	473	3	US-09-621-976-2359	Sequence 2359, App
C 712	11.4	81.4	1830121	3	US-09-557-884-1	Sequence 1, App1	C 785	11	78.6	474	3	US-09-252-991A-1794	Sequence 1794, App
C 713	11.4	81.4	1830121	3	US-09-557-884-1	Sequence 1, App1	C 786	11	78.6	501	3	US-09-270-767-9764	Sequence 9764, App
C 714	11.4	81.4	1830121	3	US-09-643-990A-1	Sequence 1, App1	C 787	11	78.6	501	3	US-09-270-767-25046	Sequence 25046, App
C 715	11.4	81.4	1830121	3	US-09-643-990A-1	Sequence 1, App1	C 788	11	78.6	510	3	US-09-252-991A-8655	Sequence 8655, App
C 716	11.4	81.4	1830121	3	US-10-158-865-1	Sequence 1, App1	C 789	11	78.6	513	3	US-09-270-767-9282	Sequence 9282, App
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ALIGNMENTS

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RESULT 1
US-09-949-016-147054/c
; Sequence 147054, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 147054
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-147054
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Best Local Similarity 76.9%; Pred. No. 3.7e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
US-09-801-042-1/c
; Sequence 1, Application US/09801042
; Patent No. 6630332
; GENERAL INFORMATION:
; APPLICANT: RIERING, MECHTHILD
; APPLICANT: THIERBACH, GEORG
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; APPLICANT: VAN DER REST, MICHEL EDUARD
; APPLICANT: MOLENAAR, DOUWE
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE
; FILE REFERENCE: MAS/21133/800410
; CURRENT APPLICATION NUMBER: US/09/801,042
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/229,329
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: DE 100 34 833.5
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: DE 101 03874.7
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 12
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; TYPE: DNA
; ORGANISM: Escherichia coli
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; LOCATION: (7)..(1593)
; OTHER INFORMATION: mqo gene
US-09-801-042-1
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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16941
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; ORGANISM: Human
US-09-949-016-16941
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Best Local Similarity 76.9%; Pred. No. 5.9e+02;
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; Sequence 15868, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
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;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: C0001307
;; CURRENT APPLICATION NUMBER: US/09/949, 016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
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;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-15868

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Best Local Similarity 76.9%; Pred. No. 7.7e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
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;; Sequence 27123, Application US/09270767
;; Patent No. 6703491
;; GENERAL INFORMATION:
;; APPLICANT: Homburger et al.
;; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;; FILE REFERENCE: File Reference: 7326-094
;; CURRENT APPLICATION NUMBER: US/09/270,767
;; CURRENT FILING DATE: 1998-03-17
;; NUMBER OF SEQ ID NOS: 62517
;; SOFTWARE: PatentIn Ver. 2.0
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;; LENGTH: 140
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US-09-270-767-27123

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Best Local Similarity 71.4%; Pred. No. 7.1e+02;
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Db 19 CGTACTGCACTAG 32

RESULT 6
US-09-513-999C-2299/c
;; Sequence 2299, Application US/09513999C
;; Patent No. 6783961
;; GENERAL INFORMATION:
;; APPLICANT: Dumas Mline Edwards, J.B.
;; APPLICANT: Duclert, A.Y.
;; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
;; Patent No. 6783961
;; FILE REFERENCE: 59, US2, REG
;; CURRENT APPLICATION NUMBER: US/09/513,999C
;; CURRENT FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/122,487
;; PRIOR FILING DATE: 1999-02-26
;; NUMBER OF SEQ ID NOS: 36681
;; SOFTWARE: Patent.pm
;; SEQ ID NO 2299

;; LENGTH: 323
;; TYPE: DNA
;; ORGANISM: Homo sapiens
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;; LOCATION: 23..322
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;; NAME/KEY: misc_feature
;; LOCATION: 9
;; OTHER INFORMATION: m=a or c
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 246
;; OTHER INFORMATION: r=a or g
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 247
;; OTHER INFORMATION: r=a or g
;; FEATURE:
;; NAME/KEY: UNSURE
;; LOCATION: 75
;; OTHER INFORMATION: Xaa=Glu or Gly
US-09-513-999C-2299

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Best Local Similarity 71.4%; Pred. No. 7.9e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Db 44 CGTACTGCACTCG 31

RESULT 7
US-08-303-861-15
;; Sequence 15, Application US/08303861
;; Patent No. 6086902
;; GENERAL INFORMATION:
;; APPLICANT: ZAMB, TIMOTHY
;; APPLICANT: LIANG, XIAOPING
;; APPLICANT: BABIUK, LORNE A.
;; TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE I
;; TITLE OF INVENTION: VACCINES
;; NUMBER OF SEQUENCES: 21
;; CORRESPONDENCE ADDRESS:
;; ADDRESSER: MORRISON & FORSTER
;; STREET: 755 Page Mill Road
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94304-1018
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/303,861
;; FILING DATE: 09-SEP-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: PARK, FREDERICK K.
;; REGISTRATION NUMBER: 35,636
;; REFERENCE/DOCKET NUMBER: 29310-20020.20
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 813-5600
;; TELEFAX: (415) 494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 349 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single

TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 157..348
US-08-303-861-15

Query Match 88.6%; Score 12.4; DB 3; Length 349;
Best Local Similarity 78.6%; Pred. No. 8e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14
Db 332 CGTACTGCAACACG 345

RESULT 8
US-09-621-976-681/C
Sequence 681, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Mline Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSER.054PR2
CURRENT FILING DATE: US/09/621.976
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 681
LENGTH: 399
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 13..399
US-09-621-976-681

Query Match 88.6%; Score 12.4; DB 3; Length 399;
Best Local Similarity 71.4%; Pred. No. 8.1e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14
Db 34 CGTACTGCAACTCG 21

RESULT 9
US-09-252-991A-79/C
Sequence 79, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: US/09/252.991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 79
LENGTH: 435
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-79

Query Match 88.6%; Score 12.4; DB 3; Length 435;
Best Local Similarity 78.6%; Pred. No. 8.2e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14
Db 378 CGAAGTCGCACTCG 365

RESULT 10
US-09-252-991A-1326/C
Sequence 1326, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: US/09/252.991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 1326
LENGTH: 504
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1326

Query Match 88.6%; Score 12.4; DB 3; Length 504;
Best Local Similarity 71.4%; Pred. No. 8.4e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14
Db 213 CGTACTGCACTCG 200

RESULT 11
US-09-252-991A-233/C
Sequence 233, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: US/09/252.991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 233
LENGTH: 543
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-233

Query Match 88.6%; Score 12.4; DB 3; Length 543;
Best Local Similarity 71.4%; Pred. No. 8.5e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14
Db 180 CGTACTGCAATTCG 167

RESULT 12
US-09-252-991A-7705
Sequence 7705, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7705
; LENGTH: 543
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7705

Query Match 88.6%; Score 12.4; DB 3; Length 543;
Best Local Similarity 71.4%; Pred. No. 8.5e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCACTCG 14
||:|||||:
Db 151 CGTCTGCACTCG 164

RESULT 13
US-09-270-767-5447/c
; Sequence 5447, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-084
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5447
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-5447

Query Match 88.6%; Score 12.4; DB 3; Length 597;
Best Local Similarity 71.4%; Pred. No. 8.6e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCACTCG 14
||:|||||:
Db 357 CGTCTGCACTCG 344

RESULT 14
US-09-270-767-20729/c
; Sequence 20729, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 20729
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-20729

Query Match 88.6%; Score 12.4; DB 3; Length 597;
Best Local Similarity 71.4%; Pred. No. 8.6e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCACTCG 14
||:|||||:
Db 357 CGTCTGCACTCG 344

RESULT 15
US-09-252-991A-100
; Sequence 100, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 100
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-100

Query Match 88.6%; Score 12.4; DB 3; Length 669;
Best Local Similarity 78.6%; Pred. No. 8.7e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCACTCG 14
||:|||||:
Db 285 CGAATGCACTCG 298

RESULT 16
US-09-252-991A-9718/c
; Sequence 9718, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9718
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9718

Query Match 88.6%; Score 12.4; DB 3; Length 696;
Best Local Similarity 78.6%; Pred. No. 8.7e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCACTCG 14
||:|||||:
Db 682 CGAATGCACTCG 669

RESULT 17
US-09-252-991A-14097/c
; Sequence 14097, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 14097
LENGTH: 726
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14097

Query Match 88.6%; Score 12.4; DB 3; Length 726;
Best Local Similarity 71.4%; Pred. No. 8.8e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCACTCG 14
||:|||||:|
Db 524 CCGACTGCACTCG 511

RESULT 18
US-09-270-767-11527
Sequence 11527, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11527
LENGTH: 737
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-11527

Query Match 88.6%; Score 12.4; DB 3; Length 737;
Best Local Similarity 71.4%; Pred. No. 8.8e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCACTCG 14
||:|||||:|
Db 616 CCGACTGCACTCG 629

RESULT 19
US-09-252-991A-94
Sequence 94, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 94
LENGTH: 756
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-94

Query Match 88.6%; Score 12.4; DB 3; Length 756;
Best Local Similarity 78.6%; Pred. No. 8.8e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCACTCG 14
||:|||||:|
Db 199 CGAATGCACTCG 212

RESULT 20
US-09-252-991A-6447/c
Sequence 6447, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6447
LENGTH: 834
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6447

Query Match 88.6%; Score 12.4; DB 3; Length 834;
Best Local Similarity 78.6%; Pred. No. 8.9e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCACTCG 14
||:|||||:|
Db 307 CCGACTGCACTCG 294

RESULT 21
US-09-902-540-5805
Sequence 5805, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 2001-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 5805
LENGTH: 867
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-5805

Query Match 88.6%; Score 12.4; DB 3; Length 867;
Best Local Similarity 78.6%; Pred. No. 9e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCACTCG 14
||:|||||:|
Db 702 CCGACTGCACTCG 715

RESULT 22
US-09-252-991A-6103
; Sequence 6103, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6103
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6103

Query Match 88.6%; Score 12.4; DB 3; Length 930;
Best Local Similarity 78.6%; Pred. No. 9.1e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUG 14
||:|||||:
Db 417 CGTACTGCACACCG 430

RESULT 23
US-09-902-540-7341
; Sequence 7341, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(115849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 7341
; LENGTH: 1005
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-7341

Query Match 88.6%; Score 12.4; DB 3; Length 1005;
Best Local Similarity 71.4%; Pred. No. 9.1e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUG 14
||:|||||:
Db 612 CGTCTGCACACTCG 625

RESULT 24
US-09-902-540-70
; Sequence 70, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(115849)B

CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 70
LENGTH: 1007
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-70

Query Match 88.6%; Score 12.4; DB 3; Length 1007;
Best Local Similarity 71.4%; Pred. No. 9.1e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUG 14
||:|||||:
Db 614 CGTCTGCACACTCG 627

RESULT 25
US-09-107-532A-2165
; Sequence 2165, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A. Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Arinello, Pamela Deneka
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 893-5007
; TELEFAX: (781) 893-8277
; INFORMATION FOR SEQ ID NO: 2165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1017 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...1017
; SEQUENCE DESCRIPTION: SEQ ID NO: 2165:
US-09-107-532A-2165

Query Match 88.6%; Score 12.4; DB 3; Length 1017;
Best Local Similarity 71.4%; Pred. No. 9.2e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCACTCG 14
Db 924 CGTACTGCACTCG 937

RESULT 26

US-09-252-991A-90/C
Sequence 90, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 90
LENGTH: 1065
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-90

Query Match 88.6%; Score 12.4; DB 3; Length 1065;
Best Local Similarity 78.6%; Pred. No. 9.2e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCACTCG 14
Db 253 CGAAGTCACTCG 240

RESULT 27

US-09-489-039A-2883
Sequence 2883, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 2883
LENGTH: 1104
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2883

Query Match 88.6%; Score 12.4; DB 3; Length 1104;
Best Local Similarity 78.6%; Pred. No. 9.2e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCACTCG 14
Db 509 CGTACGCACTCG 522

RESULT 28

US-09-252-991A-6183
Sequence 6183, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6183
LENGTH: 1137
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6183

Query Match 88.6%; Score 12.4; DB 3; Length 1137;
Best Local Similarity 78.6%; Pred. No. 9.3e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCACTCG 14
Db 14 CGTACTGCACTCG 27

RESULT 29

US-09-252-991A-13050
Sequence 13050, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13050
LENGTH: 1152
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13050

Query Match 88.6%; Score 12.4; DB 3; Length 1152;
Best Local Similarity 71.4%; Pred. No. 9.3e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCACTCG 14
Db 422 CGTCTGCACTCG 435

RESULT 30

US-09-252-991A-7557
Sequence 7557, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7557
LENGTH: 1203
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7557

Query Match 88.6%; Score 12.4; DB 3; Length 1203;
Best Local Similarity 71.4%; Pred. No. 9.3e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14
||:|||||:
DB 189 CGTCTGCACTCG 202

RESULT 31
US-09-252-991A-9574
Sequence 9574, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 9574
LENGTH: 1203
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9574

Query Match 88.6%; Score 12.4; DB 3; Length 1203;
Best Local Similarity 78.6%; Pred. No. 9.3e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14
||:|||||:
DB 492 CGAAGTCACTCG 505

RESULT 32
US-09-996-008B-1
Sequence 1, Application US/09996008B
Patent No. 6830907
GENERAL INFORMATION:
APPLICANT: Mitsuhashi, Kazuya
APPLICANT: Yamashita, Hiroaki
APPLICANT: Kimoto, No. 6830907Hiro
TITLE OF INVENTION: MUTANTS OF MYCOBACTERIUM VACCAR- DERIVED
FILE REFERENCE: 14879-093001
CURRENT APPLICATION NUMBER: US/09/996,008B
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: JP 2000-363894
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: JP 2001-254631
PRIOR FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1206
TYPE: DNA
ORGANISM: Mycobacterium vaccae
US-09-996-008B-1

Query Match 88.6%; Score 12.4; DB 3; Length 1206;

Best Local Similarity 71.4%; Pred. No. 9.4e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14
||:|||||:
DB 431 CCTCTGCACTCG 444

RESULT 33
US-09-252-991A-13225
Sequence 13225, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13225
LENGTH: 1233
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13225

Query Match 88.6%; Score 12.4; DB 3; Length 1233;
Best Local Similarity 71.4%; Pred. No. 9.4e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14
||:|||||:
DB 1177 CGTCTGCACTCG 1190

RESULT 34
US-09-252-991A-7784/c
Sequence 7784, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7784
LENGTH: 1314
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7784

Query Match 88.6%; Score 12.4; DB 3; Length 1314;
Best Local Similarity 71.4%; Pred. No. 9.5e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14
||:|||||:
DB 1024 CGTCTGCACTCG 1011

RESULT 35
US-09-489-039A-4444
Sequence 4444, Application US/09489039A

Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 4444
; LENGTH: 1359
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-4444

Query Match 88.6%; Score 12.4; DB 3; Length 1359;
Best Local Similarity 71.4%; Pred. No. 9.5e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14
||:|||||:|
Db 975 CGTACTGCACTCG 988

RESULT 36
US-09-252-991A-12900
; Sequence 12900, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12900
; LENGTH: 1563
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12900

Query Match 88.6%; Score 12.4; DB 3; Length 1563;
Best Local Similarity 71.4%; Pred. No. 9.7e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14
||:|||||:|
Db 1530 CGTCTGCACTCG 1543

RESULT 37
US-09-252-991A-104
; Sequence 104, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 104
; LENGTH: 1629
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-104

Query Match 88.6%; Score 12.4; DB 3; Length 1629;
Best Local Similarity 78.6%; Pred. No. 9.7e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14
||:|||||:|
Db 50 CGAAGTCACTCG 63

RESULT 38
US-09-252-991A-252/C
; Sequence 252, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 252
; LENGTH: 1737
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-252

Query Match 88.6%; Score 12.4; DB 3; Length 1737;
Best Local Similarity 71.4%; Pred. No. 9.8e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14
||:|||||:|
Db 463 CGTACTGCAATTCG 450

RESULT 39
US-09-252-991A-279
; Sequence 279, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 279
; LENGTH: 1737
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-279

Query Match 88.6%; Score 12.4; DB 3; Length 1737;
Best Local Similarity 71.4%; Pred. No. 9.8e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14

DB 1452 CGTACTGCAATCG 1465

RESULT 40
US-09-252-991A-12189/c
; Sequence 12189, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12189
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12189

Query Match 88.6%; Score 12.4; DB 3; Length 1776;
Best Local Similarity 71.4%; Pred. No. 9.8e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAATCG 14
DB 1637 CGTCTGCAATCG 1624

RESULT 41
US-09-252-991A-4152
; Sequence 4152, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4152
; LENGTH: 1800
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4152

Query Match 88.6%; Score 12.4; DB 3; Length 1800;
Best Local Similarity 71.4%; Pred. No. 9.8e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAATCG 14
DB 1143 CGTACTGCAATCG 1156

RESULT 42
US-09-252-991A-1375/c
; Sequence 1375, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1375
; LENGTH: 1827
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1375

Query Match 88.6%; Score 12.4; DB 3; Length 1827;
Best Local Similarity 71.4%; Pred. No. 9.9e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAATCG 14
DB 1754 CGTACTGCAATCG 1741

RESULT 43
US-09-252-991A-1416/c
; Sequence 1416, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1416
; LENGTH: 2262
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1416

Query Match 88.6%; Score 12.4; DB 3; Length 2262;
Best Local Similarity 71.4%; Pred. No. 1e+03;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAATCG 14
DB 1708 CGTACTGCAATCG 1695

RESULT 44
US-09-252-991A-12254/c
; Sequence 12254, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12254
; LENGTH: 2298

```

; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12254

Query Match      88.6%; Score 12.4; DB 3; Length 2298;
Best Local Similarity 71.4%; Pred. No. 1e+03;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy      1 CGUACUGCAACUG 14
       ||:|||||:|
Db      2185 CGTCTCGCACTCG 2172

RESULT 45
US-09-252-991A-9636/c
; Sequence 9636, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9636
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9636

Query Match      88.6%; Score 12.4; DB 3; Length 2346;
Best Local Similarity 78.6%; Pred. No. 1e+03;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy      1 CGUACUGCAACUG 14
       |||:|||:|
Db      438 CGAAGTGCACCTCG 425

RESULT 46
US-09-252-991A-12355
; Sequence 12355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12355
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12355

Query Match      88.6%; Score 12.4; DB 3; Length 2346;
Best Local Similarity 71.4%; Pred. No. 1e+03;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy      1 CGUACUGCAACUG 14
       ||:|||||:|
Db      297 CGTCTCGCACTCG 310
```

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RESULT 47
US-09-489-039A-1363
; Sequence 1363, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 1363
; LENGTH: 2370
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-1363

Query Match      88.6%; Score 12.4; DB 3; Length 2370;
Best Local Similarity 71.4%; Pred. No. 1e+03;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy      1 CGUACUGCAACUG 14
       ||:|||||:|
Db      684 CGTCTCGCACTCG 697

RESULT 48
US-09-252-991A-1192
; Sequence 1192, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1192
; LENGTH: 2391
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1192

Query Match      88.6%; Score 12.4; DB 3; Length 2391;
Best Local Similarity 71.4%; Pred. No. 1e+03;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy      1 CGUACUGCAACUG 14
       ||:|||||:|
Db      1098 CGTCTCGCACTCG 1111

RESULT 49
US-09-252-991A-4456/c
; Sequence 4456, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
```

PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 4456
 LENGTH: 2472
 TYPE: DNA
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-4456

Query Match 88.6%; Score 12.4; DB 3; Length 2472;
 Best Local Similarity 71.4%; Pred. No. 1e+03;
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14
 DB 715 CGTACTGCATTCG 702

RESULT 50

US-09-620-312D-272/c
 Sequence 272, Application US/09620312D
 Patent No. 6569662

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
 APPLICANT: Liu, Chenghua
 APPLICANT: Asundi, Vinod
 APPLICANT: Zhang, Jie
 APPLICANT: Ren, Feiyan
 APPLICANT: Chen, Rui-hong
 APPLICANT: Zhao, Qing A.
 APPLICANT: Weinman, Tom
 APPLICANT: Xue, Aidong J.
 APPLICANT: Yang, Yonghong
 APPLICANT: Wang, Jian-Rui
 APPLICANT: Zhou, Ping
 APPLICANT: Ma, Yundong
 APPLICANT: Wang, Dunrui
 APPLICANT: Wang, Zhiwei
 APPLICANT: John Tillinghast
 APPLICANT: Drmanac, Radoje T.
 TITLE OF INVENTION: No. 6569662el Nucleic Acids and
 FILE REFERENCE: 784CIP2B
 CURRENT APPLICATION NUMBER: US/09/620,312D
 CURRENT FILING DATE: 2000-07-19
 PRIOR APPLICATION NUMBER: 09/552,317
 PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: 09/488,725
 PRIOR FILING DATE: 2000-01-21
 NUMBER OF SEQ ID NOS: 1105
 SOFTWARE: PL_FL_genes Version 1.0
 SEQ ID NO 272
 LENGTH: 2495

TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (411)..(812)
 US-09-620-312D-272

Query Match 88.6%; Score 12.4; DB 3; Length 2495;
 Best Local Similarity 71.4%; Pred. No. 1e+03;
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14
 DB 88 CGTACTGCATTCG 75

Search completed: March 18, 2006, 18:39:44
 Job time : 77.5769 secs

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OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:35:23 ; Search time 1318.15 Seconds
(without alignments)
496.922 Million cell updates/sec

Title: US-10-800-926-2

Perfect score: 14

Sequence: 1 cguacugcaucug 14

Scoring table: IDENTITY_NTC
Gapex 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	14	100.0	419	7	CF849219 PMAA009XM
3	14	100.0	525	3	BI602980 603249479
4	14	100.0	547	3	BI873693 963110B09
5	14	100.0	564	2	BE568772 601342118
6	14	100.0	564	10	CZ662415 OM_Ba021
7	14	100.0	587	5	BQ456457 Kc39a08.Y
8	14	100.0	614	2	BF422183 Fw1.12.G1
9	14	100.0	670	10	CZ660542 OM_Ba021
10	14	100.0	670	9	BZ563771 BZ563772 BCGP49TR
11	14	100.0	711	7	BH565722 BCGP49TR
12	14	100.0	730	7	CF849609 PMAA011XC
13	14	100.0	751	10	CW525116 OP_Ba004
14	14	100.0	759	9	BH435200 BCGZM10TR
15	14	100.0	776	10	CW528167 OP_Ba002
16	14	100.0	851	10	CW780591 OP_Ba008
17	14	100.0	855	10	CW519957 OP_Ba002
18	14	100.0	859	2	BF031922 601555533
19	14	100.0	884	2	BF207946 601862463
20	14	100.0	916	10	CW776517 SP_0106.A
21	14	100.0	943	9	AZ209474 SP_0106.A
22	14	100.0	1195	8	DN693741 CGX90-B12

23	14	100.0	1200	8	DN663186
24	14	100.0	1211	8	DN738151
25	14	100.0	1289	8	DN660653
26	13	92.9	157	9	AO661032
27	13	92.9	205	7	CR555866
28	13	92.9	255	5	BU640724
29	13	92.9	285	6	CA374069
30	13	92.9	290	10	CW452335
31	13	92.9	292	10	CW772355
32	13	92.9	344	1	AJ578024
33	13	92.9	345	5	BY111672
34	13	92.9	364	8	DR073074
35	13	92.9	366	7	CV724006
36	13	92.9	367	7	CK749390
37	13	92.9	368	11	FR0030316
38	13	92.9	369	6	CD733604
39	13	92.9	376	2	BI120564
40	13	92.9	379	1	AI059369
41	13	92.9	399	1	AM425513
42	13	92.9	402	3	BM032972
43	13	92.9	403	9	AQ123512
44	13	92.9	408	5	BM915405
45	13	92.9	409	5	BQ852614
46	13	92.9	410	3	BJ646387
47	13	92.9	413	10	CL555282
48	13	92.9	426	1	AJ679628
49	13	92.9	437	1	AM929623
50	13	92.9	459	7	CV723505
51	13	92.9	460	2	BF398311
52	13	92.9	463	2	BF389981
53	13	92.9	463	3	AQ431011
54	13	92.9	465	3	BI658245
55	13	92.9	466	7	CO520101
56	13	92.9	469	6	CF509531
57	13	92.9	470	10	CW449589
58	13	92.9	474	5	BU426615
59	13	92.9	475	5	AZ212523
60	13	92.9	477	7	CV723433
61	13	92.9	479	7	CV724150
62	13	92.9	480	6	CB536466
63	13	92.9	497	1	AM061392
64	13	92.9	500	3	BP185556
65	13	92.9	500	3	BP186086
66	13	92.9	500	3	BP187269
67	13	92.9	500	3	BP187391
68	13	92.9	500	3	BP188449
69	13	92.9	503	2	CG590908
70	13	92.9	503	2	BG659795
71	13	92.9	503	9	BH785265
72	13	92.9	506	6	CA371538
73	13	92.9	507	1	AM004087
74	13	92.9	512	2	BR031816
75	13	92.9	517	3	BM033583
76	13	92.9	521	9	AQ289494
77	13	92.9	521	9	BH765203
78	13	92.9	521	10	AG915387
79	13	92.9	523	6	CF066281
80	13	92.9	524	3	BO088045
81	13	92.9	527	7	CW477104
82	13	92.9	528	8	DR955809
83	13	92.9	528	8	CC309426
84	13	92.9	529	7	CB719309
85	13	92.9	529	6	CK737648
86	13	92.9	532	6	CD083741
87	13	92.9	535	6	CA758576
88	13	92.9	537	1	AL865005
89	13	92.9	537	1	AL875997
90	13	92.9	537	1	BP184473
91	13	92.9	538	1	AV604121
92	13	92.9	538	6	CB934921
93	13	92.9	539	10	CW031907
94	13	92.9	540	10	CW629939
95	13	92.9	542	9	AQ509742

96	13	548	7	CN467225	CN467225 CB 01 VR	169	13	688	5	BW942458	BW942458
97	13	549	1	AMC54043	AMC54043 103261 MA	170	13	689	2	BE228384	BE228384
98	13	550	7	CN46725	CN46725 CB 01 VR	171	13	689	10	CM177588	CM177588
99	13	550	1	AM654044	AM654044 103262 MA	172	13	690	3	BJ803349	BJ803349
100	13	551	2	BE557270	BE557270 EK97H04.Y	173	13	691	3	BH995300	BH995300
101	13	550	2	BE557250	BE557250 EK97H03.Y	174	13	694	7	CV637847	CV637847
102	13	553	11	AM018127	AM018127 614067C06	175	13	694	7	CV647112	CV647112
103	13	553	11	TA780C10	TA780C10 T. brucei	176	13	697	4	AY432168	AY432168
104	13	561	3	BJ101572	BJ101572 BJ101572	177	13	697	4	AY432168	AY432168
105	13	566	9	BH583561	BH583561 BGRBP407F	178	13	697	4	AY432168	AY432168
106	13	566	9	AQ711536	AQ711536 HS_5358_B	179	13	698	8	DR817431	DR817431
107	13	569	6	CF190100	CF190100 K7G04J2.X	180	13	703	7	CN232315	CN232315
108	13	569	6	AQ887057	AQ887057 HS_5548_B	181	13	704	8	CV439019	CV439019
109	13	573	8	CX717002	CX717002 1333467.N	182	13	705	8	CV824083	CV824083
110	13	574	8	BZ569812	BZ569812 3590.1.72	183	13	706	9	BH436661	BH436661
111	13	576	8	CX418757	CX418757 JGI_XZG65	184	13	706	10	CM418230	CM418230
112	13	577	8	BH191034	BH191034 TC3-40K14	185	13	707	10	CM418230	CM418230
113	13	578	3	BJ658058	BJ658058 BJ658058	186	13	711	8	DR813636	DR813636
114	13	582	10	CZ664573	CZ664573 OM_Ba021	187	13	711	10	CM750914	CM750914
115	13	584	10	CM150544	CM150544 104_551.1	188	13	711	10	CM750914	CM750914
116	13	587	9	AQ688502	AQ688502 nbx0077F	189	13	711	10	CM750914	CM750914
117	13	589	7	CO528867	CO528867 3530.1.19	190	13	713	10	CM418229	CM418229
118	13	595	3	BJ042040	BJ042040 BJ042040	191	13	723	6	CD803412	CD803412
119	13	596	1	AM741393	AM741393 ur54d01.x	192	13	723	7	CO529627	CO529627
120	13	596	8	CX418758	CX418758 JGI_XZG65	193	13	725	9	BZ337062	BZ337062
121	13	600	5	BZ892284	BZ892284 HM2_0179.	194	13	726	9	CL708094	CL708094
122	13	601	5	BU400278	BU400278 64139591	195	13	730	5	BW784120	BW784120
123	13	602	1	A1133308	A1133308 HAI910.Hu	196	13	730	9	BH385439	BH385439
124	13	602	11	DR5121T	DR5121T Danilo Ter	197	13	730	10	CM015366	CM015366
125	13	606	3	BI393321	BI393321 PGP1n.pko	198	13	734	10	AG183248	AG183248
126	13	609	1	AL679884	AL679884 AL679884	199	13	736	9	AQ290167	AQ290167
127	13	609	1	CM483909	CM483909 fdb001f2	200	13	739	9	DR813790	DR813790
128	13	610	10	CG522963	CG522963 CGXCN41TV	201	13	740	7	CN727123	CN727123
129	13	611	9	AQ543601	AQ543601 RPCI-11-3	202	13	740	8	CM454978	CM454978
130	13	614	10	CM201410	CM201410 104_627.1	203	13	740	10	CZ781676	CZ781676
131	13	616	10	CZ630710	CZ630710 OM_Ba017	204	13	742	10	BZ085659	BZ085659
132	13	616	10	CZ708893	CZ708893 OM_Ba012	205	13	742	10	DR970990	DR970990
133	13	616	10	CL464626	CL464626 OR_CBA006	206	13	744	8	BZ362590	BZ362590
134	13	617	9	BI347827	BI347827 de48f09.x	207	13	744	10	CL770586	CL770586
135	13	619	9	CC141398	CC141398 NDU_14021	208	13	745	10	BZ003839	BZ003839
136	13	620	7	CO524641	CO524641 3530.1.16	209	13	745	11	CR830386	CR830386
137	13	627	7	CO975415	CO975415 Bdg90N16B	210	13	747	7	CO527731	CO527731
138	13	631	1	A1774062	A1774062 BSR255162	211	13	749	8	DR978727	DR978727
139	13	631	1	AM476684	AM476684 uc81c03.y	212	13	753	5	BZ764403	BZ764403
140	13	632	3	BM605111	BM605111 170006870	213	13	753	5	BH055256	BH055256
141	13	636	9	CC059056	CC059056 1118f09.b	214	13	755	9	BH519128	BH519128
142	13	637	6	CA199614	CA199614 SCRFPL103	215	13	758	8	DR956314	DR956314
143	13	640	2	BC292260	BC292260 60236707	216	13	759	10	CL865497	CL865497
144	13	641	2	BC292260	BC292260 60236707	217	13	769	10	CL865497	CL865497
145	13	642	9	CC335534	CC335534 OGUCAS0TH	218	13	770	7	CO518704	CO518704
146	13	646	10	AG975145	AG975145 Drosophila	219	13	770	7	CO518704	CO518704
147	13	651	3	BU123372	BU123372 BU123372	220	13	774	9	CC906501	CC906501
148	13	651	3	BU123372	BU123372 BU123372	221	13	777	10	CM832821	CM832821
149	13	652	10	CL834896	CL834896 OR_CBA005	222	13	780	7	CN324854	CN324854
150	13	652	10	CZ240024	CZ240024 A1Aa-aag3	223	13	780	7	CK603293	CK603293
151	13	657	7	CV611970	CV611970 L_A1-aa0	224	13	780	7	CO521217	CO521217
152	13	657	7	CV611970	CV611970 L_A1-aa0	225	13	781	7	CO521217	CO521217
153	13	659	8	CX233841	CX233841 MEM14919	226	13	781	10	CG439299	CG439299
154	13	659	8	CX930272	CX930272 JGI_CAA07	227	13	785	8	DR792703	DR792703
155	13	660	3	BM064027	BM064027 KS01062C0	228	13	785	8	DR958676	DR958676
156	13	661	9	BH681509	BH681509 BGRBP407F	229	13	789	8	DR957798	DR957798
157	13	662	10	CL190555	CL190555 104_408.1	230	13	789	8	BH54570	BH54570
158	13	664	3	BU769134	BU769134 BU769134	231	13	792	11	CR216292	CR216292
159	13	667	9	AQ159092	AQ159092 nbx0012P	232	13	792	11	CR216292	CR216292
160	13	669	6	CB554423	CB554423 MMSBP0024	233	13	793	7	CO524137	CO524137
161	13	670	6	CA067268	CA067268 SCRFPL101	234	13	794	11	CR200005	CR200005
162	13	675	7	CM657296	CM657296 rt47906.y	235	13	797	2	BG781482	BG781482
163	13	676	10	CM229382	CM229382 104_670.1	236	13	799	8	DR955033	DR955033
164	13	682	10	CL830859	CL830859 OR_CBA005	237	13	804	8	DR804046	DR804046
165	13	683	3	BI650943	BI650943 603297273	238	13	806	10	CZ871318	CZ871318
166	13	686	3	BU661351	BU661351 BU661351	239	13	810	8	DR802647	DR802647
167	13	687	10	AG329549	AG329549 MMS mubcu	240	13	811	8	CM839154	CM839154
168	13	687	10	AG329549	AG329549 MMS mubcu	241	13	811	8	CM839154	CM839154

C 242	13	92.9	811	8	DR968237	ZM	BRP008	DR968237	ZM	BRP008	315	12.4	88.6	188	1	AA218591
C 243	13	92.9	813	6	CF676734	CCAD766TR		CF676734	CCAD766TR		316	12.4	88.6	191	6	BM288010
C 244	13	92.9	813	8	CX924665	JG1 CAANI		CX924665	JG1 CAANI		317	12.4	88.6	195	3	CB337879
C 245	13	92.9	816	8	CX020327	BST938646		CX020327	BST938646		318	12.4	88.6	197	8	DN845077
C 246	13	92.9	817	8	DR965755	ZM	BRP008	DR965755	ZM	BRP008	319	12.4	88.6	202	7	DN845077
C 247	13	92.9	818	9	BH529662	BOGR487P		BH529662	BOGR487P		320	12.4	88.6	205	8	DN845077
C 248	13	92.9	819	6	BU251499	603402852		BU251499	603402852		321	12.4	88.6	205	10	CG018573
C 249	13	92.9	819	6	CF681181	CCAD555TR		CF681181	CCAD555TR		322	12.4	88.6	208	7	CG018573
C 250	13	92.9	819	6	CO521506	3530 1 14		CO521506	3530 1 14		323	12.4	88.6	209	4	AK181678
C 251	13	92.9	821	8	DR815170	ZM	BRP004	DR815170	ZM	BRP004	324	12.4	88.6	213	7	BZ263938
C 252	13	92.9	824	9	AQ362718	ndxb0050D		AQ362718	ndxb0050D		325	12.4	88.6	215	7	CV368695
C 253	13	92.9	827	10	CL696141	PR1018B		CL696141	PR1018B		326	12.4	88.6	223	3	BI470080
C 254	13	92.9	831	3	BI465005	603206401		BI465005	603206401		327	12.4	88.6	228	1	AJ685525
C 255	13	92.9	832	8	CX926915	CGA1		CX926915	CGA1		328	12.4	88.6	229	3	BM085146
C 256	13	92.9	835	10	CZ227886	AIANA-aac7		CZ227886	AIANA-aac7		329	12.4	88.6	231	6	CF650225
C 257	13	92.9	835	10	CG315519	CG315519		CG315519	CG315519		330	12.4	88.6	235	2	BB539355
C 258	13	92.9	835	11	CR234233	Reverse		CR234233	Reverse		331	12.4	88.6	238	2	BB584088
C 259	13	92.9	837	10	AG046244	Pan trogl		AG046244	Pan trogl		332	12.4	88.6	240	7	CR766177
C 260	13	92.9	839	7	CO521859	3530 1 14		CO521859	3530 1 14		333	12.4	88.6	241	10	CL221923
C 261	13	92.9	841	8	DR972051	ZM	BRP009	DR972051	ZM	BRP009	334	12.4	88.6	245	7	CK740234
C 262	13	92.9	842	8	DR970169	ZM	BRP009	DR970169	ZM	BRP009	335	12.4	88.6	248	6	CA966779
C 263	13	92.9	846	8	DR801499	ZM	BRP002	DR801499	ZM	BRP002	336	12.4	88.6	250	10	CL534767
C 264	13	92.9	847	8	DR785242	ZM	BRP000	DR785242	ZM	BRP000	337	12.4	88.6	254	7	CK103504
C 265	13	92.9	848	7	CO389091	AGENCOURT		CO389091	AGENCOURT		338	12.4	88.6	255	7	CK051332
C 266	13	92.9	857	8	CX668188	UCRCPOL 0		CX668188	UCRCPOL 0		339	12.4	88.6	256	6	CB369744
C 267	13	92.9	859	7	CN167308	AGENCOURT		CN167308	AGENCOURT		340	12.4	88.6	257	8	CX535926
C 268	13	92.9	860	5	BU177009	603855288		BU177009	603855288		341	12.4	88.6	257	11	CR161926
C 269	13	92.9	867	8	DR806905	ZM	BRP003	DR806905	ZM	BRP003	342	12.4	88.6	258	8	NB1469
C 270	13	92.9	868	8	DR821293	ZM	BRP006	DR821293	ZM	BRP006	343	12.4	88.6	259	1	AM126779
C 271	13	92.9	871	8	DR802784	ZM	BRP002	DR802784	ZM	BRP002	344	12.4	88.6	261	8	CX535971
C 272	13	92.9	874	10	AG154151	Pan trogl		AG154151	Pan trogl		345	12.4	88.6	261	5	CX535972
C 273	13	92.9	876	8	DR970603	ZM	BRP006	DR970603	ZM	BRP006	346	12.4	88.6	266	5	BM585631
C 274	13	92.9	879	8	DR824819	ZM	BRP006	DR824819	ZM	BRP006	347	12.4	88.6	269	10	CG807449
C 275	13	92.9	879	8	DR826292	ZM	BRP006	DR826292	ZM	BRP006	348	12.4	88.6	270	7	CO060744
C 276	13	92.9	893	9	BZ083437	11F57h07		BZ083437	11F57h07		349	12.4	88.6	272	8	CX535880
C 277	13	92.9	895	6	CA792343	AGENCOURT		CA792343	AGENCOURT		350	12.4	88.6	272	8	BE890274
C 278	13	92.9	898	8	DR803425	ZM	BRP002	DR803425	ZM	BRP002	351	12.4	88.6	274	3	BI971944
C 279	13	92.9	905	10	CG376614	QZC181TV		CG376614	QZC181TV		352	12.4	88.6	278	3	BM276570
C 280	13	92.9	910	8	DR811586	ZM	BRP003	DR811586	ZM	BRP003	353	12.4	88.6	281	3	BM276570
C 281	13	92.9	912	10	CL969851	OBIFCC019		CL969851	OBIFCC019		354	12.4	88.6	283	10	CL167906
C 282	13	92.9	935	5	BY717171	BY717171		BY717171	BY717171		355	12.4	88.6	286	2	BI122262
C 283	13	92.9	940	5	CC636808	OCGAD66TV		CC636808	OCGAD66TV		356	12.4	88.6	286	5	BM559123
C 284	13	92.9	945	10	CN80181A	AL145547	Anopheles	AL145547	Anopheles		357	12.4	88.6	290	5	BK612537
C 285	13	92.9	963	8	DR746441	AI1 ABCL		DR746441	AI1 ABCL		358	12.4	88.6	292	4	CNS09390
C 286	13	92.9	984	5	BU555403	603475821		BU555403	603475821		359	12.4	88.6	292	9	CC666433
C 287	13	92.9	987	9	CC656799	OCGAD66TV		CC656799	OCGAD66TV		360	12.4	88.6	296	9	BZ522723
C 288	13	92.9	989	1	AL539502	AL539502		AL539502	AL539502		361	12.4	88.6	299	4	AK218365
C 289	13	92.9	989	8	DN789023	90943487		DN789023	90943487		362	12.4	88.6	300	8	DN220438
C 290	13	92.9	1004	8	DR747906	H07 AECAS		DR747906	H07 AECAS		363	12.4	88.6	302	3	BI307181
C 291	13	92.9	1024	10	CN80181A	Anopheles		AL148728	Anopheles		364	12.4	88.6	304	5	BM522436
C 292	13	92.9	1029	9	AP300877	AP300877		AP300877	AP300877		365	12.4	88.6	306	2	BR847076
C 293	13	92.9	1053	2	BF208273	601871387		BF208273	601871387		366	12.4	88.6	306	2	BB556479
C 294	13	92.9	1097	7	CR754129	CR754129		CR754129	CR754129		367	12.4	88.6	306	6	CF425710
C 295	13	92.9	1169	2	BG719984	602691342		BG719984	602691342		368	12.4	88.6	307	1	AJ976791
C 296	13	92.9	1280	10	AJ857805	Brassica		AJ857805	Brassica		369	12.4	88.6	307	8	D22632
C 297	13	92.9	1280	10	AW730293	GA	Ba001	AW730293	GA	Ba001	370	12.4	88.6	310	10	CM463769
C 298	13	92.9	1686	10	AG076369	Pan trogl		AG076369	Pan trogl		371	12.4	88.6	311	7	CV220788
C 299	13	92.9	2258	7	AM729508	AW729508		AM729508	AW729508		372	12.4	88.6	313	7	CK720865
C 300	13	92.9	2557	7	CK402923	AI1 IFInt		CK402923	AI1 IFInt		373	12.4	88.6	317	4	CNS09445
C 301	13	92.9	105	6	CF643293	D65 A09 F		CF643293	D65 A09 F		374	12.4	88.6	317	7	CNS66426
C 302	13	92.9	110	1	AM671409	I61 343 B		AM671409	I61 343 B		375	12.4	88.6	317	8	CX535810
C 303	13	92.9	137	10	CZ757339	OC Ba010		CZ757339	OC Ba010		376	12.4	88.6	320	8	CX535863
C 304	13	92.9	142	7	CV362370	PNO-OT001		CV362370	PNO-OT001		377	12.4	88.6	325	5	BM548841
C 305	13	92.9	150	6	CB091797	he96f05.9		CB091797	he96f05.9		378	12.4	88.6	328	8	CV784671
C 306	13	92.9	153	3	DN840183	KECB21-37		DN840183	KECB21-37		379	12.4	88.6	329	7	CC002282
C 307	13	92.9	158	3	BO335911	PM3-MT020		BO335911	PM3-MT020		380	12.4	88.6	329	7	CC002282
C 308	13	92.9	160	1	AA954856	SOYF012TH		AA954856	SOYF012TH		381	12.4	88.6	332	10	CM117036
C 309	13	92.9	166	10	CG816903	CG816903		CG816903	CG816903		382	12.4	88.6	332	7	BM542948
C 310	13	92.9	168	8	DN158682	CGW04EB01		DN158682	CGW04EB01		383	12.4	88.6	334	5	BM567926
C 311	13	92.9	170	8	DR041915	NLEB000001		DR041915	NLEB000001		384	12.4	88.6	335	7	CNS66084
C 312	13	92.9	172	1	AW308569	SMOV3MCM		AW308569	SMOV3MCM		385	12.4	88.6	336	3	BM189211
C 313	13	92.9	173	2	BF918218	db74D07.y		BF918218	db74D07.y		386	12.4	88.6	336	3	BM189211
C 314	13	92.9	187	2	BF048594	db74D07.y		BF048594	db74D07.y		387	12.4	88.6	336	7	CO286728

388	12.4	88.6	337	7	CO304991	CO304991	EXK46852.	C 461	12.4	88.6	394	6	CB257259	CB257259
389	12.4	88.6	338	7	CN550823	CN550823	radsl1h10.	C 462	12.4	88.6	397	5	BY095195	BY095195
C 390	12.4	88.6	338	8	CX535866	CX535866	TUASLWMSU	C 463	12.4	88.6	398	4	CNS09978	CNS09978
C 391	12.4	88.6	338	8	Z21204	Z21204	HSAAADSWX.T	C 464	12.4	88.6	399	3	BT779784	BT779784
C 392	12.4	88.6	341	2	BG464315	BG464315	EMI_72.CO	C 465	12.4	88.6	400	1	ALJ64555	ALJ64555
C 393	12.4	88.6	341	2	CN200310	CN200310	D26 O. ma	C 466	12.4	88.6	400	1	AM790558	AM790558
C 394	12.4	88.6	343	8	N82523	N82523	TGSESTZY55d0	C 467	12.4	88.6	400	3	BM604064	BM604064
C 395	12.4	88.6	344	3	BM648661	BM648661	170006873	C 468	12.4	88.6	401	3	BO169735	BO169735
C 396	12.4	88.6	345	3	CR546396	CR546396	DKEPZ459M	C 469	12.4	88.6	401	6	CD225492	CD225492
C 397	12.4	88.6	345	8	CX535940	CX535940	TUASLWMSU	C 470	12.4	88.6	402	9	CC063995	CC063995
C 398	12.4	88.6	347	10	CL536257	CL536257	tridp016x1	C 471	12.4	88.6	403	1	AJ784102	AJ784102
C 399	12.4	88.6	348	1	AM256101	AM256101	687062B08	C 472	12.4	88.6	403	2	BG464116	BG464116
C 400	12.4	88.6	348	8	CX535885	CX535885	TUASLWMSU	C 473	12.4	88.6	405	8	CX535823	CX535823
C 401	12.4	88.6	349	7	CN9568821	CN9568821	16318_123	C 474	12.4	88.6	405	8	DN479285	DN479285
C 402	12.4	88.6	351	8	CX535867	CX535867	TUASLWMSU	C 475	12.4	88.6	406	9	AZ213929	AZ213929
C 403	12.4	88.6	353	5	BY024392	BY024392	AL462815.T. bruce1	C 476	12.4	88.6	407	8	DN929781	DN929781
C 404	12.4	88.6	354	11	TA119H09P	TA119H09P	AL462815.T. bruce1	C 477	12.4	88.6	407	10	CN808876	CN808876
C 405	12.4	88.6	355	2	BF463462	BF463462	UI-M-CG0P	C 478	12.4	88.6	408	1	AL161133	AL161133
C 406	12.4	88.6	355	7	CO190626	CO190626	EXK048859.	C 479	12.4	88.6	409	9	BM528248	BM528248
C 407	12.4	88.6	356	8	DR828194	DR828194	ZM.BPB007	C 480	12.4	88.6	409	7	CN776388	CN776388
C 408	12.4	88.6	357	10	CN809669	CN809669	Pine_4303	C 481	12.4	88.6	410	1	AM509808	AM509808
C 409	12.4	88.6	358	8	CX535982	CX535982	TUASLWMSU	C 482	12.4	88.6	412	1	AM509808	AM509808
C 410	12.4	88.6	359	2	BE245283	BE245283	TCBAP1E24	C 483	12.4	88.6	415	7	CN569386	CN569386
C 411	12.4	88.6	361	1	AV706346	AV706346	AV706346	C 484	12.4	88.6	416	5	BK466497	BK466497
C 412	12.4	88.6	361	4	CNS08028	CNS08028	Single re	C 485	12.4	88.6	417	9	CC679563	CC679563
C 413	12.4	88.6	362	1	AI975815	AI975815	EST270409	C 486	12.4	88.6	418	5	AM261294	AM261294
C 414	12.4	88.6	362	6	CA235406	CA235406	SCCFL409	C 487	12.4	88.6	418	5	BY275905	BY275905
C 415	12.4	88.6	364	7	CX922920	CX922920	PJImgc_01	C 488	12.4	88.6	418	8	DR706064	DR706064
C 416	12.4	88.6	365	7	CN569197	CN569197	rad46909.	C 489	12.4	88.6	420	8	BQ040290	BQ040290
C 417	12.4	88.6	367	7	CV220789	CV220789	EST804699	C 490	12.4	88.6	421	3	BM369794	BM369794
C 418	12.4	88.6	368	7	CO962577	CO962577	BE120N30	C 491	12.4	88.6	421	6	CD685508	CD685508
C 419	12.4	88.6	368	8	U38007	U38007	OSU18007.FD	C 492	12.4	88.6	421	9	CN941969	CN941969
C 420	12.4	88.6	369	2	BE187748	BE187748	CRC03-R	C 493	12.4	88.6	421	7	AZ409243	AZ409243
C 421	12.4	88.6	370	6	CA194482	CA194482	SCRFBI02	C 494	12.4	88.6	421	9	BP393397	BP393397
C 422	12.4	88.6	371	7	CO289065	CO289065	EXK07022.	C 495	12.4	88.6	423	2	AO640950	AO640950
C 423	12.4	88.6	372	5	CA940071	CA940071	ru77c12.Y	C 496	12.4	88.6	424	1	AI850762	AI850762
C 424	12.4	88.6	373	6	BY071167	BY071167	BY071167	C 497	12.4	88.6	425	1	DR440172	DR440172
C 425	12.4	88.6	373	7	CV468199	CV468199	eat_1 van	C 498	12.4	88.6	425	8	CZ489167	CZ489167
C 426	12.4	88.6	374	10	CG177987	CG177987	PU1D04TB	C 499	12.4	88.6	425	10	BM368934	BM368934
C 427	12.4	88.6	374	9	AZ404909	AZ404909	IM0173M16	C 500	12.4	88.6	426	3	U92742	U92742
C 428	12.4	88.6	375	5	BM583165	BM583165	BM583165	C 501	12.4	88.6	426	7	CN550735	CN550735
C 429	12.4	88.6	375	5	CO756306	CO756306	MDfrc1047	C 502	12.4	88.6	427	7	CV266051	CV266051
C 430	12.4	88.6	376	10	CL975272	CL975272	CL975272	C 503	12.4	88.6	427	8	CX535962	CX535962
C 431	12.4	88.6	379	9	BZ235623	BZ235623	CH230-518	C 504	12.4	88.6	427	7	CM041704	CM041704
C 432	12.4	88.6	380	5	BY278800	BY278800	BI278800	C 505	12.4	88.6	428	1	AV424703	AV424703
C 433	12.4	88.6	380	7	CN922432	CN922432	000410AEL	C 506	12.4	88.6	428	7	AM18453	AM18453
C 434	12.4	88.6	381	9	BM808073	BM808073	hv21f11.b	C 507	12.4	88.6	428	9	AZ882820	AZ882820
C 435	12.4	88.6	382	8	BM030426	BM030426	494796.MA	C 508	12.4	88.6	430	1	AM312991	AM312991
C 436	12.4	88.6	382	8	DR432127	DR432127	max52d02.	C 509	12.4	88.6	430	9	CC529992	CC529992
C 437	12.4	88.6	385	5	BM578149	BM578149	BM578149	C 510	12.4	88.6	432	8	CX535929	CX535929
C 438	12.4	88.6	386	7	CN896612	CN896612	010629MAZ	C 511	12.4	88.6	434	8	BZ498281	BZ498281
C 439	12.4	88.6	386	7	CV468467	CV468467	eat_1 van	C 512	12.4	88.6	435	3	BJ322083	BJ322083
C 440	12.4	88.6	386	9	AZ488442	AZ488442	IM0318A14	C 513	12.4	88.6	436	6	CA713705	CA713705
C 441	12.4	88.6	388	3	BM133039	BM133039	TGBSTxyb1	C 514	12.4	88.6	437	1	AM124654	AM124654
C 442	12.4	88.6	388	3	BM133039	BM133039	TGBSTxyb1	C 515	12.4	88.6	437	7	CR628549	CR628549
C 443	12.4	88.6	388	3	CB779386	CB779386	AMGNNTC.N	C 516	12.4	88.6	437	10	AG914085	AG914085
C 444	12.4	88.6	389	3	BP822136	BP822136	BP822136	C 517	12.4	88.6	437	10	AG914085	AG914085
C 445	12.4	88.6	390	1	AV801914	AV801914	AV801914	C 518	12.4	88.6	437	10	AG914085	AG914085
C 446	12.4	88.6	390	6	CA287929	CA287929	SCSFS206	C 519	12.4	88.6	440	5	BM573435	BM573435
C 447	12.4	88.6	390	6	CV939194	CV939194	PMrPcC_06	C 520	12.4	88.6	440	8	DR064446	DR064446
C 448	12.4	88.6	391	3	BP942219	BP942219	BP942219	C 521	12.4	88.6	441	1	BM149024	BM149024
C 449	12.4	88.6	391	9	CC872892	CC872892	NDL_101A8	C 522	12.4	88.6	442	6	CB001278	CB001278
C 450	12.4	88.6	392	6	CA278414	CA278414	SCBFS203	C 523	12.4	88.6	442	6	CR644661	CR644661
C 451	12.4	88.6	392	10	CL184392	CL184392	CL184392	C 524	12.4	88.6	442	6	CR644661	CR644661
C 452	12.4	88.6	393	3	BI487648	BI487648	gC68C09.Y	C 525	12.4	88.6	442	7	CN961370	CN961370
C 453	12.4	88.6	393	5	C24870	C24870	C24870	C 526	12.4	88.6	443	8	CX535889	CX535889
C 454	12.4	88.6	393	5	CB192267	CB192267	py27b01.Y	C 527	12.4	88.6	443	8	CX535970	CX535970
C 455	12.4	88.6	393	6	CB777267	CB777267	AMGNNTC.N	C 528	12.4	88.6	443	8	CF646747	CF646747
C 456	12.4	88.6	393	6	CD479790	CD479790	eca01-22m	C 529	12.4	88.6	445	2	BF728957	BF728957
C 457	12.4	88.6	393	7	CN241339	CN241339	EST007205	C 530	12.4	88.6	449	1	AA152278	AA152278
C 458	12.4	88.6	393	8	CX535967	CX535967	TUASLWMSU	C 531	12.4	88.6	450	1	AL910478	AL910478
C 459	12.4	88.6	394	4	CNS08KM3	CNS08KM3	Single re	C 532	12.4	88.6	450	1	AM097551	AM097551
C 460	12.4	88.6	394	4	CNS08KM3	CNS08KM3	Single re	C 533	12.4	88.6	450	1	AM097551	AM097551

534	12.4	88.6	451	1	AM678429	WS1_15_B0	607	12.4	88.6	489	6	CB620092	CB620092	OSIIRA05A
C 535	12.4	88.6	451	3	BP953093	BP953093	C 608	12.4	88.6	489	6	CD812768	CD812768	BN10_023P
C 536	12.4	88.6	452	1	AM180544	AM180544	C 609	12.4	88.6	489	8	DR063983	DR063983	1P71405.G
C 537	12.4	88.6	452	2	BR452931	BR452931	C 610	12.4	88.6	489	9	AZ952539	AZ952539	2M0217121
C 538	12.4	88.6	453	2	BG278241	BG278241	C 611	12.4	88.6	489	11	TA2404020	TA2404020	AL48166 T. Bruce1
C 539	12.4	88.6	454	2	CNS0968X	BN044580 Single re	C 612	12.4	88.6	490	7	CO723413	CO723413	MDdb5002j
C 540	12.4	88.6	454	6	CA683287	CA683287	C 613	12.4	88.6	490	9	AC0902188	AC0902188	LMAPV1_1
C 541	12.4	88.6	454	6	CB191541	CB191541	C 614	12.4	88.6	491	5	BM0309984	BM0309984	BM0309984
C 542	12.4	88.6	455	1	AU138553	AU138553	C 615	12.4	88.6	491	7	CNS60887	CNS60887	taf83c04.
C 543	12.4	88.6	455	7	CO313690	CO313690	C 616	12.4	88.6	492	3	BE168197	BE168197	BM0309984
C 544	12.4	88.6	455	7	CR546380	CR546380	C 617	12.4	88.6	493	2	BE76718	BE76718	MY-19-E-0
C 545	12.4	88.6	455	11	CR498212	CR498212	C 618	12.4	88.6	494	1	AJ680262	AJ680262	AJ680262
C 546	12.4	88.6	456	1	AJ683384	AJ683384	C 619	12.4	88.6	494	3	BM033047	BM033047	kh62403.Y
C 547	12.4	88.6	456	1	AM620580	AM620580	C 620	12.4	88.6	495	2	BM030261	BM030261	AC0962221
C 548	12.4	88.6	456	5	BU332428	BU332428	C 621	12.4	88.6	495	2	BM69191	BM69191	LERGR08TP
C 549	12.4	88.6	456	9	AZ916672	AZ916672	C 622	12.4	88.6	495	7	CO520798	CO520798	BM69191
C 550	12.4	88.6	457	1	AL910479	AL910479	C 623	12.4	88.6	496	5	BU439231	BU439231	604145103
C 551	12.4	88.6	457	6	CD229653	CD229653	C 624	12.4	88.6	496	5	AC0962221	AC0962221	LERGR08TP
C 552	12.4	88.6	457	7	CN241794	CN241794	C 625	12.4	88.6	497	3	BI583362	BI583362	RH21959.5
C 553	12.4	88.6	457	10	CZ151873	CZ151873	C 626	12.4	88.6	498	9	AZ803332	AZ803332	2M0063G04
C 554	12.4	88.6	458	1	AI944441	AI944441	C 627	12.4	88.6	498	9	BH226355	BH226355	1006131P1
C 555	12.4	88.6	458	1	AM678428	AM678428	C 628	12.4	88.6	499	2	BG465821	BG465821	RH122_45
C 556	12.4	88.6	458	6	CA704082	CA704082	C 629	12.4	88.6	499	2	BE498706	BE498706	WHE0965.G
C 557	12.4	88.6	459	1	AV391824	AV391824	C 630	12.4	88.6	499	4	CNS091LY	CNS091LY	Single re
C 558	12.4	88.6	459	6	CA584142	CA584142	C 631	12.4	88.6	499	11	CR211283	CR211283	Reverse s
C 559	12.4	88.6	460	3	BM534122	BM534122	C 632	12.4	88.6	500	1	AI975422	AI975422	SCURFL03
C 560	12.4	88.6	461	3	BI569021	BI569021	C 633	12.4	88.6	500	3	BP190016	BP190016	g33b08.Y
C 561	12.4	88.6	461	6	CD229678	CD229678	C 634	12.4	88.6	500	6	CA110921	CA110921	WdK2c.PK0
C 562	12.4	88.6	463	5	BY560253	BY560253	C 635	12.4	88.6	500	7	CNS61268	CNS61268	taf80h08.
C 563	12.4	88.6	463	7	CN910725	CN910725	C 636	12.4	88.6	500	11	TA94B010	TA94B010	T. Bruce1
C 564	12.4	88.6	463	8	DN972346	DN972346	C 637	12.4	88.6	501	1	CA099463	CA099463	SCURFL03
C 565	12.4	88.6	464	7	CK593005	CK593005	C 638	12.4	88.6	501	6	AM476659	AM476659	ga3b08.Y
C 566	12.4	88.6	464	8	CX192387	CX192387	C 639	12.4	88.6	502	1	CB965195	CB965195	NL17_H07
C 567	12.4	88.6	464	10	CM739878	CM739878	C 640	12.4	88.6	502	6	CD433926	CD433926	EL01N0316
C 568	12.4	88.6	465	7	CK035932	CK035932	C 641	12.4	88.6	502	8	CK535908	CK535908	TLUASLVMSu
C 569	12.4	88.6	468	6	CD736149	CD736149	C 642	12.4	88.6	503	1	BH030409	BH030409	RPCI-24-2
C 570	12.4	88.6	468	6	CF599032	CF599032	C 643	12.4	88.6	503	9	AI438438	AI438438	486006A12
C 571	12.4	88.6	468	7	CN891632	CN891632	C 644	12.4	88.6	503	6	CA222793	CA222793	SCERFLA03
C 572	12.4	88.6	470	1	AM000587	AM000587	C 645	12.4	88.6	503	6	CB222793	CB222793	SCERFLA03
C 573	12.4	88.6	471	6	CF079914	CF079914	C 646	12.4	88.6	504	3	BI162386	BI162386	BJ162386
C 574	12.4	88.6	472	3	BM634330	BM634330	C 647	12.4	88.6	504	7	BQ041291	BQ041291	gd20C03.Y
C 575	12.4	88.6	472	3	BO088433	BO088433	C 648	12.4	88.6	504	3	CNS68692	CNS68692	taf96e05.
C 576	12.4	88.6	472	7	CN244510	CN244510	C 649	12.4	88.6	504	8	CK535829	CK535829	TLUASLVMSu
C 577	12.4	88.6	473	3	BU173979	BU173979	C 650	12.4	88.6	504	9	AO902189	AO902189	LMAPV1_1
C 578	12.4	88.6	473	3	BM601956	BM601956	C 651	12.4	88.6	505	3	BM032911	BM032911	kh60906.Y
C 579	12.4	88.6	473	6	CD220332	CD220332	C 652	12.4	88.6	505	6	CF015164	CF015164	QBL21h01.
C 580	12.4	88.6	473	7	CN659372	CN659372	C 653	12.4	88.6	505	9	AO209308	AO209308	HS_3237.B
C 581	12.4	88.6	474	5	BM913534	BM913534	C 654	12.4	88.6	506	2	BE481549	BE481549	167048.BA
C 582	12.4	88.6	475	10	BM968630	BM968630	C 655	12.4	88.6	506	6	CD223335	CD223335	CCCL_26.B
C 583	12.4	88.6	476	7	CK593625	CK593625	C 656	12.4	88.6	507	6	CB239184	CB239184	TGBSTZY5
C 584	12.4	88.6	476	9	BZ164075	BZ164075	C 657	12.4	88.6	507	8	CNS35837	CNS35837	TLUASLVMSu
C 585	12.4	88.6	478	2	BF393862	BF393862	C 658	12.4	88.6	507	10	CL920847	CL920847	QA_ABA002
C 586	12.4	88.6	479	2	BG355564	BG355564	C 659	12.4	88.6	507	11	CR127183	CR127183	Reverse s
C 587	12.4	88.6	479	7	CF928552	CF928552	C 660	12.4	88.6	508	3	BT758071	BT758071	AO232B04-
C 588	12.4	88.6	479	7	CNS66990	CNS66990	C 661	12.4	88.6	508	7	CF897951	CF897951	AO232B04-
C 589	12.4	88.6	480	7	BM669010	BM669010	C 662	12.4	88.6	508	9	BH260596	BH260596	CH230-75E
C 590	12.4	88.6	480	7	CM614985	CM614985	C 663	12.4	88.6	509	6	CB416248	CB416248	SCAB_6341
C 591	12.4	88.6	481	7	CO309880	CO309880	C 664	12.4	88.6	509	9	AO661119	AO661119	Sheared D
C 592	12.4	88.6	481	8	DN851142	DN851142	C 665	12.4	88.6	510	1	AU140068	AU140068	AU140068
C 593	12.4	88.6	482	1	AI530525	AI530525	C 666	12.4	88.6	511	3	BM361126	BM361126	AO0490-R
C 594	12.4	88.6	482	1	AM123712	AM123712	C 667	12.4	88.6	511	6	CD224564	CD224564	CCCL_34.F
C 595	12.4	88.6	482	8	CX535904	CX535904	C 668	12.4	88.6	511	7	CY129430	CY129430	Md6r600K
C 596	12.4	88.6	482	8	BM360227	BM360227	C 669	12.4	88.6	512	5	BQ809132	BQ809132	1030006B0
C 597	12.4	88.6	483	3	BM360227	BM360227	C 670	12.4	88.6	512	7	CO343904	CO343904	EP18326.3
C 598	12.4	88.6	484	1	AV643342	AV643342	C 671	12.4	88.6	513	7	CO320858	CO320858	BM288525.
C 599	12.4	88.6	486	7	CNS66263	CNS66263	C 672	12.4	88.6	513	8	CX535828	CX535828	TLUASLVMSu
C 600	12.4	88.6	487	1	AM258138	AM258138	C 673	12.4	88.6	513	10	CL534691	CL534691	tx1b012xp
C 601	12.4	88.6	487	2	BG355443	BG355443	C 674	12.4	88.6	514	3	BM642224	BM642224	170006B73
C 602	12.4	88.6	487	3	BM369291	BM369291	C 675	12.4	88.6	514	7	CN137199	CN137199	OX1_18_HI
C 603	12.4	88.6	487	8	CV952126	CV952126	C 676	12.4	88.6	515	6	CA232784	CA232784	SCR0FL306
C 604	12.4	88.6	487	9	BH899362	BH899362	C 677	12.4	88.6	515	6	CD155416	CD155416	ML1_004IU
C 605	12.4	88.6	488	2	BF413852	BF413852	C 678	12.4	88.6	517	1	AM244188	AM244188	687050D10
C 606	12.4	88.6	489	1	AJ737889	AJ737889	C 679	12.4	88.6	517	1	AM244188	AM244188	687050D10

C 680	12.4	88.6	517	6	CA214502	SCUTFL105	C 753	12.4	88.6	546	9	AA048055
C 681	12.4	88.6	517	6	CA829247	1114040E0	C 754	12.4	88.6	546	9	BZ658892
C 682	12.4	88.6	518	3	BQ164232	1091017H0	C 755	12.4	88.6	547	3	BUS521139
C 683	12.4	88.6	518	7	CK341281	K0228B03-	C 756	12.4	88.6	547	7	CV013589
C 684	12.4	88.6	518	7	CK371872	1a120b11.	C 757	12.4	88.6	547	10	CM575138
C 685	12.4	88.6	518	9	AQ398809	mcph0017X	C 758	12.4	88.6	548	1	AM787862
C 686	12.4	88.6	519	3	BU752012	BJ752012	C 759	12.4	88.6	548	2	BG278750
C 687	12.4	88.6	519	6	CA274004	SCRLSD101	C 760	12.4	88.6	548	4	AY431329
C 688	12.4	88.6	519	8	CK864955	CK864955 dp2revr0	C 761	12.4	88.6	548	6	CB099667
C 689	12.4	88.6	521	3	BU505268	BU505268	C 762	12.4	88.6	548	6	CB099667
C 690	12.4	88.6	521	3	BO340075	MR4-NN119	C 763	12.4	88.6	548	9	CBS08919
C 691	12.4	88.6	522	1	AUD35114	AUD35114	C 764	12.4	88.6	549	3	BIS080549
C 692	12.4	88.6	522	1	CK212684	tae51f10.	C 765	12.4	88.6	549	3	BIS87761
C 693	12.4	88.6	523	2	BG487867	RH12_60	C 766	12.4	88.6	549	3	BI170227
C 694	12.4	88.6	523	6	CA238099	SCMCF1500	C 767	12.4	88.6	549	6	CB191570
C 695	12.4	88.6	524	2	BG264187	daa36c10.	C 768	12.4	88.6	549	6	CV959764
C 696	12.4	88.6	524	3	BU192988	BU192988	C 769	12.4	88.6	550	8	CV909566
C 697	12.4	88.6	524	7	CO752355	Mdfc3024g	C 770	12.4	88.6	550	4	CNS08276
C 698	12.4	88.6	524	8	CKX35959	CKX35959 TULASV8U	C 771	12.4	88.6	550	4	CNS08276
C 699	12.4	88.6	524	8	CKX864671	dp2revr0	C 772	12.4	88.6	550	6	CD378631
C 700	12.4	88.6	524	8	7T8819	7T8819_yc9609_r1	C 773	12.4	88.6	550	7	CV203916
C 701	12.4	88.6	524	11	DE019878	Branch10s	C 774	12.4	88.6	550	7	CV203916
C 702	12.4	88.6	525	7	CNS64423	tao17b05.	C 775	12.4	88.6	550	8	CV911329
C 703	12.4	88.6	525	9	BZ895555	NARP12_01	C 776	12.4	88.6	550	8	CV962541
C 704	12.4	88.6	527	6	CD223511	CCCL_28_B	C 777	12.4	88.6	551	2	BG883885
C 705	12.4	88.6	528	7	CN241823	EST007690	C 778	12.4	88.6	551	8	DN481950
C 706	12.4	88.6	528	9	CC063690	CC063690 fgma003d0	C 779	12.4	88.6	551	9	A2611050
C 707	12.4	88.6	529	3	BP262997	BP262997	C 780	12.4	88.6	552	6	CD225046
C 708	12.4	88.6	530	10	CT663620	PR10144d	C 781	12.4	88.6	552	11	DR111418
C 709	12.4	88.6	531	7	CN845976	PG07006C0	C 782	12.4	88.6	552	4	CNS09NXX
C 710	12.4	88.6	531	7	CRS37496	DKE7p459H	C 783	12.4	88.6	553	4	CNS067P2
C 711	12.4	88.6	532	2	BG047595	OVI_25_H0	C 784	12.4	88.6	553	10	CM964000
C 712	12.4	88.6	532	2	BG712501	PJ11n_pK0	C 785	12.4	88.6	553	1	AJ558626
C 713	12.4	88.6	532	2	BB772427	BB772427	C 786	12.4	88.6	553	1	AJ558626
C 714	12.4	88.6	532	3	BU752011	BU752011	C 787	12.4	88.6	555	3	BIS27763
C 715	12.4	88.6	532	3	CO392394	MS#6_B06	C 788	12.4	88.6	555	5	BG857114
C 716	12.4	88.6	533	8	CV788778	zaa50b09.	C 789	12.4	88.6	555	9	BH144050
C 717	12.4	88.6	533	11	TA315A020		C 790	12.4	88.6	555	11	TA3578A03P
C 718	12.4	88.6	534	3	B1552986	603193620	C 791	12.4	88.6	555	3	BP366809
C 719	12.4	88.6	534	3	BM743732	K-EST0017	C 792	12.4	88.6	556	7	CO533532
C 720	12.4	88.6	534	3	BZ732243	BZ732243 OGPR644T	C 793	12.4	88.6	557	2	B1232994
C 721	12.4	88.6	534	3	BU603162	BU603162	C 794	12.4	88.6	557	3	BMS19821
C 722	12.4	88.6	536	8	CV931712	PM058A10	C 795	12.4	88.6	558	7	CV065266
C 723	12.4	88.6	536	9	BH387291	AG-ND-126	C 796	12.4	88.6	559	6	CB384262
C 724	12.4	88.6	536	10	CZ306692	ZMMBF0002	C 797	12.4	88.6	559	7	AM0249729
C 725	12.4	88.6	536	11	CR147509	Reverse s	C 798	12.4	88.6	560	1	AM025609
C 726	12.4	88.6	537	7	CV014774	TL027G09	C 799	12.4	88.6	560	3	BP257609
C 727	12.4	88.6	537	7	AZ145287	SP_0014_B	C 800	12.4	88.6	560	6	CD223024
C 728	12.4	88.6	538	8	CV961982	P7PCY_80	C 801	12.4	88.6	560	7	CN249792
C 729	12.4	88.6	539	6	CD227029	CCCL_49_E	C 802	12.4	88.6	560	9	CB240815
C 730	12.4	88.6	539	6	B1346270	3C5138_MA	C 803	12.4	88.6	560	9	AO577673
C 731	12.4	88.6	540	6	CB295108	CB295108 12B280X5	C 804	12.4	88.6	561	1	AA552428
C 732	12.4	88.6	540	6	AZ999351	2M0286X8	C 805	12.4	88.6	562	1	AL931925
C 733	12.4	88.6	541	1	AV631555	AV631555	C 806	12.4	88.6	562	3	BI188567
C 734	12.4	88.6	541	7	CNS63844	taf95d03.	C 807	12.4	88.6	562	7	CNS66190
C 735	12.4	88.6	541	7	CNS63985	taf95d03.	C 808	12.4	88.6	562	8	CV787714
C 736	12.4	88.6	543	3	BG659968	62681515	C 809	12.4	88.6	562	10	CZ914481
C 737	12.4	88.6	543	3	BU606154	BU606154	C 810	12.4	88.6	562	10	CL587375
C 738	12.4	88.6	543	8	DR064150	DR064150 dp74f06_g	C 811	12.4	88.6	563	7	CP966742
C 739	12.4	88.6	544	2	BG548151	602575306	C 812	12.4	88.6	563	10	CZ828472
C 740	12.4	88.6	544	2	BE661487	BE661487 1191_GmaX	C 813	12.4	88.6	563	10	CL587375
C 741	12.4	88.6	544	10	BZ511160	BOMQO42TR	C 814	12.4	88.6	563	10	CL1956721
C 742	12.4	88.6	544	10	AG919210	Drosoph11	C 815	12.4	88.6	564	4	CP052454
C 743	12.4	88.6	545	3	BU954996	BU954996	C 816	12.4	88.6	564	6	CP052454
C 744	12.4	88.6	545	6	CA133837	SCRURKT200	C 817	12.4	88.6	564	8	DR706057
C 745	12.4	88.6	545	7	CNS66485	taf93c12.	C 818	12.4	88.6	566	3	BM361129
C 746	12.4	88.6	545	7	CNS67373	ta8g08B09.	C 819	12.4	88.6	566	7	CV498625
C 747	12.4	88.6	545	8	CO984897	GM89022B2	C 820	12.4	88.6	566	8	CV913016
C 748	12.4	88.6	545	8	CKX535953	CKX535953 TULASV8U	C 821	12.4	88.6	566	8	DN141365
C 749	12.4	88.6	546	3	BU591453	BU591453	C 822	12.4	88.6	566	8	DN557110
C 750	12.4	88.6	546	6	CD219762	CCCL_58_B	C 823	12.4	88.6	566	8	DR439741
C 751	12.4	88.6	546	7	CD222388	CCCL_21_B	C 824	12.4	88.6	567	1	AW331845
C 752	12.4	88.6	546	7	CN909427	030123AB1	C 825	12.4	88.6	567	2	BG285108
C 680	12.4	88.6	517	6	CA214502	SCUTFL105	C 753	12.4	88.6	546	9	AA048055
C 681	12.4	88.6	517	6	CA829247	1114040E0	C 754	12.4	88.6	546	9	BZ658892
C 682	12.4	88.6	518	3	BQ164232	1091017H0	C 755	12.4	88.6	547	3	BUS521139
C 683	12.4	88.6	518	7	CK341281	K0228B03-	C 756	12.4	88.6	547	7	CV013589
C 684	12.4	88.6	518	7	CK371872	1a120b11.	C 757	12.4	88.6	547	10	CM575138
C 685	12.4	88.6	518	9	AQ398809	mcph0017X	C 758	12.4	88.6	548	1	AM787862
C 686	12.4	88.6	519	3	BU752012	BJ752012	C 759	12.4	88.6	548	2	BG278750
C 687	12.4	88.6	519	6	CA274004	SCRLSD101	C 760	12.4	88.6	548	4	AY431329
C 688	12.4	88.6	519	8	CK864955	CK864955 dp2revr0	C 761	12.4	88.6	548	6	CB099667
C 689	12.4	88.6	521	3	BU505268	BU505268	C 762	12.4	88.6	548	6	CB099667
C 690	12.4	88.6	521	3	BO340075	MR4-NN119	C 763	12.4	88.6	548	9	CBS08919
C 691	12.4	88.6	522	1	AUD35114	AUD35114	C 764	12.4	88.6	549	3	BIS080549
C 692	12.4	88.6	522	1	CK212684	tae51f10.	C 765	12.4	88.6	549	3	BIS87761
C 693	12.4	88.6	523	2	BG487867	RH12_60	C 766	12.4	88.6	549	3	BI170227
C 694	12.4	88.6	523	6	CA238099	SCMCF1500	C 767	12.4	88.6	549	6	CB191570
C 695	12.4	88.6	524	2	BG264187	daa36c10.	C 768	12.4	88.6	549	6	CV959764
C 696	12.4	88.6	524	3	BU192988	BU192988	C 769	12.4	88.6	550	8	CV909566
C 697	12.4	88.6	524	7	CO752355	Mdfc3024g	C 770	12.4	88.6	550	4	CNS08276
C 698	12.4	88.6	524	8	CKX35959	CKX35959 TULASV8U	C 771	12.4	88.6	550	4	CNS08276
C 699	12.4	88.6	524	8	CKX864671	dp2revr0	C 772	12.4	88.6	550	6	CD378631
C 700	12.4	88.6	524	8	7T8819	7T8819_yc9609_r1	C 773	12.4	88.6	550	7	CV203916
C 701	12.4	88.6	524	11	DE019878	Branch10s	C 774	12.4	88.6	550	7	CV203916
C 702	12.4	88.6	525	7	CNS64423	tao17b05.	C 775	12.4	88.6	550	8	CV911329
C 703	12.4	88.6	525	9	BZ895555	NARP12_01	C 776	12.4	88.6	550	8	CV962541
C 704	12.4	88.6	527	6	CD223511	CCCL_28_B	C 777	12.4	88.6	551	2	BG883885
C 705	12.4	88.6	528	7	CN241823	EST007690	C 778	12.4	88.6	551	8	DN481950
C 706	12.4	88.6	528	9	CC063690	CC063690 fgma003d0	C 779	12.4	88.6	551	9	A2611050
C 707	12.4	88.6	529	3	BP262997	BP262997	C 780	12.4	88.6	552	6	CD225046

826	12.4	88.6	567	7	CN239033	EST004889	899	12.4	88.6	582	7	CN244773	EST010652
827	12.4	88.6	568	1	AM024855	AM024855	900	12.4	88.6	582	9	AO99553	RPCI-23-3
828	12.4	88.6	568	2	BE139918	BE139918	901	12.4	88.6	582	10	CL312785	CL312785 mch2-126N
829	12.4	88.6	568	6	CD43871	EL01N0432	902	12.4	88.6	583	3	BP200862	BP200862
830	12.4	88.6	568	6	CF642391	DS1_B04_F	903	12.4	88.6	583	3	BP336367	BP336367
831	12.4	88.6	568	6	CN249959	EST015880	904	12.4	88.6	583	3	BP353305	BP353305
832	12.4	88.6	568	7	CN562850	taf78a11.	905	12.4	88.6	583	3	BP362061	BP362061
833	12.4	88.6	568	8	CN897074	PA0484.m	906	12.4	88.6	583	8	BP34285	BP34285
834	12.4	88.6	569	7	CD275020	CD275020	907	12.4	88.6	583	9	AO158061	AO158061
835	12.4	88.6	569	7	CN567867	taf91f03.	908	12.4	88.6	584	3	BP342502	BP342502
836	12.4	88.6	570	2	BG699547	602679252	909	12.4	88.6	584	3	BP217354	BP217354
837	12.4	88.6	570	6	CN50GDI9	CR713489	910	12.4	88.6	584	3	BP345209	BP345209
838	12.4	88.6	570	6	CN615783	TA68538	911	12.4	88.6	584	9	AZ212340	AZ212340
839	12.4	88.6	570	7	CV468538	est_1_van	912	12.4	88.6	585	6	CF619753	CF619753
840	12.4	88.6	571	6	CB335028	CB335028	913	12.4	88.6	585	2	BG464063	BG464063
841	12.4	88.6	571	6	CN614462	CN614462	914	12.4	88.6	586	3	BP607847	BP607847
842	12.4	88.6	571	7	CO613353	CO613353	915	12.4	88.6	586	3	BM361570	BM361570
843	12.4	88.6	572	5	BQ594687	DG9-12438	916	12.4	88.6	586	3	BQ279493	BQ279493
844	12.4	88.6	572	5	BQ784111	BO784111	917	12.4	88.6	586	5	BUE64473	BUE64473
845	12.4	88.6	572	6	CP248923	CP248923	918	12.4	88.6	587	5	BM281869	BM281869
846	12.4	88.6	572	6	CP248923	CP248923	919	12.4	88.6	587	5	BM51877	BM51877
847	12.4	88.6	572	7	CF942011	CF942011	920	12.4	88.6	587	5	CL333405	CL333405
848	12.4	88.6	572	8	CX195317	11-E01939	921	12.4	88.6	588	3	BP172427	BP172427
849	12.4	88.6	572	8	CX535935	CX535935	922	12.4	88.6	588	3	BP282010	BP282010
850	12.4	88.6	572	11	TA164050	TA164050	923	12.4	88.6	588	10	CG047050	CG047050
851	12.4	88.6	573	2	BG720399	602682493	924	12.4	88.6	588	10	CG047051	CG047051
852	12.4	88.6	573	3	BI511796	BI511796	925	12.4	88.6	590	7	CN563109	CN563109
853	12.4	88.6	573	3	BM636573	BM636573	926	12.4	88.6	590	7	CV173780	CV173780
854	12.4	88.6	573	3	BP366764	BP366764	927	12.4	88.6	590	10	CF2664188	CF2664188
855	12.4	88.6	574	1	AI403567	GH23034.5	928	12.4	88.6	591	6	CF371584	CF371584
856	12.4	88.6	574	3	BJ607785	BJ607785	929	12.4	88.6	591	7	CN565950	CN565950
857	12.4	88.6	574	10	CL858920	OR_CBA008	930	12.4	88.6	591	8	CV915976	CV915976
858	12.4	88.6	574	11	LEBP009H09	BX345161	931	12.4	88.6	591	8	CV961893	CV961893
859	12.4	88.6	575	1	AA438781	AA438781	932	12.4	88.6	592	1	A1977188	A1977188
860	12.4	88.6	575	3	BM318333	BM318333	933	12.4	88.6	592	3	BM604155	BM604155
861	12.4	88.6	575	6	CF261256	NCEST3C82	934	12.4	88.6	592	3	BP353106	BP353106
862	12.4	88.6	575	7	CK841714	UI-R-BJ09	935	12.4	88.6	592	7	CV0298023	CV0298023
863	12.4	88.6	575	8	CV913870	PR022B9_8	936	12.4	88.6	592	7	CV0298023	CV0298023
864	12.4	88.6	575	8	CV915806	PF054G2_8	937	12.4	88.6	592	8	CV896829	CV896829
865	12.4	88.6	575	8	DR794621	ZM_BFP001	938	12.4	88.6	592	8	CV961890	CV961890
866	12.4	88.6	575	9	AO163656	AO163656	939	12.4	88.6	592	9	CC861110	CC861110
867	12.4	88.6	575	10	CZ116560	nbxb0007D	940	12.4	88.6	593	3	BP236830	BP236830
868	12.4	88.6	576	3	BM491747	BM491747	941	12.4	88.6	593	3	BP742569	BP742569
869	12.4	88.6	576	5	BX490839	DXP2P686D	942	12.4	88.6	593	6	CD444142	CD444142
870	12.4	88.6	576	7	CR540620	CR540620	943	12.4	88.6	593	8	CV930638	CV930638
871	12.4	88.6	576	11	CR072024	Forward_B	944	12.4	88.6	593	11	CR082194	CR082194
872	12.4	88.6	577	2	BG241337	RH122_49	945	12.4	88.6	594	1	AV383406	AV383406
873	12.4	88.6	577	7	CK604435	UT01182.3	946	12.4	88.6	594	3	BI545505	BI545505
874	12.4	88.6	579	7	CN251557	CN251557	947	12.4	88.6	594	5	BM572369	BM572369
875	12.4	88.6	579	7	CV209017	EST868727	948	12.4	88.6	594	5	CA015360	CA015360
876	12.4	88.6	579	8	CV923540	PU009C8_8	949	12.4	88.6	594	7	CN565962	CN565962
877	12.4	88.6	580	3	BU199716	BU199716	950	12.4	88.6	594	7	CN565962	CN565962
878	12.4	88.6	580	3	BP234102	BP234102	951	12.4	88.6	595	3	BP201702	BP201702
879	12.4	88.6	580	3	BP368413	BP368413	952	12.4	88.6	595	3	BP271792	BP271792
880	12.4	88.6	580	5	BX274681	BX274681	953	12.4	88.6	595	6	CD442854	CD442854
881	12.4	88.6	580	7	CN563228	taf85c04.	954	12.4	88.6	595	6	CD442854	CD442854
882	12.4	88.6	580	7	CN566825	taf98c04.	955	12.4	88.6	595	6	CD444027	CD444027
883	12.4	88.6	581	3	BP197073	BP197073	956	12.4	88.6	595	10	CM167015	CM167015
884	12.4	88.6	581	3	BP365936	BP365936	957	12.4	88.6	596	6	CD219726	CD219726
885	12.4	88.6	581	6	CA648099	wreln.pko	958	12.4	88.6	596	7	CN565376	CN565376
886	12.4	88.6	581	9	AO948815	sheared_D	959	12.4	88.6	596	7	CN566690	CN566690
887	12.4	88.6	582	1	AJ640401	AJ640401	960	12.4	88.6	597	1	AU135123	AU135123
888	12.4	88.6	582	2	BB660017	BB660017	961	12.4	88.6	597	1	BP336337	BP336337
889	12.4	88.6	582	3	BP200561	BP200561	962	12.4	88.6	597	7	CO972193	CO972193
890	12.4	88.6	582	3	BP200753	BP200753	963	12.4	88.6	597	10	AG917645	AG917645
891	12.4	88.6	582	3	BP245575	BP245575	964	12.4	88.6	598	3	BI473755	BI473755
892	12.4	88.6	582	3	BP260595	BP260595	965	12.4	88.6	598	5	BI637902	BI637902
893	12.4	88.6	582	3	BP261041	BP261041	966	12.4	88.6	598	5	BM557153	BM557153
894	12.4	88.6	582	3	BP261286	BP261286	967	12.4	88.6	599	3	BU193846	BU193846
895	12.4	88.6	582	3	BP262990	BP262990	968	12.4	88.6	599	6	CD433382	CD433382
896	12.4	88.6	582	3	BP353891	BP353891	969	12.4	88.6	599	6	CD609041	CD609041
897	12.4	88.6	582	3	BP361981	BP361981	970	12.4	88.6	599	7	CV667947	CV667947
898	12.4	88.6	582	6	CB076669	CB076669	971	12.4	88.6	599	10	AG923105	AG923105

972	12.4	88.6	600	3	BM439485	p21c.p20
973	12.4	88.6	600	6	CF644282	K18_H12_F
974	12.4	88.6	601	6	CD696157	EST12690
975	12.4	88.6	601	9	CC822319	MSB14D8
976	12.4	88.6	601	10	CM086386	104_430_1
977	12.4	88.6	602	3	BI580376	RE74560.5
978	12.4	88.6	602	3	BM599560	170006870
979	12.4	88.6	602	7	CK134865	RH05209.3
980	12.4	88.6	602	8	CV961872	PTPCPY_59
981	12.4	88.6	602	10	CG161459	PTDZ10TD
982	12.4	88.6	603	3	BI878368	1177405.X
983	12.4	88.6	603	6	BJ041252	BJ041252
984	12.4	88.6	603	6	CA118295	SCBGR109
985	12.4	88.6	603	7	CM567453	tag09e09.
986	12.4	88.6	603	7	CO868232	MAFRT3040
987	12.4	88.6	604	2	BB346469	BB346469
988	12.4	88.6	604	5	BQ875869	OQ19F17.Y
989	12.4	88.6	604	5	BX621452	BX621452
990	12.4	88.6	604	6	CD442696	EL01N0414
991	12.4	88.6	604	7	CV014619	TT025FP01
992	12.4	88.6	604	8	CV958846	PTXPXC_65
993	12.4	88.6	605	2	BI294829	UI-R-DKO-
994	12.4	88.6	605	6	CD434360	EL01N0323
995	12.4	88.6	606	6	CD212733	HS1_16_B0
996	12.4	88.6	606	7	CN306622	170004243
997	12.4	88.6	606	7	CN562993	taf80h08.
998	12.4	88.6	607	2	BI097451	949008B03
999	12.4	88.6	607	3	BJ604569	BJ604569
1000	12.4	88.6	607	5	BU462915	BU462915

ALIGNMENTS

RESULT 1
LOCUS BF764590 353 bp mRNA linear EST 12-JAN-2001
DEFINITION CM3-CS0043-041100-464-all CS0043 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF764590
VERSION BF764590.1 GI:12112490
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 353)
Dias Neto, R., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&ct=CM3-CS0043-041100-464-all&ct3=2000-11-04&ct4=1)
Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence stop: 353.

FEATURES

Location/Qualifiers

source

1. .353
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_id="CS0043"
/note="Organ: colon, est; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORS8765 PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 14; DB 2; Length 353;
Best Local Similarity 78.6%; Pred. No. 1.6e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14
||:|||||:
53 CCGACTGCACTCG 40

RESULT 2
LOCUS CF849219 419 bp mRNA linear EST 30-OCT-2003
DEFINITION pEM4009CM21f USDA-IPAFs:Expression of Phytophthora sojae genes during infection and propagation_sMA Phytophthora sojae cDNA clone sMA009M21 5, mRNA sequence.
ACCESSION CF849219
VERSION CF849219.1 GI:38064873
KEYWORDS EST.
SOURCE Phytophthora sojae
ORGANISM Phytophthora sojae
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae; Phytophthora.

REFERENCE
AUTHORS 1 (bases 1 to 419)
TITLE Tyler, B.
JOURNAL Unpublished (2003)
COMMENT Contact: Tyler B
Tyler lab

VBI
1880 Pratt Dr., Blacksburg, VA 24061, USA
Tel: 540-231-7318
Email: bmyler@vt.edu
PCR PRIMERS
FORWARD: BK reverse primer
BACKWARD: BK reverse primer
Plate: 009 row: M column: 21
Seq primer: BK reverse primer
High quality sequence stop: 419.
Location/Qualifiers

FEATURES

source

1. .419
/organism="Phytophthora sojae"
/mol_type="mRNA"
/db_xref="taxon:67593"
/clone="sMA009M21"
/tissue_type="mycelium"
/cell_line="P6497"
/dev_stage="mycelium"
/lab_host="synthetic medium"
/clone_id="USDA-IPAFs:Expression of Phytophthora sojae genes during infection and propagation_sMA"
/note="Vector: pBK-CMV; Site_1: BclRI; Site_2: XhoI"

ORIGIN

Query Match 100.0%; Score 14; DB 7; Length 419;
Best Local Similarity 78.6%; Pred. No. 1.6e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14

Db 58 CGTACTGCACTCG 71

RESULT 3
BI602980/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BI602980 525 bp mRNA linear EST 07-SEP-2001
603249479F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5301331 5',
mRNA sequence.
BI602980
BI602980.1 GI:15495919
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 525)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cga@b6-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1AM11762 row: n column: 20
High quality sequence stop: 98.
Location/Qualifiers
1. 525
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5301331"
/tissue_type="Hypothalamus"
/lab_host="DH10B"
/clone_1ib="NIH MGC 96"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTNN-3', size-selected for average
insert size 2.3 kb and normalized to RGT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 14; DB 3; Length 525;
Best Local Similarity 78.6%; Pred. No. 1.6e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14
||:|:|:|:|:|:|:
148 CGTACTGCACTCG 135

RESULT 4
BI873693
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

BI873693 547 bp mRNA linear EST 11-OCT-2001
963110809.Y1 C. reinhardtii CC-1690, Stress condition I,
normalized, lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA
sequence.
BI873693
BI873693.1 GI:16071697
EST.
Chlamydomonas reinhardtii

ORGANISM
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 547)
AUTHORS
Grossman, A., Chang, C.-W., Davies, J., Harris, B., Hauser, C.,
Lefebvre, P., McDermott, J.P., Shrago, J., Sillow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 963
JOURNAL
Unpublished (2001)
COMMENT
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
Location/Qualifiers
1. 547
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_1ib="C. reinhardtii CC-1690, Stress condition I,
normalized, lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI, Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP-N (30 min, 1hr, 4hr), TAP-S (30 min,
1hr, 4hr), TAP-P (4hr, 12hr, 24hr), NO3 to NH4 (30min,
1hr, 4hr) and NH4 to NO3 (30min, 1hr, 4hr). PolyA mRNA was
purified from each sample, pooled and cDNA synthesized.
The cDNA was directionally cloned into lambda Zap II
(Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
Zap clones by superinfection with Exsist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."

ORIGIN

Query Match 100.0%; Score 14; DB 3; Length 547;
Best Local Similarity 78.6%; Pred. No. 1.6e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14
||:|:|:|:|:|:|:
191 CGTACTGCACTCG 204

RESULT 5
BE568772/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BE568772 564 bp mRNA linear EST 15-AUG-2000
601342118F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3684052 5',
mRNA sequence.
BE568772
BE568772.1 GI:9812492
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 564)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@b6-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLM370 row: d column: 05
 High quality sequence stop: 563.
 Location/Qualifiers

FEATURES

source

1..564

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3684052"

/issue_type="carcinoma, cell line"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH MGC 53"

/note="Organ: bladder; Vector: pDNR-LIB (Clontech);

Site 1: SfiI (ggcgccgcgcgc); Site 2: SfiI

(ggccattatggc); Double-stranded cDNA was prepared from

cell line RNA. 5' and 3' adaptors were used in cloning as

follows: 5' adaptor sequence: 5'-CACGCGCATTTATGCGC-3' and

3' adaptor sequence:

5'-ATTCTAGAGCGCGCGCGCATG-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.55

kb (range 0.9-4.0 kb). 15/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA)."

ORIGIN

Query Match 100.0%; Score 14; DB 2; Length 564;
 Best Local Similarity 78.6%; Pred. No. 1.6e+03;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUGC 14
 |||:|||||:|
 Db 58 CGTACTGCACCTCG 45

RESULT 6

CZ662415

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

CZ662415 564 bp DNA linear GSS 07-JUL-2005
 OM_Ba0214P18.f OM_Ba Oryza minuta genomic clone OM_Ba0214P18 5',
 genomic survey sequence.
 CZ662415
 C2662415.1 GI:70240449
 GSS
 Oryza minuta
 Oryza minuta
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 564)
 Kim,H., Collura,K., Wasieleski,M., Byrne,M., Strum,D., Smart,D.,
 Rao,K., Luo,M., Jetty,R., Kudrna,D., Miller,C., Soderlund,C. and
 Wang,R.
 OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
 Unpublished (2005)
 Contact: Rod A. Wing
 Arizona Genomics Institute
 University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259
 Email: rwing@genome.arizona.edu
 Plate: 0214 row: P column: 18
 Class: BAC ends.
 Location/Qualifiers
 1..564
 /organism="Oryza minuta"
 /mol_type="genomic DNA"
 /db_xref="taxon:53628"
 /clone="OM_Ba0214P18"
 /tissue_type="leaves"
 /lab_host="DH10B"
 /clone_lib="OM_Ba"
 /note="Vector: pCUGRAC1; Site_1: HindIII; Site_2:

ORIGIN

HindIII"

Query Match 100.0%; Score 14; DB 10; Length 564;
 Best Local Similarity 78.6%; Pred. No. 1.6e+03;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUGC 14
 |||:|||||:|
 Db 282 CGTACTGCACCTCG 295

RESULT 7

BO456457

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BO456457 587 bp mRNA linear EST 29-MAY-2002
 ke3a08.y1 Dirofilaria immitis adult PAMP1 v1 Dirofilaria immitis
 cDNA 5' similar to TR:Q9XTH8 Q9XTH8 Y37A1B.1 PROTEIN. [1], mRNA
 sequence.
 BO456457.1 GI:21259569
 EST.
 Dirofilaria immitis (dog heartworm nematode)
 Dirofilaria immitis
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 Onchocercidae; Dirofilaria.
 1 (bases 1 to 587)
 McCarter,J., Clifton,S., Chispeili,B., Pape,D., Martin,J.,
 Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
 Bowers,Y., Gibbons,M., Ritzer,E., Bennett,J., Franklin,C.,
 Tsagarashvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
 Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
 Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
 McCann,R., Waterston,R. and Wilson,R.
 The Washington Univ. Nematode EST Project, 1999
 Unpublished (1999)
 Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 The library was constructed by Claire Murphy and Dr. James McCarter
 at Washington University, St. Louis. Adult nematodes were harvested
 from infected dogs by Dr. Prema Arasu of North Carolina State
 University, Raleigh, NC (Prema.Arasu@ncsu.edu) Total RNA was
 isolated by Merry McAlaird of Divergence, Inc., St. Louis, MO. DNA
 sequencing by: Washington University Genome Sequencing Center
 Seq primer: -40RP from Gibco
 High quality sequence stop: 421.
 Location/Qualifiers
 1..587
 /organism="Dirofilaria immitis"
 /mol_type="mRNA"
 /db_xref="taxon:6287"
 /dev stage="adult"
 /lab_host="DH10B"
 /clone_lib="Dirofilaria immitis adult PAMP1 v1"
 /note="Vector: PAMP1 (Gibco); Site 1: NotI; Site 2: SalI;
 The library was constructed by Claire Murphy and Dr. James
 McCarter at Washington University, St. Louis. The cDNA was
 made by using Dynabead oligo-dT priming (Dynal). PCR based
 library using a modified protocol from the SMART PCR cDNA
 Synthesis Kit from Clontech. Directionally cloned into the
 UDG sites of PAMP1. Adult nematodes were harvested from
 infected dogs by Dr. Prema Arasu of North Carolina State
 University, Raleigh, NC (Prema.Arasu@ncsu.edu). Total RNA
 was isolated by Merry McAlaird of Divergence, Inc., St.
 Louis, MO."

ORIGIN

Query Match 100.0%; Score 14; DB 5; Length 587;
 Best Local Similarity 78.6%; Pred. No. 1.6e+03;

Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGUACUGAACUG 14
||:|||||:|
Db 344 CCGACTGCACCTCG 357

RESULT 8
BF422183
LOCUS 614 bp mRNA linear EST 28-NOV-2000

DEFINITION BF422183
Fml_12.G12.b1.A003 floral-induced Meristem 1 (Fml) Sorghum
propinquum cDNA, mRNA sequence.

ACCESSION BF422183
VERSION BF422183.1 GI:11410172

KEYWORDS EST.
SOURCE Sorghum propinquum

ORGANISM Sorghum propinquum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE 1 (bases 1 to 614)
Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M., Marsala, C. and
Pratt, L.H.

TITLE An EST database from Sorghum: floral-induced meristems
JOURNAL Unpublished (2000)
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu

FEATURES
source
1. 614
Location/Qualifiers
/organism="Sorghum propinquum"
/mol_type="mRNA"
/db_xref="taxon:132711"
/clone_lib="floral-induced Meristem 1 (Fml)"
/note="Organ: Floral-induced meristems; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
BclRI; mature plants were placed in a growth chamber for
15 days with 16 hr darkness and 8 hr light (flowering is
induced by short-day conditions); 16 days after being
returned to the greenhouse under natural long days during
late April/early May, meristems were harvested. The
library was made from poly-A RNA in the cloning vector
lambda Zap II. Clones to be sequenced were prepared by
mass excision."

ORIGIN

Query Match 100.0%; Score 14; DB 2; Length 614;
Best Local Similarity 78.6%; Pred. No. 1.6e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGUACUGAACUG 14
||:|||||:|
Db 23 CCGACTGCACCTCG 36

RESULT 9
CZ660542
LOCUS 640 bp DNA linear GSS 07-JUL-2005
DEFINITION OM_Ba0212H16.f OM_Ba Oryza minuta genomic clone OM_Ba0212H16 5',
genomic survey sequence.
ACCESSION CZ660542
VERSION CZ660542.1 GI:70234850
KEYWORDS GSS.

SOURCE
ORGANISM Oryza minuta

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 640)
Kim, H., Collura, K., Wisesoteki, M., Byrne, M., Stum, D., Smart, D.,
Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Soderlund, C. and
Wing, R.

TITLE OMB (Oryza Map Alignment Project) - Arizona Genomics Institute
JOURNAL Unpublished (2005)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
Plate: 0212 row: H column: 16
Class: BAC ends.

FEATURES
source
1. 640
Location/Qualifiers
/organism="Oryza minuta"
/mol_type="genomic DNA"
/db_xref="taxon:63629"
/clone="OM_Ba0212H16"
/rissue_type="leaves"
/lab_host="DH10B"
/clone_lib="OM_Ba"
/note="Vector: pCUGIBAC1; Site_1: HindIII; Site_2:
HindIII"

ORIGIN

Query Match 100.0%; Score 14; DB 10; Length 640;
Best Local Similarity 78.6%; Pred. No. 1.6e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGUACUGAACUG 14
||:|||||:|
Db 282 CCGACTGCACCTCG 295

RESULT 10

LOCUS BZ563771/c 670 bp DNA linear GSS 17-DEC-2002
DEFINITION pacs2-164_4414.x3 pacs2-164 Pseudomonas aeruginosa genomic clone
pacs2-164_4414, genomic survey sequence.
ACCESSION BZ563771
VERSION BZ563771.1 GI:27188318

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 670)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence Variation among multiple isolates of
Pseudomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond

JOURNAL
COMMENT Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun;

FEATURES

source
1. 670
Location/Qualifiers
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="2-164"

ORIGIN

/db xref="taxon:287"
/clone="pac2-164.4414"
/clone_lib="pac2-164"
/note="clinical isolate 2-164 whole genomic shotgun library."

Query Match 100.0%; Score 14; DB 9; Length 670;
Best Local Similarity 78.6%; Pred. No. 1.6e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCACTCG 14
||:|||||:
Db 417 CGTACTGCACTCG 404

RESULT 11
BH565722 711 bp DNA linear GSS 14-DEC-2001
LOCUS BH565722/c
DEFINITION BOGPP49R BOG Brassica oleracea genomic clone BOGPP49, genomic survey sequence.

ACCESSION BH565722
VERSION BH565722.1 GI:17817562
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eustosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 711)
Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S., Ulteback, T.R., Mortman, J.R., White, O.R. and Town, C.D.
Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis
Genome Res. 15 (4), 487-495 (2005)

JOURNAL PUBMED 15805490

COMMENT Contact: Chris Town
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source Location/Qualifiers

1..711
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOGPP49"
/clone_lib="BOG"
/note="Vector: PHOS1; Site 1: BactXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BactXI linkers"

ORIGIN

Query Match 100.0%; Score 14; DB 9; Length 711;
Best Local Similarity 78.6%; Pred. No. 1.6e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCACTCG 14
||:|||||:
Db 165 CGTACTGCACTCG 152

RESULT 12
CF849609/c 730 bp mRNA linear EST 30-OCT-2003
LOCUS CF849609
DEFINITION pma011c23f USDA-IPAFs: Expression of Phytophthora sojae genes during infection and propagation_sma Phytophthora sojae cDNA clone sma011c23 5, mRNA sequence.
ACCESSION CF849609

VERSION CF849609.1 GI:38065263
KEYWORDS EST.
SOURCE Phytophthora sojae
ORGANISM Phytophthora sojae
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae; Phytophthora.

REFERENCE
AUTHORS 1 (bases 1 to 730)
TITLE Tyler, B.
JOURNAL Tyler, B. Not Published
COMMENT Unpublished (2003)
Contact: Tyler B
Tyler lab

VBI
1880 Pratt Dr., Blacksburg, VA 24061, USA
Tel: 540-231-7318
Email: bmtyley@vt.edu

PCR Primers
FORWARD: BK reverse primer
BACKWARD: BK reverse primer
Plate: 011 row: C column: 23
Seq primer: BK reverse primer
High quality sequence stop: 730.

FEATURES

source Location/Qualifiers
1..730
/organism="Phytophthora sojae"
/mol_type="mRNA"
/db_xref="taxon:67593"
/clone="sma011c23"
/tissue_type="mycelium"
/cell_line="P6497"
/dev_stage="mycelium"
/lab_host="synthetic medium"
/clone_lib="USDA-IPAFs: Expression of Phytophthora sojae genes during infection and propagation_sma"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 100.0%; Score 14; DB 7; Length 730;
Best Local Similarity 78.6%; Pred. No. 1.6e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCACTCG 14
||:|||||:
Db 725 CGTACTGCACTCG 712

RESULT 13
CM525116/c 751 bp DNA linear GSS 08-OCT-2004
LOCUS CM525116
DEFINITION OP_Ba0049M10.f OP_Ba Oryza punctata genomic clone OP_Ba0049M10 5', genomic survey sequence.

ACCESSION CM525116
VERSION CM525116.1 GI:53999338
KEYWORDS GSS.
SOURCE Oryza punctata
ORGANISM Oryza punctata

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriocaridaceae; Oryzaceae; Oryza.

1 (bases 1 to 751)
SanMiguel, P., Westerman, R., Kim, H., Yu, Y., Wisotski, M., Yost, D., Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C., Wang, R. and Jackson, S.A.
OMAP Project - Purdue University
Unpublished (2004)
Contact: Scott A. Jackson
Jackson Laboratory
Purdue University
915 W. State St., West Lafayette, IN 47907, USA
Tel: 7654963621
Fax: 7654967255
Email: sjackson@purdue.edu

Basecalling by phred version 0.020425.c. This sequence was derived

from the raw sequence read by clipping with Lucy version 1.19s.
Bases 52-802 of the raw sequence (length 1302) were retained after
clipping

PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161000 Std Error: 0.00
Plate: 0049 row: M column: 10
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.

FEATURES

source

Location/Qualifiers
1..751
/organism="Oryza punctata"
/mol_type="genomic DNA"
/db_xref="taxon:4537"
/clone="OP_Ba0049M10"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_1lb="OP_Ba"
/note="Vector: PACIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 100.0%; Score 14; DB 10; Length 751;
Best Local Similarity 78.6%; Pred. No. 1.6e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14
||:|||||:
Db 633 CGTACTGCACTCG 620

RESULT 14

LOCUS

BH435200 759 bp DNA linear GSS 12-DEC-2001
BOGZM10TR BOGZ Brassica oleracea genomic clone BOGZM10, genomic
survey sequence.

ACCESSION BH435200
VERSION BH435200.1 GI:117620921

KEYWORDS

SOURCE

ORGANISM Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eustosida II; Brassicales; Brassicaceae; Brassica.

REFERENCE

AUTHORS

1 (bases 1 to 759)
Ayala, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,
Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.

TITLE

Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis

JOURNAL

PUBMED

Genome Res. 15 (4), 487-495 (2005)

COMMENT

Other_GSSs: BOGZM10TF
Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

FEATURES

source

1..759
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOGZM10"
/clone_1lb="BOGZ"
/note="Vector: PHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into PHOS1 using BstXI linkers"

ORIGIN

Query Match 100.0%; Score 14; DB 9; Length 759;
Best Local Similarity 78.6%; Pred. No. 1.6e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14
||:|||||:
Db 432 CGTACTGCACTCG 445

RESULT 15

LOCUS

CW528167 776 bp DNA linear GSS 08-OCT-2004
OP_Ba0029D07.r OP_Ba Oryza punctata genomic clone OP_Ba0029D07
3,' genomic survey sequence.

ACCESSION

VERSION

CW528167.1 GI:54002389

KEYWORDS

SOURCE

ORGANISM

Oryza punctata
Oryza punctata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bharatoidae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 776)
San Miguel, P., Westerman, R., Kim, H., Yu, Y., Misosetki, M., Yost, D.,
Stum, D., Rao, K., Luo, M., Jetty, R., Kudra, D., Muller, C.,
Hatfield, J., Soderlund, C., Wing, R. and Jackson, S.A.

OMAP Project - Purdue University
Unpublished (2004)

Contact: Scott A. Jackson

Jackson Laboratory

Purdue University

915 W. State St., West Lafayette, IN 47907, USA

Tel: 765/4963621

Fax: 765/4967255

Email: sjackson@purdue.edu

Basecalling by phred version 0.020425.c. This sequence was derived
from the raw sequence read by clipping with Lucy version 1.19s.
Bases 120-895 of the raw sequence (length 1412) were retained after
clipping.

PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA

Insert Length: 161000 Std Error: 0.00

Plate: 0029 row: D column: 07

Seq primer: CAC TCA TTA GGC ACC CCA

Class: BAC ends.

Location/Qualifiers

1..776

/organism="Oryza punctata"

/mol_type="genomic DNA"

/db_xref="taxon:4537"

/clone="OP_Ba0029D07"

/tissue_type="young leaves"

/lab_host="DH10B-T1 phage resistant"

/clone_1lb="OP_Ba"

/note="Vector: PACIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 100.0%; Score 14; DB 10; Length 776;
Best Local Similarity 78.6%; Pred. No. 1.6e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14
||:|||||:
Db 663 CGTACTGCACTCG 650

RESULT 16

LOCUS

CW780591 851 bp DNA linear GSS 19-NOV-2004
OP_Ba0084F10.f OP_Ba Oryza punctata genomic clone OP_Ba0084F10
5,' genomic survey sequence.

ACCESSION

VERSION

CW780591

VERSION CW780591.1 GI:55849895
KEYWORDS GSS.
SOURCE Oryza punctata
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 851)
Santiguel, P., Westerman, R., Kim, H., Yu, Y., Wisotski, M., Yost, D., Stum, D., Rao, K., Luo, M., Jettly, R., Kudrna, D., Miller, C., Hatfield, J., Soderlund, C., Wing, R. and Jackson, S.A.
OMP Project - Purdue University
Unpublished (2004)
Contact: Scott A. Jackson
Jackson Laboratory
Purdue University
915 W. State St., West Lafayette, IN 47907, USA
Tel: 7654963621
Fax: 7654967255
Email: sjackson@purdue.edu

TITLE
JOURNAL
COMMENT

Baserecalling by phred version 0.020425.c. This sequence was derived from the raw sequence read by clipping with Lucy version 1.19s. Bases 36-886 of the raw sequence (length 1035) were retained after clipping.
plate: 0084 row: F column: 10
Seq primer: TAA TAC GAC TCA CTA TAG CG
Class: BAC ends.

ORIGIN
Location/Qualifiers
1..851
/organism="Oryza punctata"
/mol_type="genomic DNA"
/db_xref="taxon:4537"
/clone="OP_Ba0084F10"
/issue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_1lb="OP_Ba"
/note="Vector: pAG1BAC1; Site_1: HindIII; Site_2: HindIII"

Query Match 100.0%; Score 14; DB 10; Length 851;
Best Local Similarity 78.6%; Pred. No. 1.6e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUGC 14
||:|||||:
Db 662 CGTACTGCACCTCG 649

RESULT 17
CWS19957/c 855 bp DNA linear GSS 08-OCT-2004
LOCUS OP_Ba0023E10.f OP_Ba Oryza punctata genomic clone OP_Ba0023E10
DEFINITION 5', genomic survey sequence.
ACCESSION CWS19957
VERSION CWS19957
KEYWORDS GSS.
SOURCE Oryza punctata
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 855)
Santiguel, P., Westerman, R., Kim, H., Yu, Y., Wisotski, M., Yost, D., Stum, D., Rao, K., Luo, M., Jettly, R., Kudrna, D., Miller, C., Hatfield, J., Soderlund, C., Wing, R. and Jackson, S.A.
OMP Project - Purdue University
Unpublished (2004)
Contact: Scott A. Jackson
Jackson Laboratory
Purdue University
915 W. State St., West Lafayette, IN 47907, USA
Tel: 7654963621
Fax: 7654967255

Email: sjackson@purdue.edu
Baserecalling by phred version 0.020425.c. This sequence was derived from the raw sequence read by clipping with Lucy version 1.19s. Bases 41-895 of the raw sequence (length 1396) were retained after clipping.
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG CG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161000 Std Error: 0.00
Plate: 0023 row: F column: 10
Seq primer: TAA TAC GAC TCA CTA TAG CG
Class: BAC ends.

ORIGIN
Location/Qualifiers
1..855
/organism="Oryza punctata"
/mol_type="genomic DNA"
/db_xref="taxon:4537"
/clone="OP_Ba0023E10"
/issue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_1lb="OP_Ba"
/note="Vector: pAG1BAC1; Site_1: HindIII; Site_2: HindIII"

Query Match 100.0%; Score 14; DB 10; Length 855;
Best Local Similarity 78.6%; Pred. No. 1.6e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUGC 14
||:|||||:
Db 661 CGTACTGCACCTCG 648

RESULT 18
BP031922/c 859 bp mRNA linear EST 10-OCT-2000
LOCUS 60159533F1 NIH_MGC_58 Homo sapiens cDNA IMAGE:3829137 5',
DEFINITION mRNA sequence.
ACCESSION BP031922
VERSION BP031922.1 GI:10739634
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 859)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rmml.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Plate: L10M501 row: a column: 10
High quality sequence stop: 507.
Location/Qualifiers
1..859
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3829137"
/issue_type="hypemephroma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lb="NIH MGC 58"
/note="Organ: kidney; Vector: pNIR-LIB (Clontech); Site_1: SfiI (ggcgcctcgcc); Site_2: SfiI (ggcctatggcc); Site_3: SfiI (ggcgcctcgcc); Site_4: SfiI (ggcctatggcc); Site_5: Double-stranded cDNA was prepared from cell line RNA. 5'

REFERENCE 1 (bases 1 to 943)
 AUTHORS Cameron, R.A., Mahatras, G., Rast, J.P., Martinez, P., Biondi, T.R., Swartzell, S., Wallace, J.C., Pousetka, A.J., Livingston, B.T., Wray, G.A., Ettensohn, C.A., Lemach, H., Bitten, R.U., Davidson, E.H. and Hood, L.
 TITLE A sea urchin genome project: Sequence scan, virtual map, and additional resources
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
 COMMENT 10920195
 CONTACT: Cameron, R.A., Davidson, E.H., Hood, L.
 Division of Biology 156-29
 Pasadena Institute of Technology
 Pasadena California 91125, USA
 Tel: (626) 395-8421
 Fax: (626) 793-3047
 Email: acameron@caltech.edu
 Plate: 106 row: M column: 24
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 943.
 Location/Qualifiers
 1..943
 /organism="Strongylocentrotus purpuratus"
 /mol_type="genomic DNA"
 /db_xref="taxon:7668"
 /clone="Plate=106 Col=24 Row=M"
 /clone_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
 /note="Organ: sperm; Vector: BACs; 6; BAC Clones in E-Coli DH10B"

ORIGIN
 Query Match 100.0%; Score 14; DB 9; Length 943;
 Best Local Similarity 78.6%; Pred. No. 1.6e+03;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACTCG 14
 ||:|||||:
 Db 627 CGTACTGCAACTCG 614

RESULT 22
 DN63741 1195 bp mRNA linear EST 30-MAR-2005
 LOCUS CGX90-B12.5 SHGC-CGX Gasterosteus aculeatus cDNA clone
 DEFINITION
 CGX90-B12.5, mRNA sequence.
 ACCESSION DN63741
 VERSION DN63741.1 GI:62050365
 KEYWORDS
 SOURCE Gasterosteus aculeatus (three spined stickleback)
 ORGANISM
 Gasterosteus aculeatus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes; Gasterosteidae; Gasterosteus.
 1 (bases 1 to 1195)
 Kingley, D.M., Pelichel, C., Balabhadra, S., Grimwood, J., Dickson, M., Schmutz, J., and Myers, R.M.
 TITLE Expressed sequence tags from Gasterosteus aculeatus
 JOURNAL Unpublished (2003)
 COMMENT Contact: Grimwood, Jane
 Stanford Human Genome Center
 Stanford University School of Medicine
 975 S California Ave, Palo Alto, CA 94304, USA
 Tel: 650 320 5917
 Fax: 650 320 5801
 Email: jane@hgc.stanford.edu
 Plate: 90
 High quality sequence stop: 726.
 Location/Qualifiers
 1..1195
 /organism="Gasterosteus aculeatus"
 /mol_type="mRNA"

REFERENCE 1 (bases 1 to 943)
 AUTHORS Cameron, R.A., Mahatras, G., Rast, J.P., Martinez, P., Biondi, T.R., Swartzell, S., Wallace, J.C., Pousetka, A.J., Livingston, B.T., Wray, G.A., Ettensohn, C.A., Lemach, H., Bitten, R.U., Davidson, E.H. and Hood, L.
 TITLE A sea urchin genome project: Sequence scan, virtual map, and additional resources
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
 COMMENT 10920195
 CONTACT: Cameron, R.A., Davidson, E.H., Hood, L.
 Division of Biology 156-29
 Pasadena Institute of Technology
 Pasadena California 91125, USA
 Tel: (626) 395-8421
 Fax: (626) 793-3047
 Email: acameron@caltech.edu
 Plate: 106 row: M column: 24
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 943.
 Location/Qualifiers
 1..943
 /organism="Strongylocentrotus purpuratus"
 /mol_type="genomic DNA"
 /db_xref="taxon:7668"
 /clone="Plate=106 Col=24 Row=M"
 /clone_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
 /note="Organ: sperm; Vector: BACs; 6; BAC Clones in E-Coli DH10B"

ORIGIN
 Query Match 100.0%; Score 14; DB 8; Length 1195;
 Best Local Similarity 78.6%; Pred. No. 1.6e+03;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACTCG 14
 ||:|||||:
 Db 221 CGTACTGCAACTCG 234

RESULT 23
 DN63186 1200 bp mRNA linear EST 29-MAR-2005
 LOCUS CFM12-D08.5 SHGC-CFM Gasterosteus aculeatus cDNA clone
 DEFINITION
 CFM12-D08.5, mRNA sequence.
 ACCESSION DN63186
 VERSION DN63186.1 GI:61983242
 KEYWORDS
 SOURCE Gasterosteus aculeatus (three spined stickleback)
 ORGANISM
 Gasterosteus aculeatus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes; Gasterosteidae; Gasterosteus.
 1 (bases 1 to 1200)
 Kingley, D.M., Pelichel, C., Balabhadra, S., Grimwood, J., Dickson, M., Schmutz, J., and Myers, R.M.
 TITLE Expressed sequence tags from Gasterosteus aculeatus
 JOURNAL Unpublished (2003)
 COMMENT Contact: Grimwood, Jane
 Stanford Human Genome Center
 Stanford University School of Medicine
 975 S California Ave, Palo Alto, CA 94304, USA
 Tel: 650 320 5917
 Fax: 650 320 5801
 Email: jane@hgc.stanford.edu
 Plate: 12
 High quality sequence stop: 855.
 Location/Qualifiers
 1..1200
 /organism="Gasterosteus aculeatus"
 /mol_type="mRNA"
 /strain="Conner Creek sticklebacks, WA USA"
 /db_xref="taxon:69293"

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/clone="CFM12-D08"
/sex="mixed male and female"
/tissue_type="gillls"
/dev_stage="adult"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="SHGC-CFM"
/notes="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTAGTCTAGATCGGAGCGGCCGCC(T)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5' prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at: http://www.openbiosystems.com/cdna_library_construction_fa 9.php#8 The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems: http://www.openbiosystems.com/stickleback"

```

ORIGIN

Query Match 100.0%; Score 14; DB 8; Length 1200;
 Best Local Similarity 78.6%; Pred. No. 1.6e+03;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14
 ||:|||||:
 DB 240 CGTACTGCACTCG 253

RESULT 24
 DN738151 1211 bp mRNA linear EST 31-MAR-2005
 LOCUS CNB96-H05.y1d-8 SHGC-CNB *Gasterosteus aculeatus* cDNA clone
 DEFINITION DN738151
 ACCESSION DN738151
 VERSION DN738151.1 GI:62115161
 KEYWORDS EST.
 SOURCE *Gasterosteus aculeatus* (three spined stickleback)
 ORGANISM *Gasterosteus aculeatus*
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; *Gasterosteiformes*; *Gasterosteidae*; *Gasterosteus*.
 1 (bases 1 to 1211)
 Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M., Schmutz,J. and Myers,R.M.
 TITLE Expressed sequence tags from *Gasterosteus aculeatus*
 JOURNAL Unpublished (2003)
 COMMENT Contact: Grimwood, Jane
 Stanford Human Genome Center
 Stanford University School of Medicine
 975 S California Ave, Palo Alto, CA 94304, USA
 Tel: 650 320 5917
 Fax: 650 320 5801
 Email: jane@hngc.stanford.edu
 Plate: 96
 High quality sequence start: 2
 High quality sequence stop: 790.
 Location/Qualifiers
 1..1211
 /organism="*Gasterosteus aculeatus*"
 /mol_type="mRNA"
 /strain="Conner Creek sticklebacks, WA USA"
 /db_xref="taxon:69293"
 /clone="CNB96-H05"

FEATURES

```

/sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="SHGC-CNB"
/notes="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTAGTCTAGATCGGAGCGGCCGCC(T)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5' prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at: http://www.openbiosystems.com/cdna_library_construction_fa 9.php#8 The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems: http://www.openbiosystems.com/stickleback"

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ORIGIN

Query Match 100.0%; Score 14; DB 8; Length 1211;
 Best Local Similarity 78.6%; Pred. No. 1.6e+03;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14
 ||:|||||:
 DB 237 CGTACTGCACTCG 250

RESULT 25
 DN660653 1289 bp mRNA linear EST 28-MAR-2005
 LOCUS CEC48-A03.y1d-8 SHGC-CRC *Gasterosteus aculeatus* cDNA clone
 DEFINITION CEC48-A03 5', mRNA sequence.
 ACCESSION DN660653
 VERSION DN660653.1 GI:61965902
 KEYWORDS EST.
 SOURCE *Gasterosteus aculeatus* (three spined stickleback)
 ORGANISM *Gasterosteus aculeatus*
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; *Gasterosteiformes*; *Gasterosteidae*; *Gasterosteus*.
 1 (bases 1 to 1289)
 Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M., Schmutz,J. and Myers,R.M.
 TITLE Expressed sequence tags from *Gasterosteus aculeatus*
 JOURNAL Unpublished (2003)
 COMMENT Contact: Grimwood, Jane
 Stanford Human Genome Center
 Stanford University School of Medicine
 975 S California Ave, Palo Alto, CA 94304, USA
 Tel: 650 320 5917
 Fax: 650 320 5801
 Email: jane@hngc.stanford.edu
 Plate: 48
 High quality sequence start: 806.
 Location/Qualifiers
 1..1289
 /organism="*Gasterosteus aculeatus*"
 /mol_type="mRNA"
 /strain="Conner Creek sticklebacks, WA USA"
 /db_xref="taxon:69293"
 /clone="CEC48-A03"
 /sex="mixed male and female"
 /tissue_type="skin"

FEATURES

```
/dev stage="adult"
/clone_lib="DH10B (T1 phage resistant)"
/clone="vector: Express 1; Total and poly A+ RNA was
isolated from the indicated stickleback tissue, and a cDNA
library was constructed in the Express 1 plasmid vector by
Open Biosystems. First strand cDNA synthesis was primed
with an 54 bp linker primer containing an oligodT sequence
preceded by a synthetic NotI site (first strand primer:
5'-GACTACTCTTACATCGGAGCGCCGCC(T)25-3'). Following
second strand synthesis, cDNAs were made blunt at the end
corresponding to the original 5 prime end of mRNA, and
cloned directionally into the NotI and EcoRV sites of
Express 1. Note that the EcoRV site is typically destroyed
in the blunt end cloning, leaving a junction of the form
'xxATTC' (where is ATC is the second half of the EcoRV
site, and xxx is derived from the cDNA sequence). A map of
the Express 1 vector is available at:
http://www.openbiosystems.com/cdna_library_construction_fa
q.php#8 The primary library was transformed and amplified
in DH10B (T1 phage resistant) bacteria. Clones available
from Open Biosystems:
http://www.openbiosystems.com/stickleback"
```

ORIGIN

Query Match 100.0%; Score 14; DB 8; Length 1289;
Best Local Similarity 78.6%; Pred. No. 1.6e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUCG 14
||:|||||:
Db 18 CGTACTGCAACTCG 31

RESULT 26 157 bp DNA linear GSS 23-JUN-1999
A0661032/2 Sheared DNA-11G3.TF Sheared DNA Trypanosoma brucei genomic clone
LOCUS Sheared DNA-11G3, genomic survey sequence.
DEFINITION
ACCESSION A0661032
VERSION A0661032.1 GI:5168800
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE

AUTHORS

TITLE

1 (bases 1 to 157)
El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C.,
Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S.,
Donelson, J., Fraser, C. and Adams, M.
Determination of clone end sequences from Trypanosoma brucei GUTat
10.1 sheared DNA library

JOURNAL

Unpublished (1999)
Other GSSs: Sheared DNA-11G3.TF
Contact: Najib M. El-Sayed
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: nelsayed@tigr.org

COMMENT

Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tldb/mdb/lbdb/.
Seq primer: M13-Forward
Class: Shotgun.

FEATURES

source

1..157 location/Qualifiers
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREJ927/4 GUTat 10.1"
/db_xref="taxon:5691"

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/clone="Sheared DNA-11G3"
/clone_lib="Sheared DNA"
/clone="vector: pUC19; Site 1; SmaI; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREJ927/4 GUTat 10.1) was mechanically
sheared to give a tight size distribution (approx 2 kb).
The v + 1 method used for the library construction is
described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun
sequencing projects. In Genome Sequencing: A Practical
Approach, eds. M. Vaubin and B. Barrell, Oxford University
Press, 1999)."
```

ORIGIN

Query Match 92.9%; Score 13; DB 9; Length 157;
Best Local Similarity 76.9%; Pred. No. 6.3e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13
||:|||||:
Db 30 CGTACTGCAACTC 18

RESULT 27 205 bp mRNA linear EST 12-JUL-2004
CR555866 DKFZp469B092_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
LOCUS DKFZp469B092_5', mRNA sequence.
DEFINITION
ACCESSION CR555866
VERSION CR555866.1 GI:50249468
KEYWORDS EST.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Pongo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 205)
Bloecker, H., Boecker, M., Brandt, P., Mewes, H.W., Weill, B., Amld, C.,
Oeinger, A., Robo, G., Han, M. and Wiemann, S.
Pongo pygmaeus mRNA (Bloecker, H., Boecker, M., Brandt, P., et al.)
Unpublished (2004)
Contact: MIPS
MIPS
Ingolstaedter Landstr. 1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert Cloned from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email: s.wiemann@dkfz-heidelberg.de; sequenced by GSF (National
Research Centre for Biotechnology Ltd., Braunschweig/Germany)
Within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZp469B092) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clonerzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/projects/cdna/.

FEATURES

source

1..205 location/Qualifiers
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp469B092"
/clone_type="kidney"
/dev stage="adult"
/lab_host="DH10B"
/clone_lib="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_1: SfiIa; Site_2: SfiIb"

ORIGIN

Query Match 92.9%; Score 13; DB 7; Length 205;
Best Local Similarity 76.9%; Pred. No. 6.4e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13

Db ||:||||:|
49 CGTACTGCACTC 37

RESULT 28 255 bp mRNA linear EST 06-MAY-2003
BUE40724
LOCUS mgmk001XH17.f.b pmk1 in plasmidcriptii ak(-) plasmid Magnaporthe
DEFINITION grisea cDNA clone mgmk001XH17 5', mRNA sequence.
ACCESSION BUE40724
VERSION GI:30402792
KEYWORDS EST.

ORGANISM Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnetorthe grisea

REFERENCE Baktayota, Fungi; Ascomycota; Pezizomycotina, Sordariomycetes;
Sordariomycetes Incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 255)
AUTHORS Bbbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G.,
Bhatterai, K. and Dean, R.A.

TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe
grisea

JOURNAL Unpublished (2002)
COMMENT On Sep 30, 2002 this sequence version replaced gi:23353050.
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu

Chromatogram file of this sequence is available, see contact
person.Best nr hit (April. 22, 2003) ref|NP_620661.1| AV2 [South
African cassava mosaic virus] >gi|70. . . 32 3.1

PCR PRIMERS
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgmk001 row: H column: 17
Seq primer: T3

FEATURES
source Location/Qualifiers

1..255
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="NN95"
/db_xref="taxon:148305"
/clone="mgmk001XH17"
/sex="Mati-1 hermaphrodite"
/cell_type="germinated conidia"
/note="Vector: pBluescriptSK. Site_1: EcoRI, Site_2: XhoI;
Conidia germinated in hydrophobic surface membrane in 27C
for 12 hours. NN95 is a hygromycin phosphotransferase gene
replacement of the PMK1 MAP kinase gene in the Guy11
strain background (Xu and Hamer, 1996. Genes & Dev.
10:2696). Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimmed
according to the alignment, otherwise sequence quality was
assessed using phredPhrap version 991019 and trimmed
according to phd files (0.05) and for vector seq."

ORIGIN
Query Match 92.9%; Score 13; DB 5; Length 255;
Best Local Similarity 76.9%; Pred. No. 6.4e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 2 GUACUGCACTC 14
||:||||:|
224 GTCAGTCACTC 236

RESULT 29 285 bp mRNA linear EST 06-NOV-2002
CA374069
LOCUS CA374069

DEFINITION 648371 NCCGWA 1RT Oncorhynchus mykiss cDNA clone 1RT16K01_A_F01 5',
mRNA sequence.

ACCESSION CA374069
VERSION CA374069.1 GI:24690094
KEYWORDS EST.

ORGANISM Oncorhynchus mykiss (rainbow trout)
Oncorhynchus mykiss

REFERENCE Baktayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 285)
AUTHORS Rexroad, C.B. 3rd, Lee, Y., Keele, J.W., Karamycheva, S., Brown, G.,
Koop, B., Gahr, S.A., Palti, Y. and Quackenbush, J.

TITLE Sequence analysis of a rainbow trout cDNA library and creation of a
gene index

JOURNAL Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)
COMMENT Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351

Email: crexroad@nccgwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified by
cross match v0.990329.

Seq primer: AGCGGATACCAATTTCACACAGA.
Location/Qualifiers

1..285
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="1RT16K01_A_F01"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_11b="NCCGWA 1RT"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
library made from pooled tissue from brain, gill, liver,
spleen, muscle, and kidney."

ORIGIN

Query Match 92.9%; Score 13; DB 6; Length 285;
Best Local Similarity 76.9%; Pred. No. 6.5e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1 CGUACUGCACTC 13
||:||||:|
229 CGTACTGCACTC 241

RESULT 30 290 bp DNA linear GSS 02-NOV-2004
CW452335
LOCUS fbb0001f192n03k0 Sorghum methylation filtered library (libid: 104)
DEFINITION Sorghum bicolor genomic clone fbb0001f192n03, genomic survey
sequence.

ACCESSION CW452335
VERSION CW452335.1 GI:55200296
KEYWORDS GSS.

ORGANISM Sorghum bicolor (sorghum)
Sorghum bicolor

REFERENCE Baktayota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 290)
AUTHORS Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,
Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,
McKenamy, J., Smith, M., Holeman, H., Roe, B.A., Wiley, G., Korff, I.F.,
Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddelion, J.A. and
Martensen, R.A.

TITLE Sorghum genome sequencing by methylation filtration
JOURNAL Plos Biol. 3 (1), e13 (2005)
PUBMED 15660154
COMMENT Contact: Bedell JA

Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975

FEATURES

Bouice

```

/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="Atx623"
/db_xref="taxon:4558"
/clone="fab001f1r2n03"
/clone_lib="Sorghum methylation filtered library (libid:
104)"
/notes="Organ: leaf, Vector: pBSK(-); Site_1: HincII; DNA
prepared from purified nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to 5
kb fraction, ligated into HincII-digested pBSK(-) vector
and electroporated into E. coli cells. This is a
methylation filtered library."

```

ORIGIN

Query Match	92.9%	Score 13	DB 10	Length 230
Best Local Similarity	76.9%	Pred. No. 6.5e+03		
Matches 10	Conservative 3	Mismatches 0	Indels 0	Gaps 0

Qy	1	CGUACUGCACTUC	13
		: : : : :	
Db	164	CGTACTGCAACTC	176

RESULT 31	CM772355	LOCUS	DEFINITION
CM772355	292 bp	DNA	linear
CM772355	CG_BBA0089B23.f	CG_BBA_Oryza glaberrima	genomic clone
CM772355	5', genomic survey sequence.		CG_BBA0089B23

REFERENCE
AUTHORS

1 (bases 1 to 292)
Kim, H., Yu, Y., Wisotsakul, M., Byrne, M., Stum, D., Smatt, D., Rao, K.,
Luo, M., Jett, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C.
and Wing, R.

TITLE	OMAP
JOURNAL	Unpublished (2004)
COMMENT	Contact: Rod A. Wing

Sources

```
Location/Qualifiers
1. 292
/organism="Oryza glaberrima"
/mol_type="genomic DNA"
/db_xref="taxon:4538"
/clone="OG_BBA0089B23"
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/tissue_type="young leaves"
/lab_host="DH10B T1 phage resistant"
/clone_id="OG_BBa"
/note="Vector: pGIRBAC1; site_1: HindIII; site_2: HindIII"
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ORIGIN

Query Match	92.9%	Score 13;	DB 10;	Length 292;
Best Local Similarity	76.9%	Pred. No. 6.5e+03;		
Matches 10;	Conservative 3;	Mismatches 0;	Indels 0;	Gaps 0

QY	2	GUACUGCAACUCG	14
		: : : : : :	
Db	55	GTA CTGCAACTCG	67

RESULT 32					
AJ578024					
LOCUS					
DEFINITION	AJ578024	344 bp	mRNA	linear	EST 04-AUG-2001
	AJ578024		<i>Platichthys flesus</i>	liver sexually	<i>Platichthys</i>
			<i>flesus</i> cDNA clone BR265	mRNA sequence.	

JOURNAL
Unpublished (2003)
COMMENT
Contact: Shearer I

FEATURES	location/Qualifiers
source	1. ,344

ORIGIN

Query Match	92.9%;	Score 13;	DB 1;	Length 344;
Best Local Similarity	76.9%;	Pred. No. 6.5e+03;		
Matches 10;	Conservative 3;	Mismatches 0;	Indels 0;	Gaps 0.

QY	2	GUACUGCAACTUCG	14
		: : : : : :	
Db	271	GTACTGCAACTCG	28

RESULT 33					
BY11672					
LOCUS	345 bp	mRNA	linear	EST 07-DEC-2007	
DEFINITION	BY11672 RIKEN full-length enriched, 15 days embryo whole body Mus musculus cDNA U33004/GI7 5', mRNA sequence.				

Bt11672
Bt11673
Bt11674
Bt11675
Bt11676
Bt11677
EST.
Mus musculus (*house mouse*)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Synbranchia; Euthera; Euarchontoglires; Glires; Rodentia;
Cognathia; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 345)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaio, H., Osato, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojohori, T., Baldarelli, R., Hill, D. P., Bul, C., Hume, D. A., Quackenbush, J., Schiraldi, L. M., Kanagin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Brad, D., Brusic, V., Choibha, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, J. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Kongaya, A., Kurochkin, I. V., Lee, Y., Lennard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numa, K., Okido, T., Pavan, W. J., Pettes, G., Pessio, G., Petrovsky, N., Pillai, R., Pontius, J. O., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Vercaro, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wyszynski, B. A., Yang, J., Yang, I., Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carrinchi, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E., and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

TITLE
JOURNAL

12466851

COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/
Alizawa, K., Akimura, T., Arakawa, T., Carrinchi, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Kono, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watanabe, A., Muramatsu, Y. and Hayashizaki, Y. Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES
SOURCE

Location/Qualifiers
1. 345
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="1330047G17"
/tissue_type="whole body"
/dev_stage="15 days embryo"

ORIGIN

/clone lib="RIKEN full-length enriched, 15 days embryo whole body"

Query Match 92.9%; Score 13; DB 5; Length 345;
Best Local Similarity 76.9%; Pred. No. 6.5e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 202 GTCCTGCAACTCG 214

RESULT 34

DR073074

LOCUS

DR073074 364 bp mRNA linear EST 06-JUN-2005
1k85f03.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3, mRNA
sequence.

DEFINITION

ACCESSION

DR073074 GI:67050923

VERSION

DR073074.1 GI:67050923

KEYWORDS

EST.
Ginkgo biloba (maidenhair tree)

ORGANISM

Ginkgo biloba
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Ginkgoales; Ginkgoaceae; Ginkgo.

REFERENCE

1 (bases 1 to 364)
Brenner, E.D., Tlupova, R. W., Runko, S. J., Katari, M. S., Dedhia, N. N., O'Shaughnessy, A. L., Ball, J. A., Martienssen, R. A., McCombie, R. W., Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Ginkgo female leaf (NYBG)
Unpublished (2005)

AUTHORS

Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21m1univRev.

TITLE

Unpublished (2005)

JOURNAL

Location/Qualifiers
1. 364
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
/clone lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Strain: ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

COMMENT

Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21m1univRev.

FEATURES

source
1. 364
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
/clone lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Strain: ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

ORIGIN

Query Match 92.9%; Score 13; DB 8; Length 364;
Best Local Similarity 76.9%; Pred. No. 6.5e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db

258 GTCCTGCAACTCG 270

RESULT 35

CV724006 366 bp mRNA linear EST 04-NOV-2004
root--05-105.g1 Rice root lambda phage cDNA library (root) Oryza
sativa (japonica cultivar-group) cDNA clone root--05-105, mRNA
sequence.

DEFINITION

CV724006 GI:55411630

VERSION

CV724006.1 GI:55411630

KEYWORDS

EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

ORGANISM

Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 366)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source

1. 366
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:3947"
/clone="root-05-105"
/issue_type="root"
/dev_stage="14 days after germination"
/lab_host="B.colli SOLR"
/clone_id="Rice root lambda phage cDNA library (root)"
/note="Vector: Bluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP vector at 5'
end with EcoRI and 3' end with XhoI site."

ORIGIN

Query Match 92.9%; Score 13; DB 7; Length 366;
Best Local Similarity 76.9%; Pred. No. 6.5e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCACTCG 14
||:|||||||
182 GTACTGCACTCG 194

RESULT 36
LOCUS CK749390 367 bp mRNA linear EST 07-JUN-2005
DEFINITION mRNA sequence.
ACCESSION CK749390
VERSION CK749390.1 GI:42639813
KEYWORDS EST.
SOURCE Nuphar advena
ORGANISM Nuphar advena
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; basal Magnoliophyta; Nymphaeales;
Nymphaeaceae; Nuphar.
1 (bases 1 to 367)
dePamphilis,C., Carlson,J., Ma,H., Frohlich,M., Tanksley,S.,
Leebens-Mack,J., Field,D., Arington,J., Zahn,L., Kong,H.,
Druckemiller,M., Landherr,L., Hu,Y., Iluc,D., Wall,K.,
Plock,S.Chloreaan,S., Albert,V., Doyle,J., Miller,W.,
Openeimer,D., Soltis,D., Soltis,P. and Theissen,G.
Generation of ESTs from early flower buds of Nuphar advena
Unpublished (2002)
Contact: Claude dePamphilis or James Leebens-Mack
Mellier Laboratory
Penn State University
208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
State University, University Park, PA 16802, USA
Tel: 814 863 6413
Fax: 814 865 9131
Email: cw43@psu.edu or jh110@psu.edu
The sequence provided is trimmed of vector and low quality regions.
Full sequence and original trace file are available from the Plant
Genome Network website (<http://pgn.cornell.edu>)
Plate: nad03-5c82 row: a column: 03
Seq primer: M13F.

FEATURES
source

Location/Qualifiers
1. 367
/organism="Nuphar advena"
/mol_type="mRNA"
/db_xref="PGN:nad03-5c82-a03"
/db_xref="taxon:77108"
/clone="nad03-5c82-a03"
/issue_type="flower buds"
/dev_stage="2.5mm"
/lab_host="SOLR"
/clone_id="nad03"
/note="Vector: Bluescript SK (+/-); Site 1: EcoRI;
Site 2: XhoI; Only floral buds with diameter of 2.5 mm of
leaves were used for RNA isolation. This is a directionally
cloned, non-normalized library. Avg. insert length: 1134;
primers: M13F and M13R; Antibiotic: 50 ug/ml Ampicillin;
Primary filter: 286 pfu total; Amplified filter: 3.2E10
pfu/ml; Mass Excised filter: 5E10 total; This library has
been generated by the Floral Genome Project (FGP). The
Floral Genome Project is funded by NSF's Plant Genome
Research Program (DBI-0115684). More information about the
project can be obtained at <http://fgp.bio.psu.edu>"

ORIGIN

Query Match 92.9%; Score 13; DB 7; Length 367;
Best Local Similarity 76.9%; Pred. No. 6.5e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUACUGCACTCG 13
||:|||||||
195 GTACTGCACTCG 207

RESULT 37
LOCUS FR0030316 368 bp DNA linear GSS 25-FEB-2004
DEFINITION Fugu rubripes GSS sequence, clone 07B20ec3, genomic survey
sequence.
ACCESSION AL026685.1 GI:3264028
VERSION AL026685
KEYWORDS GSS; genome survey sequence.
SOURCE Takifugu rubripes (Fugu rubripes)
ORGANISM Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Takifugu.
1
Bigar,G., Clark,M.S., Meek,S., Smith,S., Warner,S., Edwards,Y.J.,
Bouchlirab,N., Cottage,A., Yeo,G.S., Umranta,Y., Williams,G. and
Brenner,S.
Generation and analysis of 25 Mb of genomic DNA from the pufferfish
Fugu rubripes by sequence scanning
Genome Res. 9 (10), 960-971 (1999)
2 (bases 1 to 368)
Bigar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umranta,Y.,
Williams,G. and Brenner,S.
Direct Submission
Submitted (09-JUN-1998) MRC Human Genome Mapping Project Resource
Centre, Hinxton, Cambridge, CB10 1SB, UK. Email:
biohelp@hmp.mrc.ac.uk
Vector: Bluescript II KS
V type: phagemid
primer: KS
DSCR:
One pass dye-terminator sequencing of cosmid cloned genomic
sequence.
Location/Qualifiers
1. 368
/organism="Takifugu rubripes"
/mol_type="genomic DNA"
/db_xref="taxon:31033"

ORIGIN /clone="077E20EC3"
/clone_1lb="cosmid 077E20"

Query Match 92.9%; Score 13; DB 11; Length 368;
Best Local Similarity 76.9%; Pred. No. 6.5e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACTGCACTCG 14
DB 293 GTACTGCACTCG 305

RESULT 38
LOCUS CD733604/c 369 bp mRNA linear EST 26-JUN-2003
DEFINITION 4046300 IGAL - Chicken intestinal lymphocyte Gallus gallus cDNA
CD733604
CD733604.1 GI:32284453

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianidae; Gallus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 369)
Min, W., Lillehoj, H.S., Ashwell, C.M., Matukumalli, L.K., van
Tassel, C., and Han, J.Y.
Chicken intestinal lymphocyte EST database as a resource for the
analysis of mucosal immune function
Unpublished (2003)
Contact: Hyun S. Lillehoj
Animal Parasite Diseases Laboratory
Animal and Natural Resources Institute, USDA
Bldg. 1043, BARC-East, Beltsville, MD 20705, USA
Tel: 3015048771
Fax: 3015045103
Email: lillehoj@ars.aphis.usda.gov

Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim alt ' ' -trim fasta. Vector identified
by cross match using options -mismatch 12 -minscore 12
Plate: 50 row: F column: 07
Seq primer: ATTAGCTGACACATATAG
High quality sequence stop: 369.
Location/Qualifiers
1..369
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="white leghorn SC"
/db_xref="taxon:9031"
/clone="IGAL_50F07"
/sex="mixed"
/tissue_type="Gut"
/cell_type="lymphocyte"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_1lb="IGAL - Chicken intestinal lymphocyte"
/note="Organ: Intestine; Vector: PCMV-SPORT6; Site 1:
Site 2: NotI; Normalized library from chicken gut
infected with coccidia duodenum and middle gut."

FEATURES

Query Match 92.9%; Score 13; DB 6; Length 369;
Best Local Similarity 76.9%; Pred. No. 6.5e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACTGCACTCG 14
DB 17 GTACTGCACTCG 5

RESULT 39

B1120564/c 376 bp mRNA linear EST 31-DEC-2001
LOCUS B1120564
DEFINITION F018P35Y Populus flower cDNA library Populus trichocarpa cDNA, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
B1120564
B1120564.1 GI:18004539
EST.
Populus trichocarpa (Populus balsamifera subsp. trichocarpa)
Populus trichocarpa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT
Hertberg, M., Aspeborg, H., Erlandsson, R., Bjorkbacka, H.,
Hilonen, T., Karlsson, J., Teeri, T., Gustafsson, P., Bahlero, R.,
Jansson, S., Nilsson, O., Sundberg, B., Nilsson, P., Uhlen, M.,
Sanderberg, G. and Lundberg, J.
Gene expression in Populus
Unpublished (2001)
Contact: Erlandsson R
Department of Biotechnology
Royal Institute of Technology
Teknikringen 30, Stockholm S-10044, Sweden
Tel: 46 8 790 8287
Fax: 46 8 245452
Email: rikeri@biochem.kth.se.

FEATURES

source
Location/Qualifiers
1..376
/organism="Populus trichocarpa"
/mol_type="mRNA"
/db_xref="taxon:3694"
/tissue_type="floral buds"
/clone_1lb="Populus flower cDNA library"
/note="Organ: flower"

ORIGIN

Query Match 92.9%; Score 13; DB 2; Length 376;
Best Local Similarity 76.9%; Pred. No. 6.5e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACTGCACTCG 14
DB 175 GTACTGCACTCG 163

RESULT 40

LOCUS A1059369/c 379 bp mRNA linear EST 05-JUL-1999
DEFINITION UI-R-CI-1d-e-09-0-UI_81 UI-R-CI Rattus norvegicus cDNA clone
UI-R-CI-1d-e-09-0-UI 3', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
A1059369
A1059369.1 GI:3333146
EST.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Rattus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)

CONTACT: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu

The sequence tag present in the cDNA between the NotI site and the
oligo-dT track served to identify it as a clone from the normalized

using Dynabead oligo-dT priming (Dyna1). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of PAMPI. Dissected nematode tissues were provided by Dr. Alan Scott (ascot@jhphn.edu) of the School of Public Hygiene and Public Health at John Hopkins University in Baltimore, MD.

FEATURES

source

1..402
 /organism="Ascaris suum"
 /mol_type="mRNA"
 /db_xref="taxon:6253"
 /sex="Female"
 /tissue_type="Dissected female gonad (GZ=germinal zone, most distal region of gonad)"
 /dev_stage="Adult"
 /lab_host="DH10B"
 /clone_lib="Ascaris suum female gonad GZ PAMPI v2
 Chiapelli McCarter"
 /note="Vector: PAMPI (Gibco); Site 1: NotI; Site 2: SalI; The library was constructed by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dyna1). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of PAMPI. Dissected nematode tissues were provided by Dr. Alan Scott (ascot@jhphn.edu) of the School of Public Hygiene and Public Health at John Hopkins University in Baltimore, MD."

ORIGIN

Query Match 92.9%; Score 13; DB 3; Length 402;
 Best Local Similarity 76.9%; Pred. No. 6.6e+03;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GUACGCAACUCG 14
 ||:|||||:
 Db 243 GTACTGCAACTCG 255

RESULT 43 403 bp DNA linear GSS 22-SEP-1998
 LOCUS AO123512
 DEFINITION HS_3101_B1_E10_MR_CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3101 Col=19 Row=J, genomic survey sequence.
 ACCESSION AO123512
 VERSION AO123512.1 GI:3500678
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 403)
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 10449764
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
 Plate: 3101 row: J column: 19
 Class: BAC ends

High quality sequence stop: 403
 Location/Qualifiers
 1..403
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=3101 Col=19 Row=J"
 /sex="male"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B"

ORIGIN

Query Match 92.9%; Score 13; DB 9; Length 403;
 Best Local Similarity 76.9%; Pred. No. 6.6e+03;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GUACGCAACUCG 14
 ||:|||||:
 Db 380 GTACTGCAACTCG 392

RESULT 44 408 bp mRNA linear EST 24-MAY-2005
 LOCUS BW915405
 DEFINITION BW915405 Amphioxus Branchiostoma floridae unpublished cDNA library, neurula whole animal Branchiostoma floridae cDNA clone dbne053e07 3', mRNA sequence.
 ACCESSION BW915405
 VERSION BW915405.1 GI:66541385
 KEYWORDS EST.
 SOURCE Branchiostoma floridae (Florida lancelet)
 ORGANISM Branchiostoma floridae
 Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.
 1 (bases 1 to 408)
 Yu,J., Holland,L.Z., Shin-I,T., Kohara,Y., Satou,Y. and Satoh,N.
 Expressed genes in Branchiostoma floridae
 Unpublished (2005)
 Contact: Tadashi Shin-I
 Center For Genetic Resource Information
 National Institute of Genetics
 111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6855
 Fax: 81-559-81-6855
 Email: tehin@genes.nig.ac.jp.
 Location/Qualifiers
 1..408
 /organism="Branchiostoma floridae"
 /mol_type="mRNA"
 /db_xref="taxon:7739"
 /clone="dbne053e07"
 /tissue_type="whole animal"
 /dev_stage="neurula"
 /clone_lib="Amphioxus Branchiostoma floridae unpublished cDNA library, neurula whole animal"

FEATURES

source

Query Match 92.9%; Score 13; DB 5; Length 408;
 Best Local Similarity 76.9%; Pred. No. 6.6e+03;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GUACGCAACUCG 13
 ||:|||||:
 Db 70 GTACTGCAACTC 82

ORIGIN

RESULT 45 409 bp mRNA linear EST 14-AUG-2002
 LOCUS BO852614/c
 DEFINITION BO852614.yg.ab1 QG ABCDI lectuce salinas lactuca sativa cDNA clone OGB18102, mRNA sequence.
 ACCESSION BO852614

VERSION B0852614.1 GI:22238079
 KEYWORDS EST.
 SOURCE Lactuca sativa
 ORGANISM Lactuca sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
 Cichorieae; Lactuca.
 1 (bases 1 to 409)
 Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
 Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, D.,
 Ellstrom, P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
 Lai, Z., Church, S., Jackson, L. and Bradford, K.
 Lecture and Sunflower ESTs from the Compositae Genome Project
 http://compgenomics.ucdavis.edu/
 Unpublished (2002)
 JOURNAL Contact: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)
 Asmundoen Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
 singleton, see http://cgpb.ucdavis.edu/ for details.
 Plate: Q6818 row: 1 column: 02.
 Location/Qualifiers
 FEATURES
 source
 1..409
 /organism="Lactuca sativa"
 /mol_type="mRNA"
 /cufv="Salinas"
 /db_xref="taxon:4236"
 /clone="Q6818102"
 /lab_host="E.coli"
 /note="Vector: pBRCDMSfiAB: The library was constructed
 from 10 different sources of RNA from a single genotype.
 Separate cDNAs were generated using primers that
 incorporated unique 5' and 3' tags to distinguish each
 source of RNA. cDNAs were then pooled, size-fractionated,
 directionally cloned into a custom medium-copy vector and
 transformations made with four size classes to minimize
 size bias. Details of each source of RNA and library
 construction can be obtained at http://cgpb.ucdavis.edu/
 TAG_TISSUE=germinating seeds
 TAG_LIB=Q6818102 Lactuca sativa
 TAG_SEQ=TCGTGCGCGG"
 ORIGIN
 Query Match 92.9%; Score 13; DB 5; Length 409;
 Best Local Similarity 76.9%; Pred. No. 6.6e+03;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGUACUGCACTC 13
 ||:|||||:
 Db 231 GCTACTGCACTC 219
 RESULT 46
 B0646387 410 bp mRNA linear EST 07-OCT-2004
 LOCUS B0646387 Eptaretus burgeri adult Eptaretus burgeri cDNA clone
 DEFINITION hg106p18 5', mRNA sequence.
 ACCESSION B0646387
 VERSION B0646387.1 GI:53861248
 KEYWORDS EST.
 SOURCE Eptaretus burgeri (inshore hagfish)
 ORGANISM Eptaretus burgeri
 Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;
 Myxiniidae; Eptaretinae; Eptaretus.
 1 (bases 1 to 410)
 Suzuki, T., Shin-I, T., Kohara, Y. and Kasahara, M.
 Transcription analysis of hagfish leukocytes: a framework for
 understanding the immune system of jawless fishes

JOURNAL Dev. Comp. Immunol. 28 (10), 993-1003 (2004)
 PUBMED 15236930
 COMMENT Contact: Tadao Shin-I
 Center for Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tehini@genes.nig.ac.jp.
 Location/Qualifiers
 FEATURES
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 1..410
 /organism="Eptaretus burgeri"
 /mol_type="mRNA"
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 Best Local Similarity 76.9%; Pred. No. 6.6e+03;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GUACUGCACTC 14
 ||:|||||:
 Db 274 GCTACTGCACTC 262
 RESULT 47
 CL555282 413 bp DNA linear GSS 14-JUN-2004
 LOCUS OB_Ba0005124.f OB_Ba Oryza brachyantha genomic clone
 DEFINITION OB_Ba0005124 5', genomic survey sequence.
 ACCESSION CL555282
 VERSION CL555282.1 GI:47633696
 KEYWORDS GSS.
 SOURCE Oryza brachyantha
 ORGANISM Oryza brachyantha
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 413)
 Kim, H., Yu, Y., Shum, D., Yeast, D., Rao, K., Luo, M., Jecy, R.,
 Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.
 OMAP Project
 Unpublished (2004)
 JOURNAL Contact: Rod A. Wing
 Arizona Genomics Institute
 University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259
 Email: rwing@genome.arizona.edu
 PCR Primers
 FORWARD: TAA TAC GAC TCA TGA TGG GG
 BACKWARD: CAC TCA TTA GGC ACC CCA
 Insert Length: 145000 Std Error: 0.00
 Plates: 0005 row: 1 column: 24
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 Location/Qualifiers
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ORIGIN

Query Match 92.9%; Score 13; DB 10; Length 413;
 Best Local Similarity 76.9%; Pred. No. 6.6e+03;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGUACUGCACTC 13
 ||:|||||:
 360 CCGACTGCAACTC 372

Db 360 CCGACTGCAACTC 372

RESULT 48
 AJ679628 426 bp mRNA linear EST 29-JUN-2004
 LOCUS AJ679628 CSEORAN04 Sus scrofa cDNA clone C0001779_L06, mRNA
 DEFINITION sequence.

ACCESSION AJ679628.1 GI:49412215
 VERSION AJ679628
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
 Sus.
 1 (bases 1 to 426)
 Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
 Development of cDNA and EST resources for studying reproduction and
 embryo development in pigs and cattle
 Unpublished (2004)
 Contact: Anderson SI
 Genomics and Bioinformatics
 Roslin Institute
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
 Single pass sequencing. Bases called and trimmed with phred
 v0.020425.c. Vector identified by cross match with the -minscore 20
 and -mismatch 12 options. Vector: pBluescriptII(KS+). R. Site1: SCOR1
 R. Site2: Not1 5' Seg Primer M13P Normalised library constructed
 from pig uterus. Clones available from UK Centre for Functional
 Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
 EH25 9PS, www.arkgenomics.org.
 Location/Qualifiers
 1..426
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 /tissue_type="uterus"
 /clone_id="CSEORAN04"
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 Not1; Single pass sequencing. Normalised library
 constructed from pig uterus."

FEATURES

source

ORIGIN

Query Match 92.9%; Score 13; DB 1; Length 426;
 Best Local Similarity 76.9%; Pred. No. 6.6e+03;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GUACUGCACTC 14
 ||:|||||:
 93 GACTGCAACTC 81

Db 93 GACTGCAACTC 81

RESULT 49
 AW929623 437 bp mRNA linear EST 18-MAY-2001
 LOCUS AW929623 E87338411 tomato flower buds 8 mm to pre-anthesis, Cornell
 DEFINITION University Lycopersicon esculentum cDNA clone CTC0929 5', mRNA
 sequence.

ACCESSION AW929623
 VERSION AW929623.1 GI:8105024
 KEYWORDS EST.
 SOURCE Lycopersicon esculentum (Solanum lycopersicum)
 ORGANISM Lycopersicon esculentum

REFERENCE

AUTHORS

van der Hoeven, R.S., Bezzerides, J.L., Matern, A.L., Holt, I.B.,
 Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S.,
 Rooning, C.M., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and
 Tanksley, S.D.
 Generation of ESTs from tomato flower tissue
 Unpublished (1999)
 Contact: CUGI
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 5 prime sequence.

FEATURES

source

ORIGIN

Query Match 92.9%; Score 13; DB 1; Length 437;
 Best Local Similarity 76.9%; Pred. No. 6.6e+03;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGUACUGCACTC 13
 ||:|||||:
 321 CCGACTGCAACTC 309

Db 321 CCGACTGCAACTC 309

RESULT 50
 CV723505 459 bp mRNA linear EST 04-NOV-2004
 LOCUS CV723505 root--03-M13.g1 Rice root lambda phage cDNA library (root) Oryza
 DEFINITION sativa (japonica cultivar-group) cDNA clone root--03-M13, mRNA
 sequence.

ACCESSION CV723505
 VERSION CV723505.1 GI:55411129
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eriarthroideae; Oryzaceae; Oryza.
 1 (bases 1 to 459)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr,
 Location/Qualifiers
 1..459
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"

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/cultivar="Nackdong"
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/tissue_type="root"
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/lab_host="E.coli SOLR"
/clone_lib="Rice root lambda phage CDNA library (root)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; CDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

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ORIGIN

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Best Local Similarity 76.9%; Pred. No. 6.6e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY      2 GUACUGCAACTCG 14
      ||:||:||:||
DB      356 GTACTGCAACTCG 344

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Search completed: March 18, 2006, 20:02:46
Job time : 1384.15 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:34:54 ; Search time 281.346 Seconds
(without alignments)
331.640 Million cell updates/sec

Title: US-10-800-926-2
Perfect score: 14
Sequence: 1 cguacugcaacug 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 segs, 333346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : N_Geneseq_21.*
1: geneseqn19908:*
2: geneseqn19908:*
3: geneseqn20008:*
4: geneseqn20010:*
5: geneseqn20010:*
6: geneseqn20020:*
7: geneseqn20020:*
8: geneseqn20030:*
9: geneseqn20030:*
10: geneseqn20030:*
11: geneseqn20030:*
12: geneseqn20040:*
13: geneseqn20040:*
14: geneseqn20050:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	100.0	14	ADM79935	Adm79935 Bacterial
2	14	100.0	14	ADM60734	Adm60734 Bacterial
3	14	100.0	14	ADM49626	Adm49626 Bacterial
4	14	100.0	14	ACA25094	ACA25094 Prokaryot
5	14	100.0	14	ADM55136	Adm55136 Bacterial
6	14	100.0	14	ACA45239	ACA45239 Prokaryot
7	14	100.0	14	ADM44189	Adm44189 Knock-down
8	14	100.0	14	ABN51005	Abn51005 Mouse spl
9	14	100.0	14	ACD68769	ACD68769 E. coli K
10	14	100.0	14	ACD68770	ACD68770 E. coli K
11	14	100.0	14	AA61183	AA61183 Formate d
12	14	100.0	14	ADM51056	Adm51056 Bacterial
13	14	100.0	14	ADM5906	Adm5906 Aspergill
14	14	100.0	14	AA573079	AA573079 DNA encod
15	14	100.0	14	ADR85319	ADR85319 Aspergill
16	14	100.0	14	AA53074	AA53074 Human sec
17	14	100.0	14	AA52489	AA52489 E. coli D
18	14	100.0	14	ACA32562	ACA32562 Prokaryot
19	14	100.0	14	ABK13893	Abk13893 Gene enco

20	c	13	92.9	1732	5	AA592825	AA592825 DNA encod
21	c	13	92.9	1919	5	AA590081	AA590081 DNA encod
22	c	13	92.9	1945	4	AA14703	AA14703 Probe #46
23	c	13	92.9	1945	4	AB56435	AB56435 Human foe
24	c	13	92.9	1945	4	AA136072	AA136072 Probe #47
25	c	13	92.9	1945	4	AB45908	AB45908 Human bre
26	c	13	92.9	1945	4	ABA26067	ABA26067 Probe #45
27	c	13	92.9	1945	4	AAK30108	AAK30108 Human bon
28	c	13	92.9	1945	4	AAK04600	AAK04600 Human bra
29	c	13	92.9	1945	4	AB529757	AB529757 Human liv
30	c	13	92.9	1945	5	AA104509	AA104509 Probe #45
31	c	13	92.9	1945	5	AB504688	AB504688 Human gen
32	c	13	92.9	2000	10	ACC61225	ACC61225 Gene sequ
33	c	13	92.9	2000	10	ADK63219	ADK63219 Disease t
34	c	13	92.9	2133	5	AA588191	AA588191 DNA encod
35	c	13	92.9	2263	2	AA193775	AA193775 PSD-93 co
36	c	13	92.9	3222	5	AA590082	AA590082 DNA encod
37	c	13	92.9	3443	13	ADR84732	ADR84732 Aspergill
38	c	13	92.9	14063	2	AAK20500	AAK20500 Polynucle
39	c	13	92.9	83493	14	AD213310	AD213310 Murine ca
40	c	13	92.9	84707	6	AB67196_6	AB67196_6
41	c	13	92.9	110000	6	ABQ69245_26	ABQ69245_26
42	c	13	92.9	110000	14	AB339175_12	AB339175_12
43	c	13	92.9	110000	14	AB42401_12	AB42401_12
44	c	13	92.9	110000	14	AB42736_6	AB42736_6
45	c	13	92.9	184368	14	AB35722_6	AB35722_6
46	c	13	92.9	207461	14	AB339170	AB339170
47	c	12.6	90.0	201	13	AD537261	AD537261 Human aut
48	c	12.6	90.0	2290	13	AAA28552	AAA28552 Human aut
49	c	12.6	90.0	29871	13	AD536480	AD536480 Human opt
50	c	12.6	90.0	321019	13	AD536450	AD536450 Human aut
51	c	12.6	90.0	100	8	ACD68918	ACD68918 E. coli K
52	c	12.4	88.6	100	8	ACD71764	ACD71764 E. coli K
53	c	12.4	88.6	100	8	ACD68919	ACD68919 E. coli K
54	c	12.4	88.6	100	8	ABN16733	ABN16733 Human ORF
55	c	12.4	88.6	283	3	AA59127	AA59127 Human sec
56	c	12.4	88.6	323	13	ADT71332	ADT71332 Variant r
57	c	12.4	88.6	339	13	AA78164	AA78164 VP4 gene
58	c	12.4	88.6	349	2	AA59127	AA59127 Partial n
59	c	12.4	88.6	365	12	ADP92282	ADP92282 Cotton ex
60	c	12.4	88.6	373	5	AB572705	AB572705 Human gen
61	c	12.4	88.6	375	5	ABA18180	ABA18180 Human ner
62	c	12.4	88.6	381	4	AAK73299	AAK73299 Human imm
63	c	12.4	88.6	386	2	AA729011	AA729011 Fragment
64	c	12.4	88.6	435	11	ABD01475	ABD01475 Pseudomon
65	c	12.4	88.6	438	9	ABK16449	ABK16449 Gram pos
66	c	12.4	88.6	478	9	ACH41779	ACH41779 Human foe
67	c	12.4	88.6	504	11	ABD02722	ABD02722 Pseudomon
68	c	12.4	88.6	515	13	AD083881	AD083881 Plant ful
69	c	12.4	88.6	535	4	AAK91915	AAK91915 Human CDN
70	c	12.4	88.6	535	4	AAK93946	AAK93946 Human CDN
71	c	12.4	88.6	535	12	ADL28342	ADL28342 5' end of
72	c	12.4	88.6	535	12	ADL30373	ADL30373 5' end of
73	c	12.4	88.6	543	11	ABD09101	ABD09101 Pseudomon
74	c	12.4	88.6	543	11	ABD01629	ABD01629 Pseudomon
75	c	12.4	88.6	557	2	AAQ13766	AAQ13766 Ribosome
76	c	12.4	88.6	558	4	AA582309	AA582309 E. coli D
77	c	12.4	88.6	558	4	AA552309	AA552309 Prokaryot
78	c	12.4	88.6	630	8	ACA42760	ACA42760 Prokaryot
79	c	12.4	88.6	645	4	ABLA4295	ABLA4295 Drosophila
80	c	12.4	88.6	648	4	AAK93254	AAK93254 Human CDN
81	c	12.4	88.6	648	12	ADL29681	ADL29681 5' end of
82	c	12.4	88.6	669	11	ABD01496	ABD01496 Pseudomon
83	c	12.4	88.6	696	11	ABD11114	ABD11114 Pseudomon
84	c	12.4	88.6	726	11	ABD15493	ABD15493 Pseudomon
85	c	12.4	88.6	743	4	AAK91935	AAK91935 Human CDN
86	c	12.4	88.6	743	4	AAK93345	AAK93345 Human CDN

C 93	12.4	88.6	743	12	ADL29772	Adl29772 5' end of	166	12.4	88.6	1392	8	ACA25081	ACA25081 Prokaryot
C 94	12.4	88.6	743	12	ADL28362	Adl28362 5' end of	167	12.4	88.6	1397	13	ADX48052	Adx48052 Plant full
C 95	12.4	88.6	756	11	ABD01490	Abd01490 Pseudomon	168	12.4	88.6	1411	13	ADX49753	Adx49753 Plant full
C 96	12.4	88.6	783	5	AAS65673	Aas65673 DNA encod	C 169	12.4	88.6	1498	13	ADO84587	Ado84587 Plant full
C 97	12.4	88.6	798	4	AAK92066	AAK92066 Human CDN	C 170	12.4	88.6	1541	13	ADO9585	Ado9585 Plant full
C 98	12.4	88.6	798	4	AAK94005	AAK94005 Human CDN	C 171	12.4	88.6	1557	13	ADO91743	Ado91743 Polyetid
C 99	12.4	88.6	798	12	ADL30432	Adl30432 3' end of	C 172	12.4	88.6	1557	13	ASE87035	AsE87035 Streptomy
C 100	12.4	88.6	798	12	ADL28493	Adl28493 5' end of	C 173	12.4	88.6	1557	13	ASE86832	AsE86832 Streptomy
C 101	12.4	88.6	819	14	AEA20721	Aea20721 Novel hum	C 174	12.4	88.6	1563	11	AAE54183	AAE54183 Pseudom
C 102	12.4	88.6	832	14	ADVE0576	Adve0576 Muscari a	C 175	12.4	88.6	1572	4	ACA42427	ACA42427 Prokaryot
C 103	12.4	88.6	834	11	ABD07843	Abd07843 Pseudomon	C 176	12.4	88.6	1572	8	ACA42427	ACA42427 Prokaryot
C 104	12.4	88.6	867	11	ACU69342	Acu69342 M. xanthu	C 177	12.4	88.6	1583	13	ADL11789	Adl11789 Plant full
C 105	12.4	88.6	879	13	ADT41605	Adt41605 Bacterial	C 178	12.4	88.6	1584	6	ABR6019	ABR6019 S. coelic
C 106	12.4	88.6	879	13	ADT41605	Adt41605 Bacterial	C 179	12.4	88.6	1584	10	ADH10706	Adh10706 Streptomy
C 107	12.4	88.6	889	6	ABO68459	Abog68459 Bacteria	C 180	12.4	88.6	1624	13	ADO84672	Ado84672 Plant full
C 108	12.4	88.6	906	4	AAK93936	AAK93936 Human CDN	C 181	12.4	88.6	1627	13	ADO84726	Ado84726 Plant full
C 109	12.4	88.6	906	4	AAK93235	AAK93235 Human CDN	C 182	12.4	88.6	1629	11	ABD01500	Abd01500 Pseudomon
C 110	12.4	88.6	906	4	AAK91977	AAK91977 Human CDN	C 183	12.4	88.6	1645	13	ADG60467	ADG60467 Bacterial
C 111	12.4	88.6	906	12	ADL29662	Adl29662 5' end of	C 184	12.4	88.6	1707	8	ACA25819	ACA25819
C 112	12.4	88.6	906	12	ADL28404	Adl28404 5' end of	C 185	12.4	88.6	1713	2	AAZ20661	AAZ20661
C 113	12.4	88.6	906	12	ADL30363	Adl30363 5' end of	C 186	12.4	88.6	1737	11	ABD01648	ABD01648
C 114	12.4	88.6	915	13	ADSG3257	Adsg3257 Bacterial	C 187	12.4	88.6	1737	11	ABD01675	ABD01675
C 115	12.4	88.6	915	13	ADSG5956	Adsg5956 Bacterial	C 188	12.4	88.6	1743	8	ACA36283	ACA36283 Prokaryot
C 116	12.4	88.6	915	13	ADSG2456	Adsg2456 Bacterial	C 189	12.4	88.6	1770	9	ADB75639	ADB75639 Rhodococ
C 117	12.4	88.6	927	13	ADSG2777	Adsg2777 Bacterial	C 190	12.4	88.6	1776	11	ABD13585	ABD13585 Pseudomon
C 118	12.4	88.6	927	13	ADSG3642	Adsg3642 Bacterial	C 191	12.4	88.6	1782	9	ADA48275	Ada48275 Rice gene
C 119	12.4	88.6	930	11	ABD07499	Abd07499 Pseudomon	C 192	12.4	88.6	1800	11	ABD05548	ABD05548 Pseudomon
C 120	12.4	88.6	960	4	ABLO8433	ABLO8433 Drosophila	C 193	12.4	88.6	1827	11	ABD02771	ABD02771
C 121	12.4	88.6	1005	14	ACU70878	Acu70878 M. xanthu	C 194	12.4	88.6	1925	5	AAH72967	AAH72967 Human cer
C 122	12.4	88.6	1007	14	ACU63607	Acu63607 M. xanthu	C 195	12.4	88.6	1926	5	AAH80027	AAH80027 DNA encod
C 123	12.4	88.6	1017	10	ADC92538	Adc92538 R. faeciu	C 196	12.4	88.6	1959	13	ADG49381	ADG49381 Bacterial
C 124	12.4	88.6	1028	8	ABZ37536	Abz37536 Streptomy	C 197	12.4	88.6	2160	14	ADZ10724	ADZ10724 DNA encod
C 125	12.4	88.6	1032	8	ABZ37536	Abz37536 Streptomy	C 198	12.4	88.6	2262	11	ABD02812	ABD02812 Pseudomon
C 126	12.4	88.6	1035	10	ABZ67710	Abz67710 Orthosomy	C 199	12.4	88.6	2263	4	AAH23076	AAH23076
C 127	12.4	88.6	1065	5	AAH78324	AAH78324 DNA encod	C 200	12.4	88.6	2288	11	ABD13650	ABD13650 Pseudomon
C 128	12.4	88.6	1085	11	ABD01486	Abd01486 Pseudomon	C 201	12.4	88.6	2302	4	AAH34939	AAH34939
C 129	12.4	88.6	1086	11	ABZ39803	Abz39803 N. gonorr	C 202	12.4	88.6	2346	11	ABD11032	ABD11032
C 130	12.4	88.6	1092	13	ADSG1348	Adsg1348 Maize ear	C 203	12.4	88.6	2346	11	ABD13751	ABD13751
C 131	12.4	88.6	1104	11	ACH97088	Ach97088 Klebsiell	C 204	12.4	88.6	2370	11	ACH95568	ACH95568
C 132	12.4	88.6	1137	11	ABD07579	Abd07579 Pseudomon	C 205	12.4	88.6	2391	11	ABD02588	ABD02588
C 133	12.4	88.6	1144	8	ABZ79953	ABZ79953 Mycobacte	C 206	12.4	88.6	2406	8	ABZ79958	ABZ79958
C 134	12.4	88.6	1152	8	ACA41012	ACA41012 Prokaryot	C 207	12.4	88.6	2409	2	AAK34178	AAK34178 Mycobacte
C 135	12.4	88.6	1185	11	ABD14446	ABD14446 Pseudomon	C 208	12.4	88.6	2409	13	ADU16958	ADU16958 M. tuberc
C 136	12.4	88.6	1185	4	AAH54272	AAH54272 Pseudomon	C 209	12.4	88.6	2416	4	AAH57446	AAH57446 Human lun
C 137	12.4	88.6	1185	9	ACA42593	ACA42593 Prokaryot	C 210	12.4	88.6	2451	2	AAH34179	AAH34179 Mycobacte
C 138	12.4	88.6	1195	9	AAI60901	AAI60901 Human com	C 211	12.4	88.6	2451	13	ADU16960	ADU16960 M. tuberc
C 139	12.4	88.6	1203	11	ABD08953	Abd08953 Pseudomon	C 212	12.4	88.6	2472	11	ABD05852	ABD05852 Pseudomon
C 140	12.4	88.6	1206	11	ABD10970	Abd10970 Pseudomon	C 213	12.4	88.6	2495	4	AAI58392	AAI58392 Human pol
C 141	12.4	88.6	1206	2	AAV29010	AAV29010 Formate d	C 214	12.4	88.6	2495	5	ADQ98602	ADQ98602 DNA encod
C 142	12.4	88.6	1206	6	ABK68663	ABK68663 DNA encod	C 215	12.4	88.6	2495	5	ADBA8362	ADBA8362 Novel hum
C 143	12.4	88.6	1206	12	ADL15943	Adl15943 Coenzyme-	C 216	12.4	88.6	2502	5	AAH82516	AAH82516 DNA encod
C 144	12.4	88.6	1206	12	ADOS7977	Ados7977 Mycobacte	C 217	12.4	88.6	2508	8	ACA45230	ACA45230 Prokaryot
C 145	12.4	88.6	1233	11	ABD14621	Abd14621 Pseudomon	C 218	12.4	88.6	2520	4	AAK94335	AAK94335 Human full
C 146	12.4	88.6	1254	13	ADOB1753	Adob1753 Plant full	C 219	12.4	88.6	2520	12	ADU30994	ADU30994 Full leng
C 147	12.4	88.6	1264	8	ACC70828	Acc70828 Thiobacil	C 220	12.4	88.6	2543	4	AAK94301	AAK94301 Human full
C 148	12.4	88.6	1264	3	ADK62241	Adk62241 Plant full	C 221	12.4	88.6	2543	12	ADL30927	ADL30927 Full leng
C 149	12.4	88.6	1285	13	ADOB4465	Adob4465 Plant full	C 222	12.4	88.6	2547	4	AAK94315	AAK94315 Human full
C 150	12.4	88.6	1287	4	AAH54131	AAH54131 Pseudomon	C 223	12.4	88.6	2547	12	ADL30954	ADL30954 Full leng
C 151	12.4	88.6	1287	8	ACA42311	ACA42311 Prokaryot	C 224	12.4	88.6	2553	13	ADG61679	ADG61679 Bacteria
C 152	12.4	88.6	1287	12	ADH97101	Adh97101 P. aerugi	C 225	12.4	88.6	2556	6	ABQ70793	ABQ70793 Bacteria
C 153	12.4	88.6	1287	12	ADH97103	Adh97103 P. aerugi	C 226	12.4	88.6	2563	4	AAK94914	AAK94914 Human full
C 154	12.4	88.6	1287	14	AEIC13456	Aeic13456 P. aerugi	C 227	12.4	88.6	2563	12	ADL32107	ADL32107 Full leng
C 155	12.4	88.6	1287	14	AEIC13458	Aeic13458 P. aerugi	C 228	12.4	88.6	2571	8	ACA35386	ACA35386 Prokaryot
C 156	12.4	88.6	1300	13	ADOB84562	Adob84562 Plant full	C 229	12.4	88.6	2595	8	ACA23758	ACA23758 Prokaryot
C 157	12.4	88.6	1302	14	ADV11962	Adv11962 A. fumigat	C 230	12.4	88.6	2595	8	ACA26252	ACA26252 Prokaryot
C 158	12.4	88.6	1314	11	ABD09180	Abd09180 Pseudomon	C 231	12.4	88.6	2604	4	AAI60178	AAI60178 Human pol
C 159	12.4	88.6	1314	11	ACU7663	Acu7663 Rice abio	C 232	12.4	88.6	2622	11	ACH98789	ACH98789 Klebsiell
C 160	12.4	88.6	1324	13	ADK09661	Adk09661 Plant full	C 233	12.4	88.6	2634	13	ADT43081	ADT43081 Bacteria
C 161	12.4	88.6	1326	11	ACA23850	ACA23850 Prokaryot	C 234	12.4	88.6	2645	4	ABLO5493	ABLO5493 Drosophila
C 162	12.4	88.6	1359	8	ACH98649	Ach98649 Klebsiell	C 235	12.4	88.6	2645	10	ADK11404	ADK11404 Drosophila
C 163	12.4	88.6	1363	13	ADK34937	Adk34937 Plant full	C 236	12.4	88.6	2721	13	ADT46438	ADT46438 Bacteria
C 164	12.4	88.6	1365	13	ADT41687	Adt41687 Bacteria	C 237	12.4	88.6	2806	8	ABZ79957	ABZ79957 Mycobacte
C 165	12.4	88.6	1374	13	ADK11685	Adk11685 Plant full	C 238	12.4	88.6	2838	11	ABD15524	ABD15524 Pseudomon

C 239	12.4	88.6	2841	13	ADR40446	Adi40446 Human ino	C 312	12.4	88.6	110000	12	ADM46123_11	Continuation (12 o
C 240	12.4	88.6	2852	4	ABL14294	Abli14294 Drosophill	C 313	12.4	88.6	110000	12	ADM47209_09	Continuation (10 o
C 241	12.4	88.6	2861	4	ABL15226	Abli15226 Drosophill	C 314	12.4	88.6	110000	12	ADM46464_10	Continuation (11 o
C 242	12.4	88.6	2874	4	ABL11169	Abli11169 Drosophill	C 315	12.4	88.6	110000	12	ADM46464_11	Continuation (12 o
C 243	12.4	88.6	2927	13	ACN41952	Acn41952 Human dta	C 316	12.4	88.6	110000	12	ADM46464_11	Continuation (10 o
C 244	12.4	88.6	2934	11	ABD01480	Abd01480 Pseudomon	C 317	12.4	88.6	117213	2	AAV62176	AAV62176 HSV-2 str
C 245	12.4	88.6	2992	13	ACN41953	Acn41953 Human dta	C 318	12.4	88.6	156638	6	ABQ81850	ABQ81850 Bifidobac
C 246	12.4	88.6	3010	14	ABR87633	AbR87633 Human ino	C 319	12.4	88.6	164051	13	ADQ091695	ADQ091695 Polyketid
C 247	12.4	88.6	3148	4	ABL25824	Abi25824 Drosophill	C 320	12.4	88.6	164051	13	ABR86865	ABR86865 Streptomy
C 248	12.4	88.6	3244	4	ABL08432	Abi08432 Drosophill	C 321	12.4	88.6	164051	13	ABR86865	ABR86865 Streptomy
C 249	12.4	88.6	3244	6	ABL19730	Abi19730 Mouse isc	C 322	12.4	88.6	170170	10	ADL13643	ADL13643 Osteoarth
C 250	12.4	88.6	3398	4	ABL05964	Abi05964 Drosophill	C 323	12.4	88.6	326002	13	ABD32843	ABD32843 Human can
C 251	12.4	88.6	3468	5	AA594247	AA594247 DNA encod	C 324	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 252	12.4	88.6	3472	4	ABL07626	Abi07626 Drosophill	C 325	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 253	12.4	88.6	3480	14	ADV11961	Adv11961 A fumigat	C 326	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 254	12.4	88.6	3507	4	ABL13699	Abi13699 Drosophill	C 327	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 255	12.4	88.6	3710	4	ABL13193	Abi13193 Drosophill	C 328	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 256	12.4	88.6	3773	4	ABL07215	Abi07215 Drosophill	C 329	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 257	12.4	88.6	3812	5	AA593388	AA593388 DNA encod	C 330	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 258	12.4	88.6	3897	11	ABD15404	Abd15404 Pseudomon	C 331	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 259	12.4	88.6	3939	5	ABD08638	Abd08638 Human kin	C 332	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 260	12.4	88.6	4029	8	ACA51034	Acas1034 Prokaryot	C 333	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 261	12.4	88.6	4092	8	ACA51862	Acas1862 Prokaryot	C 334	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 262	12.4	88.6	4143	4	AA563308	AA563308 Salmomell	C 335	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 263	12.4	88.6	4251	5	AA589655	AA589655 DNA encod	C 336	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 264	12.4	88.6	4285	8	ABT17985	Abt17985 Aspergill	C 337	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 265	12.4	88.6	4357	12	AD145254	Adi145254 Rice isop	C 338	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 266	12.4	88.6	4525	10	ADF74213	Adf74213 Human mov	C 339	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 267	12.4	88.6	4651	8	ABT19799	Abt19799 Aspergill	C 340	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 268	12.4	88.6	4859	4	AA103936	AA103936 Human rep	C 341	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 269	12.4	88.6	4859	5	AA540336	AA540336 DNA encod	C 342	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 270	12.4	88.6	4859	11	AD070952	Adi070952 Human pro	C 343	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 271	12.4	88.6	5188	4	ABL11168	Abi11168 Drosophill	C 344	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 272	12.4	88.6	5773	12	ABE87435	Adp64435 L casei p	C 345	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 273	12.4	88.6	5875	14	ABE87631	AbE87631 Human ino	C 346	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 274	12.4	88.6	6203	16	ACL64348	Ac164348 M. xanthu	C 347	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 275	12.4	88.6	6239	4	ABX3553	Abx3553 Human bre	C 348	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 276	12.4	88.6	6465	8	ACA24261	AcA24261 Prokaryot	C 349	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 277	12.4	88.6	7114	4	ABL07214	Abi07214 Drosophill	C 350	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 278	12.4	88.6	7365	4	ABL11950	Abi11950 Drosophill	C 351	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 279	12.4	88.6	8544	4	ABL07154	Abi07154 Drosophill	C 352	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 280	12.4	88.6	8802	4	ABL13698	Abi13698 Drosophill	C 353	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 281	12.4	88.6	11204	4	AA546245	AA546245 DNA encod	C 354	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 282	12.4	88.6	14283	4	ABL05492	Abi05492 Drosophill	C 355	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 283	12.4	88.6	15042	4	ABL22246	Abi22246 Drosophill	C 356	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 284	12.4	88.6	15711	4	ABL26112	Abi26112 Drosophill	C 357	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 285	12.4	88.6	16141	4	AAK91491	Aak91491 Human dig	C 358	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 286	12.4	88.6	16141	4	AAK73262	Aak73262 Human imm	C 359	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 287	12.4	88.6	16439	4	ABL13192	Abi13192 Drosophill	C 360	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 288	12.4	88.6	22118	8	ADA14746	Ada14746 Mouse 455	C 361	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 289	12.4	88.6	22118	9	ADA37415	Ada37415 Origin of	C 362	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 290	12.4	88.6	22118	10	AD61410	Ad61410 Mouse rib	C 363	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 291	12.4	88.6	22118	10	AD710518	Ad710518 Mouse rib	C 364	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 292	12.4	88.6	22118	10	ACC44659	Acc44659 Mouse rib	C 365	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 293	12.4	88.6	22118	13	ADR43998	Adr43998 Mouse pre	C 366	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 294	12.4	88.6	22118	14	ABE25474	AbE25474 Mouse 455	C 367	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 295	12.4	88.6	28432	4	ABL05010	Abi05010 Drosophill	C 368	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 296	12.4	88.6	45055	10	ABZ6808	Abz6808 Orthosomy	C 369	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 297	12.4	88.6	59816	8	ABZ37516	Abz37516 Streptomy	C 370	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 298	12.4	88.6	59816	8	ABZ37515	Abz37515 Streptomy	C 371	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 299	12.4	88.6	60873	3	AAA81469	AAa81469 N. mening	C 372	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 300	12.4	88.6	64482	12	AD059515	Ad059515 Human can	C 373	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 301	12.4	88.6	64482	14	AD213896	Ad213896 Murine ca	C 374	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 302	12.4	88.6	72704	14	ACL64810	Ac164810 M. xanthu	C 375	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 303	12.4	88.6	103765	4	AA199683_43	AA199683_43	C 376	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 304	12.4	88.6	110000	3	AA199683_12	AA199683_12	C 377	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 305	12.4	88.6	110000	6	AA199682_43	AA199682_43	C 378	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 306	12.4	88.6	110000	11	AA199682_18	AA199682_18	C 379	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 307	12.4	88.6	110000	11	AA199682_12	AA199682_12	C 380	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 308	12.4	88.6	110000	12	ADN46845_11	ADN46845_11	C 381	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 309	12.4	88.6	110000	12	ADN46845_11	ADN46845_11	C 382	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 310	12.4	88.6	110000	12	ADN47591_09	ADN47591_09	C 383	12.4	88.6	349980	5	AA221610	AA221610 Neisseria
C 311	12.4	88.6	110000	12	ADN46123_10	ADN46123_10	C 384	12.4	88.6	349980	5	AA221610	AA221610 Neisseria

385	12	85.7	995	14	ABE66688	Ab666688 Rice geno	458	12	85.7	2288	4	ABU27079	AbU27079 Drosophill
c 386	12	85.7	1039	13	ADX11555	Adx115555 Plant full	c 459	12	85.7	2289	6	ABK28655	AbK28655 Human cDN
c 387	12	85.7	1079	2	AAx20676	Aax20676 Polynucle	c 460	12	85.7	2311	3	AAx38012	AAx38012 Rat WAR-1
c 388	12	85.7	1092	4	AAf74781	Aaf74781 Rat WAR-1	c 461	12	85.7	2315	4	AAH15998	AAH15998 Human cDN
c 389	12	85.7	1146	8	ACA37829	AcA37829 Prokaryot	c 462	12	85.7	2394	10	ADC89717	AdC89717 L. johnso
c 390	12	85.7	1168	13	ADX46327	Adx46327 Plant full	c 463	12	85.7	2419	4	AAH14594	AAH14594 Human cDN
c 391	12	85.7	1179	4	ABU04417	AbU04417 Drosophill	c 464	12	85.7	2419	6	ABV77974	AbV77974 Hypoxia-r
c 392	12	85.7	1179	13	ADS96589	AdS96589 Drosophill	c 465	12	85.7	2425	13	ADX61617	AdX61617 Plant full
c 393	12	85.7	1185	3	AAZ56367	Aaz56367 Escherich	c 466	12	85.7	2460	2	AAZ23692	Aaz23692 D. melano
c 394	12	85.7	1293	4	ABA88909	AbA88909 Escherich	c 467	12	85.7	2460	2	AAZ88270	AAZ88270 Drosophill
c 395	12	85.7	1338	4	AAH52950	Aah52950 S. epider	c 468	12	85.7	2472	11	ACL28203	AcL28203 Rice abio
c 396	12	85.7	1341	13	ADX61915	Adx61915 Plant full	c 469	12	85.7	2501	4	ABU06799	AbU06799 Drosophill
c 397	12	85.7	1356	6	ABN92161	Abn92161 Staphyloc	c 470	12	85.7	2551	4	ABU27080	AbU27080 Drosophill
c 398	12	85.7	1356	13	AD8017882	Ad8017882 Staphyloc	c 471	12	85.7	2567	10	ADG16967	AdG16967 Oncorhync
c 399	12	85.7	1362	13	ADX47723	Adx47723 Plant full	c 472	12	85.7	2571	4	AAI26650	AAI26650 Human bre
c 400	12	85.7	1368	9	ACD19166	AcD19166 B. coli 0	c 473	12	85.7	2584	13	ADO82147	AdO82147 Plant full
c 401	12	85.7	1368	10	ADC01591	Adc01591 Enterobac	c 474	12	85.7	2602	10	ADB64196	AdB64196 Human gen
c 402	12	85.7	1378	4	ABA88908	AbA88908 Escherich	c 475	12	85.7	2724	5	AA578437	AA578437 DNA encod
c 403	12	85.7	1413	10	ADP58398	AdP58398 Human pol	c 476	12	85.7	2724	5	AA568040	AA568040 DNA encod
c 404	12	85.7	1431	2	AAT85635	Aat85635 Balanus a	c 477	12	85.7	2793	12	ADP22447	AdP22447 Sea-squid
c 405	12	85.7	1434	8	ADA32352	Ada32352 DNA encod	c 478	12	85.7	2818	4	AAH54648	AAH54648 S. epider
c 406	12	85.7	1453	8	ABX63157	Abx63157 Human cDN	c 479	12	85.7	2850	8	ACC42476	Acc42476 Human C1Q
c 407	12	85.7	1457	2	AAZ06764	Aaz06764 Phosphodi	c 480	12	85.7	2900	10	ADC89716	AdC89716 L. johnso
c 408	12	85.7	1523	6	AB579007	Ab579007 B. coli C	c 481	12	85.7	2960	6	ABR92144	AbR92144 Cyclo-o
c 409	12	85.7	1523	10	ADH80574	AdH80574 Escherich	c 482	12	85.7	2960	14	ADK07065	AdK07065 Cyclo-o
c 410	12	85.7	1537	4	AAI58673	Aai58673 Human pol	c 483	12	85.7	2978	12	ADRI6891	AdRI6891 Acetomoni
c 411	12	85.7	1537	5	ADQ98891	Adq98891 DNA encod	c 484	12	85.7	3030	3	AAH54637	AAH54637 S. epider
c 412	12	85.7	1537	9	ADB48651	AdB48651 Novel hum	c 485	12	85.7	3108	3	AAA97632	AAa97632 Mouse neu
c 413	12	85.7	1560	8	AB275094	Ab275094 Mouse emb	c 486	12	85.7	3150	4	AAH54529	AAh54529 S. epider
c 414	12	85.7	1602	12	ADO26194	AdQ26194 Human pho	c 487	12	85.7	3348	6	ABZ11420	AbZ11420 Human pol
c 415	12	85.7	1636	2	AAx37992	Aax37992 Human sec	c 488	12	85.7	3348	6	ADM43938	AdM43938 Novel hum
c 416	12	85.7	1636	8	ADA40396	Ada40396 Human sec	c 489	12	85.7	3353	5	ABX71421	AbX71421 Human tes
c 417	12	85.7	1636	8	ACC50766	Acc50766 Human sec	c 490	12	85.7	3387	2	AAx55540	AAx55540 Invertebr
c 418	12	85.7	1636	9	ADA11488	Ada11488 Human cDN	c 491	12	85.7	3437	4	ABL18960	AbL18960 Drosophill
c 419	12	85.7	1653	10	ADJ95081	AdJ95081 Novel NOV	c 492	12	85.7	3511	6	ABZ11574	AbZ11574 Human pol
c 420	12	85.7	1676	11	ACL29320	AcL29320 Rice abio	c 493	12	85.7	3511	5	ADM44092	AdM44092 Novel hum
c 421	12	85.7	1677	14	ACL71310	AcL71310 M. xanthu	c 494	12	85.7	3523	12	ABV24226	AbV24226 Human pro
c 422	12	85.7	1702	6	ABN59709	Abn59709 Novel hum	c 495	12	85.7	3523	3	ABV25694	AbV25694 Human pro
c 423	12	85.7	1728	4	ABL28131	AbL28131 Drosophill	c 496	12	85.7	3546	11	ACN88654	AcN88654 Breast ca
c 424	12	85.7	1730	4	AAI60459	Aai60459 Human pol	c 497	12	85.7	3562	4	ABU04416	AbU04416 Drosophill
c 425	12	85.7	1770	2	AAx98028	Aax98028 Human sec	c 498	12	85.7	3615	4	ABU20427	AbU20427 Drosophill
c 426	12	85.7	1770	8	AAH14148	Aah14148 Human cDN	c 499	12	85.7	3668	10	ADD24893	AdD24893 Human sec
c 427	12	85.7	1770	8	ADA39936	Ada39936 Human sec	c 500	12	85.7	3699	3	AAZ89623	AAZ89623 A. gossyp
c 428	12	85.7	1770	8	ACC50515	Acc50515 Human sec	c 501	12	85.7	3747	13	ACN42292	AcN42292 Human dia
c 429	12	85.7	1770	8	ADA11593	Ada11593 Human cDN	c 502	12	85.7	3828	4	AAH18018	AAH18018 Human cDN
c 430	12	85.7	1782	12	ADQ25930	AdQ25930 Human pho	c 503	12	85.7	3828	10	ABX08753	AbX08753 Angiogene
c 431	12	85.7	1782	13	ADR46215	Adr46215 Human pho	c 504	12	85.7	3828	13	ADP56190	AdP56190 Human PRO
c 432	12	85.7	1852	3	AACT7519	Aac7519 Human ORF	c 505	12	85.7	3828	14	AEA36243	AEa36243 Human nuc
c 433	12	85.7	1872	10	ADJ95079	AdJ95079 Novel NOV	c 506	12	85.7	3881	6	ABU58814	AbU58814 Fungal me
c 434	12	85.7	1887	2	AAZ06762	Aaz06762 Phosphodi	c 507	12	85.7	4121	2	AAx29140	Aax29140 Hypoxia-r
c 435	12	85.7	1892	10	ABX78371	Abx78371 Corn stre	c 508	12	85.7	4121	9	ACH00173	AcH00173 Rat cDNA
c 436	12	85.7	1917	13	ADRS8506	AdR8506 Aspergill	c 509	12	85.7	4121	10	ADC69803	AdC69803 Hypoxia-r
c 437	12	85.7	1929	14	ADZ85678	Adz85678 Murine pd	c 510	12	85.7	4121	10	AAZ62296	AAz62296 Human bre
c 438	12	85.7	1939	14	ADZ85826	Adz85826 Full leng	c 511	12	85.7	4290	4	ABU23008	AbU23008 Drosophill
c 439	12	85.7	1931	4	AAH17375	Aah17375 Human cDN	c 512	12	85.7	4343	4	ABU03429	AbU03429 Drosophill
c 440	12	85.7	1936	13	ADK64838	Adk64838 Plant full	c 513	12	85.7	4343	11	ADM02716	AdM02716 Human cDN
c 441	12	85.7	1967	6	AAZ06763	Aaz06763 Phosphodi	c 514	12	85.7	4482	4	ABU30306	AbU30306 Drosophill
c 442	12	85.7	1991	6	AAK92161	Abk92161 Prostata	c 515	12	85.7	4513	4	ABL28130	AbL28130 Drosophill
c 443	12	85.7	1991	12	ADO58106	AdO58106 Human pho	c 516	12	85.7	4513	13	ADR07846	AdR07846 Full leng
c 444	12	85.7	1991	13	ACN40846	AcN40846 Tumour-as	c 517	12	85.7	4562	12	ADR44010	AdR44010 Human bre
c 445	12	85.7	1997	2	AAZ09086	Aaz09086 Cyclic-GM	c 518	12	85.7	4562	14	ADX98490	AdX98490 Human bol
c 446	12	85.7	2000	8	ADA72637	Ada72637 Rice gene	c 519	12	85.7	4835	3	AAA97635	AAa97635 Mouse neu
c 447	12	85.7	2000	8	ADA72872	Ada72872 Rice gene	c 520	12	85.7	4900	4	ABU22188	AbU22188 Drosophill
c 448	12	85.7	2000	8	ADA73231	Ada73231 Rice gene	c 521	12	85.7	4900	4	AA557166	AA557166 DNA encod
c 449	12	85.7	2000	11	ACL35285	AcL35285 Rice stre	c 522	12	85.7	4900	10	ADC35890	AdC35890 Drosophill
c 450	12	85.7	2000	11	ACL36121	AcL36121 Rice stre	c 523	12	85.7	5242	12	ADK60429	AdK60429 Angiogene
c 451	12	85.7	2000	11	ACL36274	AcL36274 Rice stre	c 524	12	85.7	5242	12	ADK60730	AdK60730 Angiogene
c 452	12	85.7	2022	6	ABN66286	Abn66286 Streptoco	c 525	12	85.7	5242	12	ADP73052	AdP73052 Angiogene
c 453	12	85.7	2060	6	ABR844919	AbR84491 Aspergill	c 526	12	85.7	5242	12	ADQ96161	AdQ96161 T cell ac
c 454	12	85.7	2166	6	ABZ32442	Abz32442 Candida a	c 527	12	85.7	5736	4	ABU08443	AbU08443 Drosophill
c 455	12	85.7	2207	4	AAV29572	Aav29572 L. lactis	c 528	12	85.7	5789	13	ADP06575	AdP06575 Full leng
c 456	12	85.7	2238	4	ABU23009	AbU23009 Drosophill	c 529	12	85.7	6250	14	ACL64310	AcL64310 M. xanthu
c 457	12	85.7	2247	14	ADM11254	AdM11254 Tobacco h	c 530	12	85.7	7040	4	ABU03428	AbU03428 Drosophill

C 531	12	85.7	7176	4	ABL23012	AbL23012 Drosophila	C 604	11.4	81.4	60	6	ABN42325	Abn42325 Human sp1
C 532	12	85.7	8060	13	ADR84332	AdR84332 Aspergillus	C 605	11.4	81.4	60	6	ABN37773	Abn37773 Human sp1
C 533	12	85.7	8158	4	AAK91908	AAK91908 C. albica	C 606	11.4	81.4	65	6	ABN28477	Abn28477 Rat sp1c
C 534	12	85.7	9291	4	ABL20426	ABL20426 Drosophila	C 607	11.4	81.4	67	6	ABQ73659	Abq73659 Yersinia
C 535	12	85.7	9577	4	ABL08442	ABL08442 Drosophila	C 608	11.4	81.4	100	8	ACD80032	ACD80032 E. coli K
C 536	12	85.7	9974	2	AAK20573	AAK20573 Polynucle	C 609	11.4	81.4	100	8	ACD71765	ACD71765 E. coli K
C 537	12	85.7	10466	4	ABL06798	ABL06798 Drosophila	C 610	11.4	81.4	100	8	ACD80031	ACD80031 E. coli K
C 538	12	85.7	10523	4	AAK87458	AAK87458 Human imm	C 611	11.4	81.4	103	2	AAQ65663	AAQ65663 Alkaline
C 539	12	85.7	10523	4	AAK87455	AAK87455 Human imm	C 612	11.4	81.4	110	9	ACH03438	ACH03438 Human 1st
C 540	12	85.7	12198	10	ADBS7247	ADBS7247 Rat gene	C 613	11.4	81.4	147	8	ABK73524	ABK73524 Streptomy
C 541	12	85.7	12198	10	ADD47039	ADD47039 Rat gene	C 614	11.4	81.4	149	2	AAQ76752	AAQ76752 Human gen
C 542	12	85.7	12677	4	AAK72352	AAK72352 Human imm	C 615	11.4	81.4	156	7	ADBS66626	ADBS66626 Corn seed
C 543	12	85.7	12680	4	AAK72351	AAK72351 Human imm	C 616	11.4	81.4	159	4	AAI55222	AAI55222 Corn seed
C 544	12	85.7	13237	4	ABL17698	ABL17698 Drosophila	C 617	11.4	81.4	159	4	ABN48980	Abn48980 Human 1st
C 545	12	85.7	15468	12	ADN73144	ADN73144 Thale cte	C 618	11.4	81.4	162	4	ABN70072	Abn70072 Human foe
C 546	12	85.7	15762	4	ABL06916	ABL06916 Drosophila	C 619	11.4	81.4	162	4	AAI50188	AAI50188 Probe #18
C 547	12	85.7	17379	4	AAK71667	AAK71667 Human imm	C 620	11.4	81.4	162	4	ABN36870	ABN36870 Probe #15
C 548	12	85.7	17379	4	AAK28427	AAK28427 Genomic s	C 621	11.4	81.4	162	4	AAK44181	AAK44181 Human bon
C 549	12	85.7	17379	10	ADG41623	ADG41623 Human res	C 622	11.4	81.4	162	4	AAK18283	AAK18283 Human bra
C 550	12	85.7	17379	11	ADJ97397	ADJ97397 Human res	C 623	11.4	81.4	162	4	ABN43837	ABN43837 Human 1st
C 551	12	85.7	19278	10	ACR57551	ACR57551 Human fru	C 624	11.4	81.4	162	6	ABN18416	ABN18416 Human gen
C 552	12	85.7	20001	13	ADT77134	ADT77134 Type II d	C 625	11.4	81.4	168	2	AAQ83666	AAQ83666 Partial I
C 553	12	85.7	20001	14	ABN96527	ABN96527 Human ALD	C 626	11.4	81.4	171	2	AAQ83671	AAQ83671 Partial I
C 554	12	85.7	24081	10	AAQ54223	AAQ54223 Streptomy	C 627	11.4	81.4	173	4	AAI22832	AAI22832 Probe #12
C 555	12	85.7	26190	4	AAI98929	AAI98929 Human exc	C 628	11.4	81.4	173	4	ABN67922	ABN67922 Human foe
C 556	12	85.7	26190	5	AAI63279	AAI63279 Human kid	C 629	11.4	81.4	173	4	AAI48133	AAI48133 Probe #16
C 557	12	85.7	29559	14	ACI64791	ACI64791 M. xanthu	C 630	11.4	81.4	173	4	ABN49999	ABN49999 Human bre
C 558	12	85.7	36568	6	ABK50980	ABK50980 Human bol	C 631	11.4	81.4	173	4	AAK42068	AAK42068 Human bon
C 559	12	85.7	51698	12	ADQ97614	ADQ97614 Mouse can	C 632	11.4	81.4	173	4	AAK16317	AAK16317 Human bra
C 560	12	85.7	52101	10	AAQ54217	AAQ54217 Streptomy	C 633	11.4	81.4	173	4	ABN41672	ABN41672 Human 1st
C 561	12	85.7	53122	11	ACN43998_6	Continuation (7 of	C 634	11.4	81.4	173	5	AAI08504	AAI08504 Probe #84
C 562	12	85.7	63079	14	ADJ21509	ADJ21509 Murine ca	C 635	11.4	81.4	173	6	ABN16106	ABN16106 Human gen
C 563	12	85.7	72409	13	ABD33061	ABD33061 Human can	C 636	11.4	81.4	177	4	ABN24709	ABN24709 Drosophila
C 564	12	85.7	90616	12	ADQ97596	ADQ97596 Mouse can	C 637	11.4	81.4	180	10	ADD08988	ADD08988 Human pab
C 565	12	85.7	97291	10	ACR65317	ACR65317 Photocarb	C 638	11.4	81.4	183	1	AAQ92471	AAQ92471 Sequence
C 566	12	85.7	110000	6	ABA90521_18	Continuation (11 o	C 639	11.4	81.4	183	8	ACA25428	ACA25428 Partial I
C 567	12	85.7	110000	10	ACR67367_55	Continuation (56 o	C 640	11.4	81.4	189	8	ACA25428	ACA25428 Prokaryot
C 568	12	85.7	110000	13	ABD32665	ABD32665 Human can	C 641	11.4	81.4	191	4	ABN26727	ABN26727 Probe #16
C 569	12	85.7	112453	13	ABD32665	ABD32665 Human can	C 642	11.4	81.4	191	4	ABN74973	ABN74973 Human foe
C 570	12	85.7	112453	13	ABD32665	ABD32665 Human can	C 643	11.4	81.4	191	4	AAI55501	AAI55501 Probe #24
C 571	12	85.7	122673	14	ABE61123	ABE61123 Human PDE	C 644	11.4	81.4	191	4	ABN39663	ABN39663 Probe #18
C 572	12	85.7	143899	6	AAI38336	AAI38336 Genomic s	C 645	11.4	81.4	191	4	AAK49618	AAK49618 Human bon
C 573	12	85.7	168325	11	ACN44484	ACN44484 Mouse gen	C 646	11.4	81.4	191	4	AAK23477	AAK23477 Human bra
C 574	12	85.7	235070	11	ACN45174	ACN45174 Human gen	C 647	11.4	81.4	191	4	ABN49239	ABN49239 Human 1st
C 575	12	85.7	275790	14	ADZ00150	ADZ00150 Salmonell	C 648	11.4	81.4	191	6	ABN23106	ABN23106 Human gen
C 576	12	85.7	310268	13	ABD32548	ABD32548 Human can	C 649	11.4	81.4	192	4	AAH04728	AAH04728 Gene expr
C 577	11.6	82.9	33	12	ADJ66778	ADJ66778 Flea and	C 650	11.4	81.4	195	4	AAH35239	AAH35239 Human col
C 578	11.6	82.9	2000	8	ADAT73026	ADAT73026 Rice gene	C 651	11.4	81.4	195	10	ADH85366	ADH85366 Enterococ
C 579	11.6	82.9	2000	8	ADAT73026	ADAT73026 Rice gene	C 652	11.4	81.4	195	6	ABN76744	ABN76744 Human ORF
C 580	11.4	81.4	20	2	AAV31172	AAV31172 Bacillus	C 653	11.4	81.4	199	12	ACH83057	ACH83057 Human gen
C 581	11.4	81.4	20	2	AAV31180	AAV31180 Bacillus	C 654	11.4	81.4	203	7	ADBS6830	ADBS6830 Corn seed
C 582	11.4	81.4	20	6	ABK11818	ABK11818 Hybrid B.	C 655	11.4	81.4	206	14	ADY53863	ADY53863 Gordonia
C 583	11.4	81.4	20	6	ABK11826	ABK11826 5' exchan	C 656	11.4	81.4	227	14	ADY53861	ADY53861 Gordonia
C 584	11.4	81.4	20	10	ADH393897	ADH393897 Human gen	C 657	11.4	81.4	230	4	AAH57347	AAH57347 Human bra
C 585	11.4	81.4	20	12	ADL35186	ADL35186 B. thurin	C 658	11.4	81.4	237	5	AAH71836	AAH71836 DNA encod
C 586	11.4	81.4	20	12	ADG91969	ADG91969 PCR prime	C 659	11.4	81.4	237	13	ADBS0615	ADBS0615 Bacterial
C 587	11.4	81.4	20	12	ADG91969	ADG91969 PCR prime	C 660	11.4	81.4	243	12	ADL02685	ADL02685 DNA encod
C 588	11.4	81.4	24	6	ABQ05350	ABQ05350 oligonuc	C 661	11.4	81.4	244	12	ADP59119	ADP59119 Maize car
C 589	11.4	81.4	24	6	ABQ11596	ABQ11596 oligonuc	C 662	11.4	81.4	250	4	ABN88653	ABN88653 Escherich
C 590	11.4	81.4	24	6	ABQ05309	ABQ05309 oligonuc	C 663	11.4	81.4	255	6	ABK87533	ABK87533 Mammalian
C 591	11.4	81.4	24	6	ABQ00675	ABQ00675 oligonuc	C 664	11.4	81.4	258	8	ACA00790	ACA00790 C. glutam
C 592	11.4	81.4	24	6	ABQ11637	ABQ11637 oligonuc	C 665	11.4	81.4	264	5	AAH66623	AAH66623 C. glutam
C 593	11.4	81.4	25	2	AAI04429	AAI04429 M. tuberc	C 666	11.4	81.4	269	12	ADP62217	ADP62217 Soybean c
C 594	11.4	81.4	25	6	ABQ13132	ABQ13132 oligonuc	C 667	11.4	81.4	276	6	ABN74740	ABN74740 Corn taab
C 595	11.4	81.4	25	6	ABQ13173	ABQ13173 oligonuc	C 668	11.4	81.4	291	6	ABK38794	ABK38794 CDNA enco
C 596	11.4	81.4	25	9	ACH56700	ACH56700 DNA targ	C 669	11.4	81.4	291	8	ACA11123	ACA11123 Human lun
C 597	11.4	81.4	30	2	AAO10731	AAO10731 oligonuc	C 670	11.4	81.4	291	10	ACA02309	ACA02309 Lung can
C 598	11.4	81.4	33	2	AAO83647	AAO83647 Internal	C 671	11.4	81.4	291	13	ADH46351	ADH46351 Human lun
C 599	11.4	81.4	50	4	AAI34522	AAI34522 Human SNP	C 672	11.4	81.4	291	3	ADJ20270	ADJ20270 Human lun
C 600	11.4	81.4	50	4	AAI03083	AAI03083 1466-95 P	C 673	11.4	81.4	292	3	AAO01958	AAO01958 Human sec
C 601	11.4	81.4	51	4	AAI78257	AAI78257 Human g1	C 674	11.4	81.4	293	12	ADP62755	ADP62755 Maize car
C 602	11.4	81.4	60	6	ABQ73883	ABQ73883 Yersinia	C 675	11.4	81.4	296	6	ABN73464	ABN73464 Corn taab
C 603	11.4	81.4	60	6	ABN49744	ABN49744 Human sp1	C 676	11.4	81.4	305	6	ABN68969	ABN68969 Novel mur

677	11.4	81.4	307	5	ABA11517	Abal1517 Human ner	C 750	11.4	81.4	458	5	AA104872	AA104872 Probe #8
678	11.4	81.4	308	10	ABX85434	Abx85434 Corn ear-	C 751	11.4	81.4	458	5	AA103496	AA103496 Probe #34
C 679	11.4	81.4	321	12	AAT31177	Aat31177 Mutated O	C 752	11.4	81.4	458	6	AB803564	AB803564 Human gen
C 680	11.4	81.4	321	12	ADL93587	Adl93587 Human CD4	C 753	11.4	81.4	458	6	AB805136	AB805136 Human gen
681	11.4	81.4	328	3	AAA41530	Aaa41530 Human bec	C 754	11.4	81.4	458	9	ADN38400	ADN38400 Human gen
682	11.4	81.4	330	3	ADA49151	Ada49151 Maize gen	C 755	11.4	81.4	458	10	ADG88750	ADG88750 Corn c1m
C 683	11.4	81.4	335	2	AAV87152	AAv87152 EST clone	C 756	11.4	81.4	459	3	ACA46344	ACA46344 Arabidops
684	11.4	81.4	340	9	ACH42717	Ach42717 Human foe	C 757	11.4	81.4	459	8	ACA35048	ACA35048 Prokaryot
685	11.4	81.4	352	12	ACH93436	Ach93436 Human gen	C 758	11.4	81.4	460	4	ABA57446	ABA57446 Human foe
C 686	11.4	81.4	357	13	ACHF5010	Achf5010 Human S1R	C 759	11.4	81.4	460	4	ABA36994	ABA36994 Probe #56
687	11.4	81.4	358	6	ABO85712	Abq85712 Arabidops	C 760	11.4	81.4	460	4	ABA26950	ABA26950 Probe #54
688	11.4	81.4	365	4	AAKS6666	Aaks6666 Human imm	C 761	11.4	81.4	460	4	AAK31085	AAK31085 Human bon
C 689	11.4	81.4	369	3	AAAC6321	Aaac6321 Gene frag	C 762	11.4	81.4	460	4	AAK05484	AAK05484 Human bra
C 690	11.4	81.4	371	3	AAZ45989	Aaz45989 CDNA enco	C 763	11.4	81.4	460	4	AB830764	AB830764 Human l1v
C 691	11.4	81.4	372	14	ACL56113	Ac156113 Human col	C 764	11.4	81.4	460	6	AB805836	AB805836 Human gen
C 692	11.4	81.4	374	2	AAQ73727	Aaq73727 Retrocans	C 765	11.4	81.4	462	10	ADD08978	ADD08978 Human pan
C 693	11.4	81.4	374	4	AAK73298	Aak73298 Human imm	C 766	11.4	81.4	463	5	AAH87825	AAH87825 Pepperm1n
C 694	11.4	81.4	375	2	AAV87184	AAv87184 EST clone	C 767	11.4	81.4	463	5	ABV46070	ABV46070 Human pro
C 695	11.4	81.4	378	10	ADD08982	Add08982 Human pan	C 768	11.4	81.4	463	9	ACH45567	ACH45567 Human foe
C 696	11.4	81.4	381	9	ACH46902	Ach46902 Human inf	C 769	11.4	81.4	465	2	AAT36688	Aat36688 Osteoclas
C 697	11.4	81.4	388	9	ACH19655	Ach19655 Human adu	C 770	11.4	81.4	465	6	ABV98307	ABv98307 Human pan
698	11.4	81.4	393	10	ADF57861	Adf57861 Human pol	C 771	11.4	81.4	469	4	AAH00970	AAH00970 Leibman1
C 699	11.4	81.4	398	8	ABX36584	Abx36584 Bovine ES	C 772	11.4	81.4	469	4	AAH00972	AAH00972 Leibman1
C 700	11.4	81.4	398	10	ADH42944	Adh42944 Mouse pro	C 773	11.4	81.4	469	4	ACH13531	ACH13531 Human adu
701	11.4	81.4	403	5	AA105074	AA105074 Probe #50	C 774	11.4	81.4	471	5	ABA20385	ABA20385 Human ner
702	11.4	81.4	403	10	ADL24523	Adl24523 Intestina	C 775	11.4	81.4	480	11	ABD15066	ABd15066 Pseudomon
703	11.4	81.4	404	4	AAH12660	Aah12660 Human CDN	C 776	11.4	81.4	480	11	ACH13758	ACH13758 Human adu
C 704	11.4	81.4	405	4	AAH84616	Aah84616 B. coli g	C 777	11.4	81.4	483	9	ACH13758	ACH13758 Human adu
C 705	11.4	81.4	405	4	AAH67068	Aah67068 Novel hum	C 778	11.4	81.4	487	10	ABD50413	ABD50413 Primary r
C 706	11.4	81.4	405	8	ACA18637	Aca18637 Prokaryot	C 779	11.4	81.4	490	9	ACH33590	ACH33590 Human end
C 707	11.4	81.4	405	12	ACH83330	Ach83330 Human gen	C 780	11.4	81.4	495	13	ADX50554	ADx50554 Plant ful
C 708	11.4	81.4	406	9	ACH49185	Ach49185 Human leu	C 781	11.4	81.4	496	13	ACN50698	ACn50698 Cotton an
C 709	11.4	81.4	408	2	AAT85950	Aat85950 Human AMY	C 782	11.4	81.4	497	13	ACN50784	ACn50784 Cotton an
C 710	11.4	81.4	408	8	ABX37499	Abx37499 Bovine ES	C 783	11.4	81.4	498	6	ABK5324	ABK5324 Human col
C 711	11.4	81.4	412	8	ABX37585	Abx37585 Bovine ES	C 784	11.4	81.4	498	8	ACA26394	ACA26394 Prokaryot
C 712	11.4	81.4	412	8	ABX37585	Abx37585 Bovine ES	C 785	11.4	81.4	500	12	ACH77234	ACH77234 Human gen
713	11.4	81.4	413	5	AAH88743	Aah88743 Sucrose p	C 786	11.4	81.4	501	4	ABA62449	ABA62449 Human foe
714	11.4	81.4	415	5	AAH88743	Aah88743 Sucrose p	C 787	11.4	81.4	501	4	AA142429	AA142429 Probe #11
715	11.4	81.4	415	10	ADBS1486	Adbs1486 Primary r	C 788	11.4	81.4	501	4	ABA29783	ABA29783 Probe #82
C 716	11.4	81.4	417	8	ABX55824	Abx55824 Bovine ES	C 789	11.4	81.4	501	4	AAK36655	AAK36655 Human bon
717	11.4	81.4	421	5	ABV16272	Abv16272 Human pro	C 790	11.4	81.4	501	4	AAK10794	AAK10794 Human bra
718	11.4	81.4	421	5	AAH67574	Aah67574 Novel hum	C 791	11.4	81.4	501	4	AB836320	AB836320 Human l1v
C 719	11.4	81.4	421	5	ABQ99118	Abq99118 Human ORF	C 792	11.4	81.4	501	5	AB836320	AB836320 Human l1v
720	11.4	81.4	429	8	ABX36242	Abx36242 Bovine ES	C 793	11.4	81.4	501	5	AB836320	AB836320 Human l1v
C 721	11.4	81.4	432	2	AAT33176	Aat33176 Mutated O	C 794	11.4	81.4	501	6	AB810666	AB810666 Human gen
C 722	11.4	81.4	432	6	ABK62903	Abk62903 Rat seque	C 795	11.4	81.4	504	3	AA531976	AA531976 Neisseria
C 723	11.4	81.4	432	10	ADBS5697	Adbs5697 Toxicity-	C 796	11.4	81.4	504	10	ADCT7429	ADCT7429 DNA homol
C 724	11.4	81.4	432	10	ADBS1487	Adbs1487 Primary r	C 797	11.4	81.4	504	10	ADK56007	ADK56007 Plant DNA
C 725	11.4	81.4	438	2	AAT36689	Aat36689 Osteoclas	C 798	11.4	81.4	505	12	ADJ10782	ADj10782 Recombina
C 726	11.4	81.4	438	5	ABV38586	Abv38586 Human pro	C 799	11.4	81.4	505	12	ACH69357	ACH69357 Human gen
C 727	11.4	81.4	439	6	ABK62922	Abk62922 Rat seque	C 800	11.4	81.4	510	4	AB119531	AB119531 Drosoph11
C 728	11.4	81.4	439	10	ADBS6953	Adbs6953 Toxicity-	C 801	11.4	81.4	510	11	ACH29334	ACH29334 Drosoph11
C 729	11.4	81.4	443	4	AAK64488	Aak64488 Human imm	C 802	11.4	81.4	510	11	ACH29334	ACH29334 Drosoph11
C 730	11.4	81.4	443	5	AAK64488	Aak64488 Human imm	C 803	11.4	81.4	512	12	ADL84315	ADL84315 DNA up-re
C 731	11.4	81.4	446	9	ACH14171	Ach14171 Human adu	C 804	11.4	81.4	512	12	ADL84316	ADL84316 DNA up-re
C 732	11.4	81.4	448	9	ACH48739	Ach48739 Human leu	C 805	11.4	81.4	513	13	AAFI1322	AAFI1322 Asperg11
C 733	11.4	81.4	448	9	ACH45475	Ach45475 Human foe	C 806	11.4	81.4	513	13	ADU55363	ADU55363 Asperg11
C 734	11.4	81.4	449	13	ADX10349	Adx10349 Plant ful	C 807	11.4	81.4	513	13	ADZ93366	ADZ93366 Asperg11
C 735	11.4	81.4	450	8	ACA28963	Aca28963 Prokaryot	C 808	11.4	81.4	515	6	ABQ36137	ABQ36137 Oligonuc1
C 736	11.4	81.4	454	6	ABT11346	Abt11346 Yeast bel	C 809	11.4	81.4	515	6	ABQ36136	ABQ36136 Oligonuc1
C 737	11.4	81.4	458	4	AA113609	AA113609 Probe #35	C 810	11.4	81.4	515	6	ACH15803	ACH15803 Human adu
C 738	11.4	81.4	458	4	AA151114	AA151114 Probe #50	C 811	11.4	81.4	516	11	ACH96986	ACH96986 K1ebste11
C 739	11.4	81.4	458	4	ABA55319	Abas55319 Human foe	C 812	11.4	81.4	520	6	ABU01379	ABU01379 Murine ap
C 740	11.4	81.4	458	4	ABA56866	Abas6866 Human foe	C 813	11.4	81.4	520	13	ACN59750	ACN59750 Cotton gy
C 741	11.4	81.4	458	4	AA134970	AA134970 Probe #36	C 814	11.4	81.4	521	12	ACH79760	ACH79760 Human gen
C 742	11.4	81.4	458	4	AA136450	AA136450 Probe #51	C 815	11.4	81.4	522	8	ACA32316	ACA32316 Prokaryot
C 743	11.4	81.4	458	4	ABA44858	Abaa44858 Human bre	C 816	11.4	81.4	525	14	AA615942	AA615942 Human ost
C 744	11.4	81.4	458	4	ABA46313	Abaa6313 Human bre	C 817	11.4	81.4	525	14	AA615942	AA615942 Human ost
C 745	11.4	81.4	458	4	AAK29023	Aak29023 Human bon	C 818	11.4	81.4	528	13	ADK65644	ADK65644 DNA enco
C 746	11.4	81.4	458	4	AAK30501	Aak30501 Human bon	C 819	11.4	81.4	535	12	ADK35502	ADK35502 DNA enco
C 747	11.4	81.4	458	4	AAK35652	Aak35652 Human bra	C 820	11.4	81.4	535	12	ADK35502	ADK35502 DNA enco
C 748	11.4	81.4	458	4	AB830160	AB830160 Human l1v	C 821	11.4	81.4	536	4	AA163827	AA163827 Human pol
C 749	11.4	81.4	458	4	AB828636	AB828636 Human l1v	C 822	11.4	81.4	536	4	AA631623	AA631623 CDNA enco

C 823	11.4	81.4	536	4	ABK43817	Abk43817 DNA encod	C 896	11.4	81.4	618	13	ADV41756	Adv41756 Rat cardi
C 824	11.4	81.4	536	12	AD154204	Ad154204 CDNA encod	C 897	11.4	81.4	629	10	ACN53940	Acn53940 Cotton an
C 825	11.4	81.4	536	12	ADM24378	Adm24378 Human PRO	C 898	11.4	81.4	629	13	ACN53940	Acn53940 Cotton an
C 826	11.4	81.4	537	13	AAC74530	Aac74530 Human ORF	C 899	11.4	81.4	633	3	AAZ55544	Aaz55544 Feline ma
C 827	11.4	81.4	537	6	ABN16615	Abn16615 Human ORF	C 900	11.4	81.4	633	3	AAZ55545	Aaz55545 Feline ma
C 828	11.4	81.4	538	13	ADQ48838	Adq48838 Novel can	C 901	11.4	81.4	642	10	ADCS51237	Adc51237 Mutant P
C 829	11.4	81.4	539	9	ACH37731	Ach37731 Human end	C 902	11.4	81.4	647	4	AB118861	Ab118861 Drosophill
C 830	11.4	81.4	542	4	AAH37189	Aah37189 Human col	C 903	11.4	81.4	649	6	ABK43431	Abk43431 Human CDN
C 831	11.4	81.4	543	11	ABK53446	Abk53446 Human eos	C 904	11.4	81.4	650	5	ABG23232	Abg23232 Contig HR
C 832	11.4	81.4	543	11	ABD17593	Abd17593 Pseudomon	C 905	11.4	81.4	657	5	AA590153	Aa590153 DNA encod
C 833	11.4	81.4	546	6	ABQ44997	Abq44997 Oligonuc1	C 906	11.4	81.4	661	10	ADK55181	Adk55181 Plant DNA
C 834	11.4	81.4	546	6	ABQ44996	Abq44996 Oligonuc1	C 907	11.4	81.4	661	10	ADK57744	Adk57744 Plant DNA
C 835	11.4	81.4	547	14	ADCT6962	Adc76962 DNA homol	C 908	11.4	81.4	662	9	ACL24023	ACL24023 DNA clone
C 836	11.4	81.4	547	14	ABE66206	Abe66206 Rice geno	C 909	11.4	81.4	670	5	AAE93261	Aae93261 DNA encod
C 837	11.4	81.4	549	13	AAAC2993	Aac2993 Arabidops	C 910	11.4	81.4	671	3	AAE13513	Aae13513 Aspergill
C 838	11.4	81.4	549	13	ADQ57259	Adq57259 Novel can	C 911	11.4	81.4	671	10	ADCT6220	Adc76220 DNA homol
C 839	11.4	81.4	554	4	AA143036	Aa143036 Probe #11	C 912	11.4	81.4	671	10	ADK54118	Adk54118 Plant DNA
C 840	11.4	81.4	554	4	AB536880	Ab536880 Human liv	C 913	11.4	81.4	671	11	ADK54118	Adk54118 Plant DNA
C 841	11.4	81.4	554	6	ABQ32977	Abq32977 Oligonuc1	C 914	11.4	81.4	671	13	ADU57554	Adu57554 Insect re
C 842	11.4	81.4	554	6	ABQ32976	Abq32976 Oligonuc1	C 915	11.4	81.4	671	13	ADU57554	Adu57554 Aspergill
C 843	11.4	81.4	555	9	ACL24021	ACL24021 DNA clone	C 916	11.4	81.4	672	13	ADR61857	Adr61857 Cotton CD
C 844	11.4	81.4	557	4	AAH10202	Aah10202 Human CDN	C 917	11.4	81.4	679	13	ADT17591	Adt17591 Plant CDN
C 845	11.4	81.4	558	12	ACH79736	Ach79736 Human gen	C 918	11.4	81.4	684	13	ADT17072	Adt17072 Plant CDN
C 846	11.4	81.4	558	12	AAT33180	Aat33180 Mutated O	C 919	11.4	81.4	685	4	AAK93634	Aak93634 Human CDN
C 847	11.4	81.4	556	13	ADQ56901	Adq56901 Novel can	C 920	11.4	81.4	685	4	AAK93634	Aak93634 Human CDN
C 848	11.4	81.4	567	4	ABA60765	Ab60765 Human foe	C 921	11.4	81.4	685	12	ADL30061	Adl30061 3' end of
C 849	11.4	81.4	567	4	AA140658	Aa140658 Probe #93	C 922	11.4	81.4	685	12	ADL28387	Adl28387 5' end of
C 850	11.4	81.4	567	4	ABA28814	Ab28814 Probe #72	C 923	11.4	81.4	690	3	AA646413	Aa646413 Open read
C 851	11.4	81.4	567	4	AAK34942	Aak34942 Human bon	C 924	11.4	81.4	690	8	ACC47178	Acc47178 Rat APOB
C 852	11.4	81.4	567	4	AAK09051	Aak09051 Human bra	C 925	11.4	81.4	692	1	AAAN91781	Aan91781 DNA probe
C 853	11.4	81.4	567	4	AB534696	Ab534696 Human liv	C 926	11.4	81.4	705	5	AA691529	Aa691529 DNA encod
C 854	11.4	81.4	567	6	AB509443	Ab509443 Human gen	C 927	11.4	81.4	708	4	ABA89034	Ab89034 Escherich
C 855	11.4	81.4	567	10	AAU56260	Aau56260 Bovine IT	C 928	11.4	81.4	710	12	ADU42783	Adu42783 Plant CDN
C 856	11.4	81.4	569	12	ADU44194	Ad44194 Plant cDN	C 929	11.4	81.4	714	12	ACH90889	Ach90889 Human gen
C 857	11.4	81.4	570	12	ADQ92040	Adq92040 Human aut	C 930	11.4	81.4	715	13	ADK48180	Adk48180 Plant ful
C 858	11.4	81.4	571	10	ADK53242	Adk53242 Plant DNA	C 931	11.4	81.4	717	11	ABD01748	Abd01748 Pseudomon
C 859	11.4	81.4	577	9	AAE08377	Aae08377 Fusarium	C 932	11.4	81.4	720	4	AAK61014	Aak61014 Human imm
C 860	11.4	81.4	577	9	ACL24026	ACL24026 DNA clone	C 933	11.4	81.4	725	12	ADN61658	Adn61658 Triclicum
C 861	11.4	81.4	577	13	ADU52418	Adu52418 Fusarium	C 934	11.4	81.4	725	12	ADN61658	Adn61658 Triclicum
C 862	11.4	81.4	577	13	ADU52418	Adu52418 Fusarium	C 935	11.4	81.4	726	9	ADA31746	Ada31746 DNA encod
C 863	11.4	81.4	577	14	ADZ90421	Adz90421 Fusarium	C 936	11.4	81.4	734	8	ABZ56782	Abz56782 Aspergill
C 864	11.4	81.4	579	6	ABO38415	Abg38415 Oligonuc1	C 937	11.4	81.4	735	6	ABK78568	Abk78568 Bacillu
C 865	11.4	81.4	579	6	ABO38414	Abg38414 Oligonuc1	C 938	11.4	81.4	738	13	ADT46477	Adt46477 Bacterial
C 866	11.4	81.4	579	12	ACH69630	Ach69630 Human gen	C 939	11.4	81.4	745	10	ADCT6226	Adc76226 DNA homol
C 867	11.4	81.4	583	10	ADCT5095	Adc75095 N bentham	C 940	11.4	81.4	745	10	ADK54127	Adk54127 Plant DNA
C 868	11.4	81.4	583	10	ADCT5095	Adc75095 N bentham	C 941	11.4	81.4	745	12	ADU67303	Adu67303 Human ova
C 869	11.4	81.4	583	11	ADCT5095	Adc75095 N bentham	C 942	11.4	81.4	746	11	ADU67303	Adu67303 Human ova
C 870	11.4	81.4	583	13	ADCT5095	Adc75095 N bentham	C 943	11.4	81.4	753	8	ACA25336	ACA25336 Prokaryot
C 871	11.4	81.4	583	13	ADCT5095	Adc75095 N bentham	C 944	11.4	81.4	754	6	ABQ34281	Abq34281 Oligonuc1
C 872	11.4	81.4	584	13	ADK48762	Adk48762 Plant ful	C 945	11.4	81.4	754	6	ABQ34280	Abq34280 Oligonuc1
C 873	11.4	81.4	586	13	ADK33248	Adk33248 Plant ful	C 946	11.4	81.4	756	12	ADH03222	Adh03222 Tenaurin
C 874	11.4	81.4	587	13	ACN53211	Acn53211 Cotton an	C 947	11.4	81.4	756	12	ADH03222	Adh03222 Tenaurin
C 875	11.4	81.4	589	6	ABL81829	Ab181829 Human col	C 948	11.4	81.4	762	10	ABZ52160	Abz52160 Aspergill
C 876	11.4	81.4	590	4	AAH03555	Aah03555 Human CDN	C 949	11.4	81.4	762	10	ADFO1339	Adfo1339 Bacterial
C 877	11.4	81.4	593	13	ACN54303	Acn54303 Cotton an	C 950	11.4	81.4	765	13	ADK30282	Adk30282 Plant ful
C 878	11.4	81.4	594	12	AAT33175	Aat33175 Mutated O	C 951	11.4	81.4	767	13	ADK48221	Adk48221 Plant ful
C 879	11.4	81.4	594	11	ACL34332	ACL34332 Rice abio	C 952	11.4	81.4	768	8	ACA45592	ACA45592 Prokaryot
C 880	11.4	81.4	597	13	AAV21146	Aav21146 Internal	C 953	11.4	81.4	774	11	ABD01709	Abd01709 Pseudomon
C 881	11.4	81.4	598	12	AAV21146	Aav21146 Internal	C 954	11.4	81.4	777	13	ADK4963	Adk4963 Cotton CD
C 882	11.4	81.4	598	12	AAV21170	Aav21170 Internal	C 955	11.4	81.4	779	13	ADK4963	Adk4963 Cotton CD
C 883	11.4	81.4	599	13	ADK56645	Adk56645 Cotton CD	C 956	11.4	81.4	780	3	AAZ55543	Aaz55543 Feline CD
C 884	11.4	81.4	600	6	ABQ66395	Abq66395 Arabidops	C 957	11.4	81.4	780	3	AAZ55542	Aaz55542 Feline CD
C 885	11.4	81.4	600	9	AAZ57189	Aaz57189 Mycobacte	C 958	11.4	81.4	783	10	ADT90010	Adt90010 Human gen
C 886	11.4	81.4	600	12	ADN61660	Adn61660 Triclicum	C 959	11.4	81.4	783	10	ADT90010	Adt90010 Human gen
C 887	11.4	81.4	602	13	ACN46478	Acn46478 Cotton pr	C 960	11.4	81.4	789	2	AAK40044	Aak40044 Prostate
C 888	11.4	81.4	604	14	ADK16770	Adk16770 Human can	C 961	11.4	81.4	790	6	ABO52667	Abg52667 Oligonuc1
C 889	11.4	81.4	608	6	ABN25395	Abn25395 Human ORF	C 962	11.4	81.4	800	6	ABO52666	Abg52666 Oligonuc1
C 890	11.4	81.4	609	3	ABZ41453	Abz41453 N gonorr	C 963	11.4	81.4	802	2	AAK40045	Aak40045 Prostate
C 891	11.4	81.4	612	3	AAZ53967	Aaz53967 Neisseria	C 964	11.4	81.4	804	12	ACH90938	Ach90938 Human gen
C 892	11.4	81.4	612	12	ADQ36932	Adq36932 Cell prol	C 965	11.4	81.4	804	12	ACH90938	Ach90938 Human gen
C 893	11.4	81.4	612	12	ADQ36932	Adq36932 Cell stre	C 966	11.4	81.4	807	11	AB124401	Ab124401 Drosophill
C 894	11.4	81.4	613	13	ADK33151	Adk33151 Plant ful	C 967	11.4	81.4	807	11	ADK33151	Adk33151 Plant ful
C 895	11.4	81.4	618	10	ABQ80467	Abq80467 Rat subti	C 968	11.4	81.4	814	6	AB564931	Ab564931 Rice ribo

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C 969 11.4 81.4 816 4 AAD03962 Ad03962 Human act
C 970 11.4 81.4 816 6 ABS73266 Abs73266 DNA encod
C 971 11.4 81.4 816 12 ADP28828 Adp28828 Human sec
C 972 11.4 81.4 816 12 ADQ83359 Adq83359 Human tum
C 973 11.4 81.4 816 13 ACN39435 Acn39435 Tumour-as
C 974 11.4 81.4 816 2 AAT33174 Aat33174 Mutated O
C 975 11.4 81.4 821 10 ADB52632 Adb52632 Primary r
C 976 11.4 81.4 821 11 ADW21810 Adw21810 Rat hepat
C 977 11.4 81.4 825 10 ABZ38826 Abz38826 N. gonorr
C 978 11.4 81.4 828 3 AAZ53604 Aaz53604 Neisseria
C 979 11.4 81.4 830 10 ADH28934 Adh28934 Human chr
C 980 11.4 81.4 833 12 ADG63275 Adg63275 Transcript
C 981 11.4 81.4 839 13 ADX12269 Adx12269 Plant full
C 982 11.4 81.4 841 13 ADX49038 Adx49038 Plant full
C 983 11.4 81.4 843 13 ADX48835 Adx48835 Plant full
C 984 11.4 81.4 843 4 ABL21765 Abl21765 Drosophila
C 985 11.4 81.4 849 11 ADM44906 Adm44906 Insect re
C 986 11.4 81.4 849 11 ABD02753 Abd02753 Pseudomon
C 987 11.4 81.4 854 3 AAA64412 Aaa64412 DNA encod
C 988 11.4 81.4 861 11 ACH94679 Ach94679 Klebsiell
C 989 11.4 81.4 861 12 ADC035784 Adc035784 Novel mou
C 990 11.4 81.4 867 14 ACL66762 Acl66762 M. xanthu
C 991 11.4 81.4 871 6 ABO16669 Abq16669 Oligonuc
C 992 11.4 81.4 876 12 ACF57509 Acf57509 E coli be
C 993 11.4 81.4 876 12 ADG62867 Adg62867 Apo-B RNA
C 994 11.4 81.4 879 2 AAQ71632 Aaq71632 Apo-B RNA
C 995 11.4 81.4 879 11 ABD14987 Abd14987 Pseudomon
C 996 11.4 81.4 885 3 AAZ55541 Aaz55541 Feline CD
C 997 11.4 81.4 885 3 AAZ55540 Aaz55540 Feline CD
C 998 11.4 81.4 885 10 ADC75605 Adc75605 DNA homol
C 999 11.4 81.4 886 2 AAQ82741 Aaq82741 Chicken t
1000 11.4 81.4

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ALIGNMENTS

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RESULT 1
ID ADW79935 standard; RNA; 14 BP.
XX
AC ADW79935;
XX
DT 21-APR-2005 (first entry)
XX
DE Bacterial immunomodulatory Cpg oligoribonucleotide, SEQ ID NO:2.
XX
KW Immune modulation; immune stimulation; bacterial infection;
KW endotoxin shock; antibacterial; antimicrobial; immunomodulator;
KW immunostimulant; adjuvant; ss.
XX
OS Bacteria.
XX
FH Key Location/Qualifiers
FT misc_feature 1..2
FT /tag= a
FT /note= "Cpg dinucleotide"
FT misc_feature 13..14
FT /tag= b
FT /note= "Cpg dinucleotide"
XX
XX US2005032731-A1.
XX
PD 10-FEB-2005.
XX
PF 15-MAR-2004; 2004US-00800926.
XX
PR 11-MAY-1993; 93US-00059745.
PR 20-JAN-1995; 95US-00376175.
PR 18-AUG-1995; 95US-00517016.
PR 29-OCT-1996; 96US-00739264.
PR 17-NOV-1998; 98US-00193653.
PR 18-JUN-2001; 2001US-00883550.

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XX (MARS/) MARSHALL W E.
XX Marshall WG;
XX WPI, 2005-161694/17.
XX
XX Composition for modulating and/or stimulating immune system of animal
XX useful for withstanding microbial infections and lethality of endotoxin
XX shock, comprises low molecular weight oligoribonucleotide from bacteria.
XX
XX Claim 5; SEQ ID NO 2; 17pp; English.
XX
XX The invention relates to a composition for modulating and/or stimulating
XX the immune system of an animal, comprising bacterial oligoribonucleotides
XX (ORN) with a molecular weight of less than 10 kD. The bacterial ORNs are
XX preferably ADW79934-ADW79936, contain Cpg motifs and are resistant to
XX RNase. Bacteria produce RNase-resistant Cpg ORNs in response to stresses
XX such as a change in environment, including the neutral pH they encounter
XX when they colonize animals. The immune systems of animals have co-evolved
XX to recognize such Cpg ORNs as being derived from bacteria, and has
XX adapted a non-toxic alerting response to their release from bacteria. The
XX invention also relates to a method for the preparation of the bacterial
XX ORNs by subjecting bacteria to one or more periods of stress, separating
XX the ORNs and media from the bacteria, and filtering the separated product
XX to remove substances with a molecular weight of more than 10 kD; and a
XX method of using the filtrate to modulate/stimulate the immune system of
XX an animal to withstand microbial infection. The composition and methods
XX of the invention are useful for modulating and/or stimulating the immune
XX system of animals (including humans, poultry and livestock), particularly
XX to withstand microbial infections or the onset of endotoxin shock. The
XX compositions may be administered orally (e.g., as a food supplement) or
XX parentally, and may also be administered as an adjuvant for oral or
XX parenteral vaccines. The compositions may additionally be used topically
XX to protect against ear, nose and vaginal infections. They may further be
XX used to extend the viability of monocytes, thereby improving their
XX ability to mature into macrophages to fight infection, and may be used to
XX downregulate the cytotoxicity of macrophages to prevent them from
XX destroying normal T-cells in people with HIV infections. The composition
XX of the invention contains ORNs released by either harmless or pathogenic
XX bacteria, but is free from bacterial cells. Unlike Cpg
XX oligodeoxyribonucleotides (ODNs), the bacterial Cpg ORNs and compositions
XX containing them are non-toxic. The present sequence represents a
XX specifically claimed bacterial Cpg oligoribonucleotide present in
XX compositions of the invention.
XX
XX Sequence 14 BP; 3 A; 5 C; 3 G; 0 T; 3 U; 0 Other;
XX
XX Query Match 100.0%; Score 14; DB 14; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 4e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CGUACUGCAACUG 14
XX |||||||||
XX Db 1 CGUACUGCAACUG 14
XX
XX RESULT 2
XX ADS60734
XX ID ADS60734 standard; cDNA; 1786 BP.
XX
XX AC ADS60734;
XX
XX DT 02-DEC-2004 (first entry)
XX
XX DE Bacterial polynucleotide #12721.
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
XX cold tolerance; heat tolerance; drought tolerance; herbicide; omosis;
XX pathogen tolerance; pest tolerance; plant disease resistance;
XX cell cycle pathway modification; plant growth regulator;
XX homologous recombination; seed oil yield; protein yield; carbohydrate;
XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

```


KM bacterial polynucleotide; gene; ss.
 XX Bacteria.
 XX US2003233675-A1.
 XX 18-DEC-2003.
 XX 20-FEB-2003; 2003US-00369493.
 XX 21-FEB-2002; 2002US-0360039P.
 XX (CAOY/) CAO Y.
 XX (HINK/) HINKLE G J.
 XX (SLAT/) SLATER S C.
 XX (CHEN/) CHEN X.
 XX (GOLD/) GOLDMAN B S.
 XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX WPI; 2004-061375/06.
 XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX Claim 1; SEQ ID NO 36408; 122bp; English.
 XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition. This sequence represents a bacterial polynucleotide used in
 CC the scope of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX Sequence 1786 BP; 374 A; 597 C; 455 G; 360 T; 0 U; 0 Other;
 SQ
 QY Query Match 100.0%; Score 14; DB 13; Length 1786;
 Db Best Local Similarity 78.6%; Pred. No. 5.5e+02;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGUACUGCAACUCG 14
 ||:|||||:
 Db 128 CGTACTCGCACTCG 141
 RESULT 3
 ID ADS49626 standard; cDNA; 1981 BP.
 XX ADS49626/c
 AC ADS49626;
 XX 02-DEC-2004 (first entry)
 DT Bacterial polynucleotide #4369.
 XX

XX Recombinant DNA construct; transformed plant; improved plant property;
 KM cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KM pathogen tolerance; pest tolerance; plant disease resistance;
 KM cell cycle pathway modification; plant growth regulator;
 KM homologous recombination; seed oil yield; protein yield; carbohydrate;
 KM nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KM bacterial polynucleotide; gene; ss.
 XX Bacteria.
 XX US2003233675-A1.
 XX 18-DEC-2003.
 XX 20-FEB-2003; 2003US-00369493.
 XX 21-FEB-2002; 2002US-0360039P.
 XX (CAOY/) CAO Y.
 XX (HINK/) HINKLE G J.
 XX (SLAT/) SLATER S C.
 XX (CHEN/) CHEN X.
 XX (GOLD/) GOLDMAN B S.
 XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX WPI; 2004-061375/06.
 XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX Claim 1; SEQ ID NO 28056; 122bp; English.
 XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition. This sequence represents a bacterial polynucleotide used in
 CC the scope of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX Sequence 1981 BP; 448 A; 584 C; 648 G; 301 T; 0 U; 0 Other;
 SQ
 QY Query Match 100.0%; Score 14; DB 13; Length 1981;
 Db Best Local Similarity 78.6%; Pred. No. 5.5e+02;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGUACUGCAACUCG 14
 ||:|||||:
 Db 1510 CGTACTCGCACTCG 1497
 RESULT 4
 ID ACA25094/c

ID ACA25094 standard; DNA; 1986 BP.
 AC ACA25094;
 XX
 XX 19-JUN-2003 (first entry)
 DE Prokaryotic essential gene #6751.
 KM Antisense; ds; prokaryotic essential gene; cell proliferation;
 XX drug design; gene.
 OS Burkholderia fungorum.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 XX
 XX 21-MAR-2002; 2002MO-US009107.
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 XX (BLIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KU, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX P-PSDB; ABU21224.
 DR
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 XX Claim 14; SEQ ID NO 12964; 1766pp; English.
 XX
 XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 1986 BP; 450 A; 584 C; 651 G; 301 T; 0 U; 0 Other;

Query Match 100.0%; Score 14; DB 8; Length 1986;
 Best Local Similarity 78.6%; Pred. No. 5.5e+02;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGUACUGCACTCG 14
 DB 1510 CGTACTGCACTCG 1497
 RESULT 5
 ID ADS55136/C
 XX ADS55136 standard; cDNA; 2080 BP.
 AC ADS55136;
 XX
 XX 02-DEC-2004 (first entry)
 DE Bacterial polynucleotide #7123.
 XX
 XX Recombinant DNA construct; transformed plant; improved plant property;
 KM cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KM pathogen tolerance; pest tolerance; plant disease resistance;
 KM cell cycle pathway modification; plant growth regulator;
 KM homologous recombination; seed oil yield; protein yield; carbohydrate;
 KM nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 XX bacterial polynucleotide; gene; ss.
 XX
 OS Bacteria.
 XX
 XX US2003233675-A1.
 XX
 XX 18-DEC-2003.
 XX
 XX 20-FEB-2003; 2003US-00369493.
 XX
 XX 21-FEB-2002; 2002US-0360039P.
 XX
 XX
 XX (CAOY/) CAO Y.
 XX (HINK/) HINKLE G J.
 XX (SLAT/) SLATER S C.
 XX (CHEN/) CHEN X.
 XX (GOLD/) GOLDMAN B S.
 XX
 XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 PT WPI; 2004-061375/06.
 PT
 PT New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 XX Claim 1; SEQ ID NO 30810; 122pp; English.
 XX
 XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan

CC production. This sequence represents a bacterial polynucleotide used in
 CC the scope of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 2080 BP; 474 A; 610 C; 680 G; 316 T; 0 U; 0 Other;

Query Match 100.0%; Score 14; DB 13; Length 2080;

Best Local Similarity 78.6%; Pred. No. 5.6e+02; Indels 0; Gaps 0;

Matches 11; Conservative 3; Mismatches 0;

QY 1 CGUACUGCAACUCG 14

Db 1510 CGTACTGCAACTCG 1497

RESULT 6
 ID ACA45239/c standard; DNA; 2460 BP.

XX ACA45239;

XX 19-JUN-2003 (first entry)

XX Prokaryotic essential gene #26896.

XX Antisense; ds; prokaryotic essential gene; cell proliferation;

XX drug design; gene.

XX Pseudomonas syringae.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (BLIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX P-PSDB; ABU41369.

XX New antisense nucleic acids, useful for identifying proteins or screening

XX PT for homologous nucleic acids required for cellular proliferation to

XX isolate candidate molecules for rational drug discovery programs.

XX Claim 14; SEQ ID NO 33109; 1766bp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

XX Sequence 2460 BP; 556 A; 704 C; 776 G; 424 T; 0 U; 0 Other;

Query Match 100.0%; Score 14; DB 8; Length 2460;

Best Local Similarity 78.6%; Pred. No. 5.6e+02; Indels 0; Gaps 0;

Matches 11; Conservative 3; Mismatches 0;

QY 1 CGUACUGCAACUCG 14

Db 1408 CGTACTGCAACTCG 1395

RESULT 7
 ID ADU44189 standard; DNA; 21 BP.

XX ADU44189;

XX 27-JUN-2005 (first entry)

XX Knock-down target sequence #9368.

XX ds; RNA production; protein production; drug development;

XX knock-down target.

XX Unidentified.

XX WO2004094636-A1.

XX 04-NOV-2004.

XX 24-APR-2003; 2003WO-BP004362.

XX 24-APR-2003; 2003WO-BP004362.

XX (GALA-) GALAPAGOS GENOMICS NV.

XX (VSCB/) VAN DER SCHUREN J.

XX Arts GJF, Lambrecht MJY, Djokic K, Clasen RJ, Mesic B;

XX Griffioen S, Bergs CTL;

XX WPI; 2004-775940/76.

XX New knockdown sequences, useful in lowering the amount of RNA and/or

XX PT protein production in cells used in drug development process.

XX Claim 11; SEQ ID NO 9430; 402bp; English.

XX The invention relates to a polynucleotide comprising an RNA sequence. The

XX CC polynucleotides, vector, libraries, and method are useful in lowering the

XX amount of RNA and/or protein production in cells used in drug development

XX process. The present sequence represents a knock-down target sequence.

XX Sequence 21 BP; 6 A; 8 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 13; Length 21;

Best Local Similarity 76.9%; Pred. No. 1.5e+03;

Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUCGCAACTCG 13
 Db 2 GCTACTGCAACTCG 14

RESULT 8
 ABRN51005
 ID ABRN51005 standard; DNA; 65 BP.

AC ABRN51005;

DT 15-JUL-2002 (first entry)

DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:23753.

KM Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.

OS Mus musculus.

PN MO200210449-A2.

PD 07-FEB-2002.

PF 20-JUL-2001; 2001WO-IB001903.

PR 28-JUL-2000; 2000US-0221607P.

PR 02-MAY-2001; 2001US-0287724P.

PA (COMP-) COMPUGEN INC.

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

DR WPI; 2002-257383/30.

PT New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNA transcribed from a transcription unit of a
 PT genome, useful for detecting tissue-, pathology-, and developmental-
 PT specific genes.

PS Example 1; SEQ ID NO 23753; 47bp; English.

CC The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
 CC)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises several
 CC oligonucleotides, each capable of hybridizing selectively to a set of
 CC messenger RNAs transcribed from a given transcription unit of the genome,
 CC which encodes one or more messenger RNA splice variants. The
 CC oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterizing the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialized mini
 CC libraries to detect transcripts of a sub-transcriptome under a particular
 CC biological or pathological state, and so allowing the detection of tissue
 CC - and pathology-specific genes such as those genes only expressed in
 CC specific tissue under a specific pathological condition; to detect
 CC developmental specific genes; and to detect RNA transcripts and splice
 CC variants of a transcriptome of a patient suffering from a particular
 CC disorder. ABRN27253 to ABRN59589 represent oligonucleotide sequences from
 CC rats, humans and mice, which are used in the exemplification of the
 CC present invention. N.B. The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

CC Sequence 65 BP; 17 A; 23 C; 10 G; 15 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 6; Length 65;
 Best Local Similarity 76.9%; Pred. No. 1.7e+03;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUCGCAACTCG 14
 Db 31 GCTACTGCAACTCG 43

RESULT 9
 ACD68769/c
 ID ACD68769 standard; DNA; 100 BP.

AC ACD68769;

DT 18-SEP-2003 (first entry)

DE E. coli K12 MG1655 biochip probe SEQ ID 39.

KM Biochip; gene expression; gut; diagnostic; detection; probe; ss.

OS Escherichia coli.

PN EP1260592-A1.

PD 27-NOV-2002.

PF 17-MAY-2001; 2001EP-00112179.

PR 17-MAY-2001; 2001EP-00112179.

PA (MMGB-) MMGB-BIOTECH AG.

PI Donner H, Drescher B, Huber A, Weber J;

DR WPI; 2003-241155/24.

PT Biochip containing probes complementary with open reading frames in
 PT Escherichia coli K12, useful for detecting gene expression and expression
 PT patterns.

PS Claim 3; Page 17; 2004pp; German.

CC This invention describes a novel biochip comprising probe spots, each
 CC containing many identical probes. The probes are nucleotide sequences of
 CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at
 CC least one includes a segment of at least 20 bases identical with, or
 CC complementary to, a segment of an open reading frame (orf) of Escherichia
 CC coli K12. The biochip is used for specific detection of gene expression
 CC in K12 and for determining the gene expression pattern, e.g. for
 CC diagnostic determination of which E. coli strains are present in the gut,
 CC and to determine the effects of e.g. growth media on gene expression. The
 CC biochip provides as comprehensive as possible detection of the K12
 CC genome, with simultaneous analysis of many different genes with a single
 CC device, and comparison of gene expression between K12 and its mutants or
 CC other E. coli strains in a single experiment. Apart from qualitative and
 CC quantitative information about gene expression, it also allows
 CC measurements of population densities for the various strains. The use of
 CC synthetic oligonucleotides for preparation of probes allows free
 CC variation in probe length and ensures high purity (and thus selectivity,
 CC reactivity and reproducibility); also synthetic probes are generally
 CC shorter than probes prepared by polymerase chain reaction. ACD68731 to
 CC ACD81540 represent oligonucleotide probes used with the biochip described
 CC in the invention

CC Sequence 100 BP; 29 A; 28 C; 29 G; 14 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 8; Length 100;
 Best Local Similarity 76.9%; Pred. No. 1.7e+03;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUCGCAACTCG 14
 Db 14 GCTACTGCAACTCG 2

RESULT 10

ACD68770/c
 ID ACD68770 standard; DNA, 100 BP.
 XX
 AC ACD68770;
 XX
 DT 18-SEP-2003 (first entry)
 XX
 DE E. coli K12 MG1655 biochip probe SEQ ID 40.
 XX
 KM Biochip; gene expression; gut; diagnostic; detection; probe; ss.
 XX
 OS Escherichia coli.
 XX
 PN EPI260592-A1.
 XX
 PD 27-NOV-2002.
 XX
 PF 17-MAY-2001; 2001EP-00112179.
 XX
 PR 17-MAY-2001; 2001EP-00112179.
 XX
 PA (MWGB-) MWGB-BIOTECH AG.
 XX
 PI Donner H, Drescher B, Huber A, Weber J;
 XX
 DR WPI; 2003-241155/24.
 XX
 PT Biochip containing probes complementary with open reading frames in
 PT Escherichia coli K12, useful for detecting gene expression and expression
 PT patterns.
 XX
 PS Claim 3; Page 17; 2004pp; German.
 XX
 CC This invention describes a novel biochip comprising probe spots, each
 CC containing many identical probes. The probes are nucleotide sequences of
 CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at
 CC least one includes a segment of at least 20 bases identical with, or
 CC complementary to, a segment of an open reading frame (orf) of Escherichia
 CC coli K12. The biochip is used for specific detection of gene expression
 CC in K12 and for determining the gene expression pattern, e.g. for
 CC diagnostic determination of which E. coli strains are present in the gut,
 CC and to determine the effects of e.g. growth media on gene expression. The
 CC biochip provides as comprehensive as possible detection of the K12
 CC genome, with simultaneous analysis of many different genes with a single
 CC device, and comparison of gene expression between K12 and its mutants or
 CC other E. coli strains in a single experiment. Apart from qualitative and
 CC quantitative information about gene expression, it also allows
 CC measurements of population densities for the various strains. The use of
 CC synthetic oligonucleotides for preparation of probes allows free
 CC variation in probe length and ensures high purity (and thus selectivity,
 CC reactivity and reproducibility); also synthetic probes are generally
 CC shorter than probes prepared by polymerase chain reaction. ACD68731 to
 CC ACD81540 represent oligonucleotide probes used with the biochip described
 CC in the invention
 XX
 SQ Sequence 100 BP; 29 A; 23 C; 34 G; 14 T; 0 U; 0 Other;
 XX
 QY Query Match 92.9%; Score 13; DB 8; Length 100;
 DB Best Local Similarity 76.9%; Pred. No. 1.7e+03;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

XX
 DE Formate dehydrogenase nucleotide sequence.
 XX
 KM Formate dehydrogenase; Hyphomicrobium; ds.
 XX
 OS Hyphomicrobium sp.
 XX
 PN JP2000245471-A.
 XX
 PD 12-SEP-2000.
 XX
 PF 01-MAR-1999; 99JP-00052548.
 XX
 PR 01-MAR-1999; 99JP-00052548.
 XX
 PA (NIRA) UNITIKA LTD.
 XX
 DR WPI; 2000-622119/60.
 XX
 DR P-PADB; AAY85650.
 XX
 PT New Hyphomicrobium sp. formate dehydrogenase gene for producing formate
 PT dehydrogenase of high specific activity, high temperature stability and
 PT high pH stability.
 XX
 PS Claim 2; Page 5-6; 9pp; Japanese.
 XX
 CC This invention relates to a gene encoding a formate dehydrogenase from
 CC Hyphomicrobium sp. A transformant containing the new gene is used for the
 CC preparation of formate dehydrogenase of high specific activity, low
 CC Michaelis constant (Km) value against formic acid and NAD⁺, high
 CC temperature stability and high pH stability. The present sequence
 CC represents the gene of the invention
 XX
 SQ Sequence 1197 BP; 290 A; 350 C; 323 G; 234 T; 0 U; 0 Other;
 XX
 QY Query Match 92.9%; Score 13; DB 3; Length 1197;
 DB Best Local Similarity 76.9%; Pred. No. 2e+03;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13
 DB 431 CGUACUGCAACUC 443
 XX
 RESULT 12
 ID ADS51056
 XX ADS51056 standard; cDNA; 1306 BP.
 XX
 AC ADS51056;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Bacterial polynucleotide #5799.
 XX
 KM Recombinant DNA construct; transformed plant; improved plant property;
 KM cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KM pathogen tolerance; pest tolerance; plant disease resistance;
 KM cell cycle pathway modification; plant growth regulator;
 KM homologous recombination; seed oil yield; protein yield; carbohydrate;
 KM nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KM bacterial polynucleotide; gene; ss.
 XX
 OS Bacteria.
 XX
 PN US2003233675-A1.
 XX
 PD 18-DEC-2003.
 XX
 PF 20-FEB-2003; 2003US-00369493.
 XX
 PR 21-FEB-2002; 2002US-0360039P.
 XX
 PA (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX WPI; 2004-061375/06.
 DR
 XX
 PT New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 PS Claim 1; SEQ ID NO 29486; 122pp; English.
 XX
 CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition. Improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polynucleotide used in
 CC the scope of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 1306 BP; 392 A; 296 C; 253 G; 365 T; 0 U; 0 Other;
 QY
 Db 1 CGUACUCGCACTC 13
 701 CGTACTGCAACTC 713
 Query Match 92.9%; Score 13; DB 13; Length 1306;
 Best Local Similarity 76.9%; Pred. No. 2e+03;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
 ADR85906/c
 ID ADR85906 standard; DNA; 1322 BP.
 XX
 AC ADR85906;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Aspergillus fumigatus essential gene open reading frame #543.
 XX
 KM Fungicide; Aspergillus fumigatus infection; Farmer's lung disease;
 OS drug screening; ds.
 XX
 OS Aspergillus fumigatus.
 XX
 PN WO2004067709-A2.
 XX
 PD 12-AUG-2004.
 XX
 PF 16-JAN-2004; 2004WO-US001099.
 XX
 PR 17-JAN-2003; 2003US-0441281P.

PR 13-JUN-2003; 2003US-0478196P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 PA (ELIT-) ELITRA CANADA LTD.
 XX
 PI Jiang B, Hu W, Lemieux S, Roemer T;
 XX
 XX WPI; 2004-594200/57.
 DR
 P-PSDB; ADR86493.
 XX
 PT New purified or isolated Aspergillus fumigatus nucleic acid molecule
 PT encoding a gene product, useful for diagnosing and/or treating invasive
 PT fungal infections, such as Farmer's lung disease.
 XX
 PS Claim 2; SEQ ID NO 2543; 164pp; English.
 XX
 CC The present invention relates to Aspergillus fumigatus genes that are
 CC essential and are potential targets for drug screening. The methods and
 CC compositions of the present invention are useful for diagnosing and/or
 CC treating invasive Aspergillus fumigatus infection, including the allergic
 CC forms of the disease, such as Farmer's lung disease. They can also be
 CC used in various drug discovery purposes, such as expression of the
 CC recombinant protein, hybridization assay and construction of nucleic acid
 CC arrays. The present sequence represents an Aspergillus fumigatus
 CC essential gene open reading frame, used during diagnosis and drug
 CC development in the invention. These genes share a high degree of sequence
 CC conservation with known essential genes of candida albicans. The sequence
 CC data for this patent is not represented in the printed specification, but
 CC was obtained in electronic format from WIPO.
 XX
 SQ Sequence 1322 BP; 277 A; 354 C; 291 G; 400 T; 0 U; 0 Other;
 QY
 Db 2 GUACUCGCACTCG 14
 57 GTACTGCAACTCG 45
 Query Match 92.9%; Score 13; DB 13; Length 1322;
 Best Local Similarity 76.9%; Pred. No. 2e+03;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
 AAS73079
 ID AAS73079 standard; cDNA; 1359 BP.
 XX
 AC AAS73079;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #8883.
 XX
 KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder; ss.
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 XX WPI; 2001-639362/73.
 DR
 P-PSDB; ABO08892.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in

```

XX fungal infections, such as Farmer's lung disease.
XX
XX Claim 3; SEQ ID NO 1543; 164pp; English.
XX
XX The present invention relates to Aspergillus fumigatus genes that are
XX essential and are potential targets for drug screening. The methods and
XX compositions of the present invention are useful for diagnosing and/or
XX treating invasive Aspergillus fumigatus infection, including the allergic
XX forms of the disease, such as Farmer's lung disease. They can also be
XX used in various drug discovery purposes, such as expression of the
XX recombinant protein, hybridization assay and construction of nucleic acid
XX arrays. The present sequence represents an Aspergillus fumigatus
XX essential gene sequence containing all introns, used during diagnosis and
XX drug development in the invention. These genes share a high degree of
XX sequence conservation with known essential genes of candida albicans. The
XX sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format from WIPO.
XX
XX Sequence 1443 BP; 313 A; 382 C; 312 G; 436 T; 0 U; 0 Other;
XX
XX Query Match 92.9%; Score 13; DB 13; Length 1443;
XX Best Local Similarity 76.9%; Pred. No. 2.1e+03;
XX Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0
XX
XX 2 GUACTGCACTCG 14
XX |:|:|:|:|:|:|
XX
XX Db 57 GTACTGCMACTCG 45
XX
XX
XX RESULT 16
XX AAF33074
XX ID AAF33074 standard; cDNA; 1488 BP.
XX
XX AAF33074;
XX
XX 23-MAR-2001 (first entry)
XX
XX Human secreted protein gene 38 SEQ ID NO:48.
XX
XX Human; secreted protein; diagnosis; cytostatic; antitumour;
XX antiarthritic; dermatological; cardiac; antiinflammatory; anti-ulcer;
XX gastrointestinal; solid tumour; rheumatoid arthritis; psoriasis;
XX diabetic retinopathy; myocardial angiogenesis; Crohn's disease; ulcer;
XX 88.
XX
XX Homo sapiens.
XX
XX WO200077237-A1.
XX
XX 21-DEC-2000.
XX
XX 01-JUN-2000; 2000WO-US014928.
XX
XX 11-JUN-1999; 99US-0138633P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (ROSE/) ROSEN C A.
XX
XX Rosen CA, Ruben SM, Komatsoulis GA;
XX
XX WPI; 2001-071280/08.
XX DR P-PSDB; AAB64703.
XX
XX Nucleic acid encoding 49 human secreted polypeptides, useful for
XX preventing, diagnosing and/or treating diseases such as tumors,
XX rheumatoid arthritis, psoriasis and diabetic retinopathy.
XX
XX Claim 1; Page 452; 520pp; English.
XX
XX The polynucleotide sequences given in AAF33037 to AAF33085 encode the
XX human secreted proteins given in AAB64666 to AAB64714. AAB64715 to
XX AAB64771 represent human secreted polypeptide sequences and proteins
XX homologous to them, which are given in the exemplification of the present

```

CC invention. Human secreted proteins have activities based on the tissues
CC and cells the genes are expressed in. Examples of activities include:
CC cytotoxic; antirheumatic; antiarthritic; dermatological; cardiant;
CC antiinflammatory; gastrointestinal; and anti-ulcer. The polynucleotides
CC and polypeptides can be used in the prevention, treatment and diagnosis
CC of diseases associated with inappropriate polypeptide expression.
CC Disorders that may be treated or prevented include solid tumours,
CC rheumatoid arthritis, psoriasis, diabetic retinopathy, myocardial
CC angiogenesis, Crohn's disease and ulcers. The polynucleotides and their
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate
CC the presence of similar nucleic acid sequences in samples, and therefore
CC which patients may be in need of restorative therapy. The polypeptides
CC may also be used as antigens in the production of antibodies against the
CC polypeptide and in assays to identify modulators (agonists and
CC antagonists) of polypeptide expression and activity. The anti-polypeptide
CC antibodies and antagonists may also be used to down regulate expression
CC and activity. AAF33028 to AAF33036 and AAB64665 represent sequences used
CC in the exemplification of the present invention

XX SQ Sequence 1488 BP; 496 A; 290 C; 253 G; 449 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 4; Length 1488;
Best Local Similarity 76.9%; Pred. No. 2.1e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGAACGCAACGAC 13
DB 658 GGAACGCAACGAC 670

RESULT 17
AAS52489/c
ID AAS52489 standard; DNA; 1647 BP.

XX AAS52489;

XX 13-FEB-2002 (first entry)

XX E. coli DNA for cellular proliferation protein #211.

XX Antisense; ds; prokaryotic cellular proliferation gene; antibiotic;
KM antibacterial; drug design.

XX Escherichia coli.

XX MO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001MO-US009180.

XX 21-MAR-2000; 2000US-0191078P.

XX 23-MAY-2000; 2000US-0206848P.

XX 26-MAY-2000; 2000US-0207727P.

XX 23-OCT-2000; 2000US-0242578P.

XX 27-NOV-2000; 2000US-0253625P.

XX 22-DEC-2000; 2000US-0257931P.

XX 16-FEB-2001; 2001US-0269308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyekind JW, Wall D, Trawick JD, Carr GJ;

XX Yamamoto RT, Xu HH;

XX WPI; 2001-611495/70.

XX P-PSDB; AAU34630.

XX New polynucleotides for the identification and development of

XX PT antibiotics, comprise sequences of antisense nucleic acids.

XX PS Claim 27; SEQ ID NO 6126; 511pp; English.

CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence encodes an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1647 BP; 400 A; 402 C; 488 G; 357 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 4; Length 1647;
Best Local Similarity 76.9%; Pred. No. 2.1e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 GGAACGCAACGAC 14
DB 1533 GGAACGCAACGAC 1521

RESULT 18
ACA32562/c
ID ACA32562 standard; DNA; 1647 BP.

XX ACA32562;

XX 19-JUN-2003 (first entry)

XX Prokaryotic essential gene #14219.

XX Antisense; ds; prokaryotic essential gene; cell proliferation;

XX drug design; gene.

XX Escherichia coli.

XX MO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002MO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342823P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyekind JW,

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX P-PSDB; ABU28692.

XX WPI; 2003-029926/02.

XX New antisense nucleic acids, useful for identifying proteins or screening

XX PT for homologous nucleic acids required for cellular proliferation to

XX isolate candidate molecules for rational drug discovery programs.

XX PS Claim 14; SEQ ID NO 20432; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 1647 BP; 400 A; 402 C; 488 G; 357 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 8; Length 1647;
Best Local Similarity 76.9%; Pred. No. 2.1e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACTCG 14
Db 1533 GTACTGCAACTCG 1521

RESULT 19
ABK13893/c
ID ABK13893 standard; DNA, 1720 BP.
XX
AC ABK13893;
XX
DT 29-AUG-2003 (revised)
DT 21-MAY-2002 (first entry)
XX
DE Gene encoding *Escherichia coli* malate:quinone oxidoreductase (mqo).
XX
XX Fermentative preparation of L-threonine; Enterobacteriaceae bacteria;
KM malate:quinone oxidoreductase; mqo; fermentation; gene; ds.
XX
OS *Escherichia coli*; strain MC4100.
XX
XX Key Location/Qualifiers
FH 7.1596
FT CDS /*tag= a
FT /product= "Mqo"
FT /EC_number= "1.1.99.16"
XX
XX WO200206459-A1.
XX
XX 24-JAN-2002.
XX
XX 16-MAY-2001; 2001WO-EP005548.
XX
XX 18-JUL-2000; 2000DE-01034833.
PR 30-JAN-2001; 2001DE-01003874.
XX
XX (DEGS) DEGUSA AG.

XX
PI Rieping M, Thierbach G, Van Der Rest ME, Molenaar D;
XX
DR WPI; 2002-217000/27.
XX
DR P-PADB; AADU5255.
XX
PT Fermentative preparation of L-threonine by employing Enterobacteriaceae
PT bacteria in which nucleotide sequence(s) that code(s) for malate:quinone
PT oxidoreductase (mqo) gene are enhanced, particularly over-expressed.
XX
PS Claim 2; Page 30-32; 39pp; English.
XX
XX The present invention relates to a process for the fermentative
CC preparation of L-threonine. The process involves employing
CC Enterobacteriaceae bacteria, particularly those which already produce L-
CC threonine, and in which the gene which encodes for the malate:quinone
CC oxidoreductase (mqo) enzyme (E.C.1.1.99.16) are enhanced, in particular
CC over-expressed. The invention employs the Enterobacteriaceae, *Escherichia*
CC *coli* as an example. The process is useful for preparing L-threonine by
CC fermentation. The present sequence encodes for the *E. coli* mqo enzyme.
CC (Updated on 29-AUG-2003 to standardise OS field)
XX

SQ Sequence 1720 BP; 414 A; 421 C; 516 G; 369 T; 0 U; 0 Other;
Query Match 92.9%; Score 13; DB 6; Length 1720;
Best Local Similarity 76.9%; Pred. No. 2.1e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACTCG 14
Db 1482 GTACTGCAACTCG 1470

RESULT 20
AAS92825/c
ID AAS92825 standard; cDNA; 1732 BP.
XX
AC AAS92825;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #28629.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KM food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
DR P-PADB; AAG28638.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 1; SEQ ID NO 28629; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain

CC	reaction (PCR), primers, oligomers, and for chromosome and gene mapping.
CC	and in recombinant production of (II). The polynucleotides are also used
CC	in diagnostics as expressed sequence tags for identifying expressed
CC	genes. (I) is useful in gene therapy techniques to restore normal
CC	activity of (II) or to treat disease states involving (II). (II) is
CC	useful for generating antibodies against it, detecting or quantitating a
CC	polypeptide in tissue, as molecular weight markers and as a food
CC	supplement. (II) and its binding partners are useful in medical imaging
CC	of sites expressing (II). (I) and (II) are useful for treating disorders
CC	involving aberrant protein expression or biological activity. The
CC	polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC	coding sequences of the invention. Note: The sequence data for this
CC	patent did not appear in the printed specification, but was obtained in
CC	electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
CC	
SQ	Sequence 1732 BP; 422 A; 452 C; 438 G; 420 T; 0 U; 0 Other;
Qy	Query Match 92.9%; Score 13; DB 5; Length 1732;
	Best Local Similarity 76.9%; Pred. No. 2.1e+03;
	Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0.
Dy	2 GUACUGCAACUCG 14
	:
Dy	1683 GTACTGCAACTCG 1671
RESULT 21	
AAS90081/c	
ID	AAS90081 standard; cDNA; 1919 BP.
XX	AAS90081;
AC	
XX	13-FEB-2002 (first entry)
DE	
XX	DNA encoding novel human diagnostic protein #25885.
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW	food supplement; medical imaging; diagnostic; genetic disorder; ss.
OS	Homo sapiens.
XX	
PN	WO200175067-A2.
PD	
XX	11-OCT-2001.
PF	
XX	30-MAR-2001; 2001WO-US008631.
PR	
XX	31-MAR-2000; 2000US-00540217.
PR	
XX	23-AUG-2000; 2000US-00649167.
PA	
XX	(HYSE-) HYSEQ INC.
PI	
DR	Dzmanac RT, Liu C, Tang YT;
DR	WPI; 2001-639362/73.
XX	P-PSDB; ABG25894.
XX	
PT	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
XX	biodiversity.
XX	
PS	Claim 1; SEQ ID NO 25885; 103pp; English.
XX	
CC	The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC	sequences. (I) is useful as hybridisation probes, polymerase chain
CC	reaction (PCR), primers, oligomers, and for chromosome and gene mapping,
CC	and in recombinant production of (II). The polynucleotides are also used

CC	in diagnostics as expressed sequence tags for identifying expressed
CC	genes. (I) is useful in gene therapy techniques to restore normal
CC	activity of (II) or to treat disease states involving (II). (II) is
CC	useful for generating antibodies against it, detecting or quantitating a
CC	polypeptide in tissue, as molecular weight markers and as a food
CC	supplement. (II) and its binding partners are useful in medical imaging
CC	of sites expressing (II). (I) and (II) are useful for treating disorders
CC	involving aberrant protein expression or biological activity. The
CC	polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequences. AAS6197-AAS94564 represent novel human diagnostic
CC	coding sequences of the invention. Note: The sequence data for this
CC	patent did not appear in the printed specification, but was obtained in
CC	electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
XX	Sequence 1919 BP; 469 A; 514 C; 488 G; 448 T; 0 U; 0 Other;
XX	
XX	Query Match 92.9%; Score 13; DB 5; Length 1919;
XX	Best Local Similarity 76.9%; Pred. No. 2.1e+03;
XX	Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0.
OY	2 GUACUGCACTCG 14
	: ::
DB	1683 GTACTGCACACTCG 1671
RESULT 22	
ID	AAIL4703
XX	AAIL4703 standard; DNA; 1945 BP.
AC	
XX	AAIL4703;
DT	
XX	12-OCT-2001 (first entry)
DS	
XX	Probe #4636 for gene expression analysis in human cervical cell sample.
XX	
KW	Probe; human; microarray; gene expression; cervical epithelial cell;
KM	cervical cancer; ss.
XX	
OS	Homo sapiens.
XX	
FN	WO200157278-A2.
PD	
XX	09-AUG-2001.
PZ	
XX	30-JAN-2001; 2001WO-US000670.
PR	
XX	04-FEB-2000; 2000US-0180312P.
PR	26-MAY-2000; 2000US-0207456P.
PR	30-JUN-2000; 2000US-00608408.
PR	03-AUG-2000; 2000US-00632366.
PR	21-SEP-2000; 2000US-0234687P.
PR	27-SEP-2000; 2000US-0236359P.
PR	04-OCT-2000; 2000GB-00024263.
PA	
XX	(MOLE-) MOLECULAR DYNAMICS INC.
PI	
XX	Penn SG, Hanzel DK, Chen W, Rank DR;
DR	
XX	WPI; 2001-488901/53.
XX	
PT	Human genome-derived single exon nucleic acid probes useful for analyzing
XX	gene expression in human cervical epithelial cells.
PS	
XX	Claim 25; SEQ ID NO 4636; 487bp; English.
CC	The present invention relates to human single exon nucleic acid probes
CC	(SENP). The present sequence is one such probe. The SENPs are derived
CC	from human HeLa cells. The SENPs can be used to produce a single exon
CC	microarray, which can be used for measuring human gene expression in a

CC sample derived from human cervical epithelial cells. By measuring gene
 CC expression, the probes are therefore useful in grading and/or staging of
 CC diseases of the cervix, notably cervical cancer. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1945 BP; 453 A; 617 C; 484 G; 391 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 4; Length 1945;

Best Local Similarity 76.9%; Pred. No. 2.1e+03;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACUCG 14
 Db 263 GTACTGCAACTCG 275

RESULT 23

ABAS6435
 ID ABAS6435 standard; DNA; 1945 BP.

XX ABAS6435;

AC 01-FEB-2002 (first entry)

DT Human foetal liver single exon nucleic acid probe #4740.

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX Homo sapiens.

OS WO200157277-A2.

XX 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US000669.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human fetal liver.

XX Claim 1; SEQ ID NO 4740; 639pp + Sequence listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring

XX human gene expression in a sample derived from human foetal liver. The

XX single exon nucleic acid probes may be used for predicting, measuring and

XX displaying gene expression in samples derived from human fetal liver. The

XX present sequence is a single exon nucleic acid probe of the invention.

XX Note: The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

Db 263 GTACTGCAACTCG 275

RESULT 24

AAI36072
 ID AAI36072 standard; DNA; 1945 BP.

XX AAI36072;

AC 17-OCT-2001 (first entry)

DT Probe #4758 used to measure gene expression in human placenta sample.

XX Probe; microarray; human; placenta; antenatal diagnosis;

XX genetic disorder; ss.

XX Homo sapiens.

OS WO200157272-A2.

XX 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US000663.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-48897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human placenta.

XX Claim 25; SEQ ID NO 4758; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENPs).

XX The present sequence is one such probe. The probes are useful for

XX producing a microarray for predicting, measuring and displaying gene

XX expression in samples derived from human placenta. The probes are useful

XX for antenatal diagnosis of human genetic disorders

XX Sequence 1945 BP; 453 A; 617 C; 484 G; 391 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 4; Length 1945;

Best Local Similarity 76.9%; Pred. No. 2.1e+03;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACUCG 14

Db 263 GTACTGCAACTCG 275

RESULT 25

ABAA5908
 ID ABAA5908 standard; DNA; 1945 BP.

XX ABAA5908;

AC 01-FEB-2002 (first entry)

DT Human breast cell single exon nucleic acid probe #4603.

XX Human; microarray; single exon probe; gene expression; breast; disease;

XX cancer; ss.

XX OS Homo sapiens.
 XX PN WO200157271-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000662.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLF-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-496933/54.
 XX PT New spatially-addressable set of single exon nucleic acid probes, useful
 PT for measuring gene expression in sample derived from human breast,
 PT comprises number of single exon nucleic acid probes.
 XX PS Claim 1; SEQ ID NO 4603; 327pp + Sequence Listing; English.
 XX CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting the
 CC probes with a collection of detectably labeled nucleic acids derived
 CC from mRNA of human breast, and then measuring the label bound to each
 CC probe of the microarray. The probes are useful for verifying the
 CC expression of regions of genomic DNA predicted to encode proteins. They
 CC are useful for gene discovery, and for determining predisposition and/or
 CC prognosing breast disease. Gene expression analysis is useful for
 CC assessing the toxicity of chemical agents on cells. The microarray of
 CC this invention presents a far greater diversity of probes for measuring
 CC gene expression, with far less bias than expressed sequence tag
 CC microarrays. The method is suitable for rapid production of functional
 CC information from genomic sequence. The present sequence is a single exon
 CC nucleic acid probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 1945 BP; 453 A; 617 C; 484 G; 391 T; 0 U; 0 Other;
 XX
 XX Query Match 92.9%; Score 13; DB 4; Length 1945;
 XX Best Local Similarity 76.9%; Pred. No. 2.1e+03;
 XX Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GUACUGCACTCG 14
 Db 263 GTACTGCACTCG 275
 XX
 XX RESULT 26
 XX ABA26067
 XX ID ABA26067 standard; DNA; 1945 BP.
 XX AC ABA26067;
 XX XX
 XX DT 23-JAN-2002 (first entry)
 XX DE Probe #4533 for gene expression analysis in human heart cell sample.
 XX KM Human; gene expression; heart; microarray; vascular system; probe;
 XX KM cardiovascular disease; hypertension; cardiac arrhythmia;
 XX KM congenital heart disease; ss.
 XX XX

OS OS Homo sapiens.
 XX PN WO200157274-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000666.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLF-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-488899/53.
 XX PT Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts.
 XX PS Claim 1; SEQ ID NO 4533; 530pp; English.
 XX CC The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart. The
 CC present sequence is one such probe. The probes may be used for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from the human heart via microarrays. By measuring gene expression, the
 CC probes are useful for predicting, diagnosing, grading, staging,
 CC monitoring and prognosing diseases of the human heart and vascular system
 CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
 CC congenital heart disease. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 1945 BP; 453 A; 617 C; 484 G; 391 T; 0 U; 0 Other;
 XX
 XX Query Match 92.9%; Score 13; DB 4; Length 1945;
 XX Best Local Similarity 76.9%; Pred. No. 2.1e+03;
 XX Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GUACUGCACTCG 14
 Db 263 GTACTGCACTCG 275
 XX
 XX RESULT 27
 XX AAK30108
 XX ID AAK30108 standard; DNA; 1945 BP.
 XX AC AAK30108;
 XX XX
 XX DT 06-NOV-2001 (first entry)
 XX DE Human bone marrow expressed single exon probe SEQ ID NO: 4665.
 XX KM Human; bone marrow expressed exon; gene expression analysis; probe;
 XX KM microarray; cancer; leukemia; lymphoma; myeloma; ss.
 XX OS Homo sapiens.
 XX PN WO200157276-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000668.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX XX

PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human bone marrow.
XX
PS Example 4; SEQ ID NO 4665; 658bp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention
XX
SQ Sequence 1945 BP; 453 A; 617 C; 484 G; 391 T; 0 U; 0 Other;
XX
Query Match 92.9%; Score 13; DB 4; Length 1945;
Best Local Similarity 76.9%; Pred. No. 2.1e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2 GUACUGCAACUG 14
Db 263 GTRCTGCACTCG 275
XX
RESULT 28
AAK04600
ID AAK04600 standard; DNA; 1945 BP.
XX
AC AAK04600;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 4591.
XX
KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains.

XX
PS Example 4; SEQ ID NO 4591; 650bp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
SQ Sequence 1945 BP; 453 A; 617 C; 484 G; 391 T; 0 U; 0 Other;
XX
Query Match 92.9%; Score 13; DB 4; Length 1945;
Best Local Similarity 76.9%; Pred. No. 2.1e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2 GUACUGCAACUG 14
Db 263 GTRCTGCACTCG 275
XX
RESULT 29
ABS29757
ID ABS29757 standard; DNA; 1945 BP.
XX
AC ABS29757;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver single exon probe, SEQ ID NO 4747.
XX
KW Human; single exon nucleic acid probe; liver; cirrhosis;
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KW coronary heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157273-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000664.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488998/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX
PS Claim 1; SEQ ID NO 4747; 658bp; English.
XX
CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABS25011-ABS51005 represent human

CC liver single exon nucleic acid probes of the invention. Note: The
CC sequence information for this patent does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1945 BP; 453 A; 617 C; 484 G; 391 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 4; Length 1945;
Best Local Similarity 76.9%; Pred. No. 2.1e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 2 GUACTGCACTCG 14
Db 263 GTACTGCACTCG 275

RESULT 30
AA104509
ID AA104509 standard; DNA; 1945 BP.
XX
AC AA104509;
XX
DT 09-OCT-2001 (first entry)
XX
DE Probe #4500 used to measure gene expression in human breast sample.
XX
KW Probe; human; breast disease; breast cancer; development disorder; ss;
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
OS Homo sapiens.
XX
PN WO200157270-A2.
XX
PD 09-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US000661.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
XX
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-476286/51.
XX
PT Novel single exon nucleic acid probe used to measuring gene expression in
XX a human breast.

PS Claim 25; SEQ ID NO 4500; 322pp; English.
XX
XX The present invention relates to novel single exon nucleic acid probes.
CC The present sequence is one such probe. The probes are useful for
CC measuring human gene expression in a human breast sample, where the probe
CC hybridises at high stringency to a nucleic acid expressed in the human
CC breast. The probes are useful for predicting, diagnosing, grading,
CC staging, monitoring and prognosing diseases of the human breast,
CC particularly those diseases with polygenic aetiology. The diseases
CC include: breast cancer, disorders of development, inflammatory diseases
CC of the breast, fibrocystic changes, proliferative breast disease and non-
CC carcinoma tumours. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1945 BP; 453 A; 617 C; 484 G; 391 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 5; Length 1945;
Best Local Similarity 76.9%; Pred. No. 2.1e+03;

Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 2 GUACTGCACTCG 14
Db 263 GTACTGCACTCG 275

RESULT 31
ABS04688
ID ABS04688 standard; DNA; 1945 BP.
XX
AC ABS04688;
XX
DT 19-AUG-2002 (first entry)
XX
XX Human genome-derived single exon probe from lung SEQ ID NO 4679.
DE
XX
XX Human; de; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.
XX
OS Homo sapiens.
XX
PN WO200186003-A2.
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US000665.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
XX
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2002-114183/15.
XX
PT Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples.

PS Claim 1; SEQ ID NO 4679; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC; the novel set of probes which hybridise at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of the
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several

CC	tissue and/or cell types using hybridisation to a single exon
CC	microarrays having a probe with the exon, where a common pattern of
CC	expression of the exons in the tissues and/or cell types indicates that
CC	the exons should be assigned to a single gene; a peptide comprising one
CC	of 12011 sequences, mentioned in the specification, or encoded by the
CC	probes/open reading frames (ORF). The probes are used for gene expression
CC	analysis, and for identifying exons in a gene, particularly using human
CC	lung derived mRNA and for the study of lung diseases such as asthma, lung
CC	cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC	disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC	tuberosus sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC	Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC	histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC	Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC	dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC	present sequence is a single exon probe of the invention. Note: The
CC	sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences
CC	
SO	Sequence 1945 BP; 453 A; 617 C; 484 G; 391 T; 0 U; 0 Other;
QY	Query Match 92.9%; Score 13; DB 6; Length 1945;
Db	Best Local Similarity 76.9%; Pred. No. 2.1e+03;
	Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0
	2 GUACUGCAACUCCG 14
	: :
	263 GTACTGCAACTCG 275
RESULT 32	
ACC61225/c	ACC61225 standard; DNA; 2000 BP.
AC	ACC61225;
XX	
DT	20-JUN-2003 (first entry)
XX	
DE	Gene sequence #SEQ ID 1232.
XX	
KM	Multiprotein complex; eukaryote; drug target; diagnosis; gene; ds.
OS	Saccharomyces cerevisiae.
FN	EP1258494-A1.
XX	
PD	20-NOV-2002.
XX	
PF	20-DEC-2001; 2001EP-00130253.
XX	
PR	15-MAY-2001; 2001EP-00111774.
XX	
PA	(CELL-) CELLZONE AG.
XX	
PI	Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;
PI	Marzloch M, Schultz JD, Superti-Furga GD;
XX	
DR	WPI; 2003-250078/25.
XX	
DR	P-PSDB; ABR53183.
XX	
PT	New isolated protein complexes useful for diagnosing a disease or
PT	disorder, or as a target for an active agent of a pharmaceutical,
PT	preferably a drug target in the treatment or prevention of disease or
PT	disorder.
XX	
PS	Disclosure; SEQ ID NO 1232; 1'bp + Sequence Listing; English.
CC	
CC	The invention relates to multiprotein complexes from eukaryotes. Proteins
CC	of the invention and DNA sequences encoding them are given in records
CC	ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are
CC	obtainable by using a protein as a bait and isolating the set of proteins
CC	which is attached thereto from cells. Such protein complexes may comprise

CC up to 30 distinct proteins. Protein complexes of the invention are useful
CC for diagnosing a disease or disorder, or as a target for an active agent
CC of a pharmaceutical, preferably a drug target in the treatment or
CC prevention of a disease or disorder. Note: The sequence data for this
CC patent is not represented in the printed specification, but is based on
CC sequence information supplied by the European Patent Office. The complete
CC document is available on CD-ROM

XX
XX Sequence 2000 BP; 681 A; 345 C; 390 G; 584 T; 0 U; 0 Other;
SQ

Query Match 92.9%; Score 13; DB 10; Length 2000;
Best Local Similarity 76.9%; Pred.No. 2.1e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0

OY 2 GUACUGCACTCG 14
 |:|:|:|:|:
DB 1296 GTACTGCAACTCG 1284

RESULT 33
ID ADR63219/C
XX ADR63219 standard; DNA; 2000 BP.
XX
XX ADR632219;
XX
DT 06-MAY-2004 (first entry)
XX
DE Disease treating protein complex-derived gene #735.
XX
KW protein complex; drug target; diagnosis; gene; ds.
XX
OS unidentified.
XX
PN EPI338608-A2.
PD 27-AUG-2003.
PP 20-DEC-2002; 2002EP-00102902.
PR 20-DEC-2001; 2001EP-00130253.
RX
RA (CELL-) CELLZOME AG.
PI Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J,
PI Marzulloch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A,
PI Michon A, Leutwein C, Rick J,
DR WPI; 2003-638460/61.
XX P-PSDB; ADR63218.

New proteins and protein complexes from eukaryotes, useful as targets in
PT drug screening, or in diagnosing or screening for the presence of a
PT disease or disorder, or a predisposition for developing a disease or
PT disorder in a subject.

Disclousre; SEQ ID NO 1470; 13pp; English.

The invention relates to novel protein complexes comprising a first and a
second protein, or its derivative, fragment, homologue or variant. The
proteins are selected from given protein complexes, which are not defined
in the specification. The variants are encoded by nucleic acids that
hybridize to the nucleic acids encoding the proteins under low stringency
conditions. The protein complexes are useful as targets for an active
agent of a pharmaceutical. These protein complexes are particularly
useful as drugs targets for the treatment or preventing of a disease or
disorder. The complexes and methods above are useful in diagnosing or
screening for the presence of a disease or disorder or a predisposition
for developing a disease or disorder in a subject. These are also useful
in screening for a drug for treatment or prevention of a disease or
disorder. The molecule that modulates the amount, activity or protein
components of the complex is useful for the manufacture of a medicament
for the treatment or prevention of a disease or disorder. This sequence
corresponds to a gene of the invention. (Note: the sequence data for this

CC patent did not form part of the printed specification but was obtained
 CC from the EPO in electronic format).

XX SQ Sequence 2000 BP; 681 A; 345 C; 390 G; 584 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 10; Length 2000;
 Best Local Similarity 76.9%; Pred. No. 2.1e+03;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GUACUGCAACUCG 14

Db 1296 GTACTGCAACTCG 1284

RESULT 34

AA588191/c
 ID AA588191 standard; CDNA; 2133 BP.

XX AC AA588191;

XX DT 13-FRB-2002 (first entry)

XX DE DNA encoding novel human diagnostic protein #23995.

XX KM Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX KM food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR P-PSDB; ABG24004.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX PS Claim 1; SEQ ID NO 23995; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AA564197-AA594564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 2133 BP; 518 A; 542 C; 579 G; 494 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 5; Length 2133;
 Best Local Similarity 76.9%; Pred. No. 2.1e+03;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GUACUGCAACUCG 14

Db 2019 GTACTGCAACTCG 2007

RESULT 35

AA93775
 ID AA93775 standard; DNA; 2963 BP.

XX AC AA93775;

XX DT 29-JUN-1998 (first entry)

XX DE PSD-93 coding sequence.

XX KM PSD-93; nNOS; neuronal nitric oxide synthase; Alzheimer's disease;

XX KM diagnosis; muscular dystrophy; skeletal muscle; Huntington's disease;

XX KM Duchenne muscular dystrophy; Becker muscular dystrophy; dystrophin;

XX KM sarcolemma; PDZ domain; neurodegenerative disease; gene therapy;

XX KM amyotrophic lateral sclerosis; ds.

XX OS Rattus sp.

XX PN Rattus sp.

XX PD 12-SEP-1997.

XX PF 06-MAR-1997; 97WO-US003897.

XX PR 08-MAR-1996; 96US-00613114.

XX PA (REGC) UNIT CALIPORNIA.

XX PI Bredt DS, Brenman JB, Chao DS;

XX DR WPI; 1997-47055/43.

XX DR P-PSDB; AA934659, AA934660, AA934661, AA934662, AA934663.

XX PT Diagnosing muscular dystrophy by detecting absence or decrease of

XX PT neuronal nitric oxide synthase (nNOS) in skeletal muscle sarcolemma -

XX PT using new nNOS binding post-synaptic density proteins, PSD-93 and PSD-95;

XX PT also used for the diagnosis, prophylaxis and treatment of stroke and

XX PT other neurodegenerative diseases.

XX PS Claim 17; Page 72-73; 124pp; English.

XX This sequence encodes the post synaptic density protein-93 (PSD-93). PSD-

93 can be used in the method of the invention, for diagnosing muscular dystrophy (MD) in a mammal by detecting absence or a decrease of neuronal nitric oxide synthase (nNOS) in a skeletal muscle sample. Patients with Duchenne or Becker MD lack normal levels of nNOS in skeletal muscle, in addition to lack of functional dystrophin. nNOS is normally targeted to the sarcolemma by associating to dystrophin (via the N-terminal PDZ domain (66 aa motif bearing homology to a heterogenous family of signalling enzymes localised at cell-cell junctions) of nNOS, interacting specifically with the PDZ domain of the alpha 1-syntrophin component). The binding proteins PSD-93 and -95 also have a PDZ domain and interact with nNOS, mediating binding of nNOS to the NMDA receptor located at synapses. The PSD proteins are involved in the development and progression of stroke and some neurodegenerative diseases (e.g. Huntington's and Alzheimer's diseases and amyotrophic lateral sclerosis), so inhibiting them (or their binding) can be used to treat etc. such diseases (associated with overactivation of NMDA receptors by excessive levels of nNOS. This method allows early diagnosis of MD. MD can now be treated by gene therapy, using only the fragment of dystrophin involved in formation of the nNOS/sarcolemma/dystrophin complex, rather than the complete dystrophin gene which is too large to manipulate

Sequence 2963 BP; 897 A; 641 C; 696 G; 729 T; 0 U; 0 Other;
Query Match 92.9%; Score 13; DB 2; Length 2963;
Best Local Similarity 76.9%; Pred. No. 2.2e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

2 GUACUGCACTCG 14
1430 GTACTGCACTCG 1442

RESULT 36
AAS90082/c
ID AAS90082 standard; cDNA; 3222 BP.
XX
AC AAS90082;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #25886.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
XX
DR P-PsDB; ABG25895.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
XX
PS Claim 1; SEQ ID NO 25886; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/publ/published_pot_sequences

Sequence 3222 BP; 727 A; 880 C; 863 G; 752 T; 0 U; 0 Other;
Query Match 92.9%; Score 13; DB 5; Length 3222;
Best Local Similarity 76.9%; Pred. No. 2.2e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

2 GUACUGCACTCG 14
2019 GTACTGCACTCG 2007

RESULT 37
ADR84732/c
ID ADR84732 standard; DNA; 3443 BP.
XX
AC ADR84732;
XX
DT 04-NOV-2004 (first entry)
XX
DE Aspergillus fumigatus essential gene genomic sequence #543.
XX
KW Fungicide; Aspergillus fumigatus infection; Farmer's lung disease; drug screening; ds.
XX
OS Aspergillus fumigatus.
XX
PN WO2004067709-A2.
XX
PD 12-AUG-2004.
XX
PF 16-JAN-2004; 2004WO-US001099.
XX
PR 17-JAN-2003; 2003US-0441281P.
XX
PR 13-JUN-2003; 2003US-0478196P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PA (ELIT-) ELITRA CANADA LTD.
XX
PI Jhang B, Hu W, Lemieux S, Roemer T;
XX
DR WPI: 2004-594200/57.
XX
DR P-PsDB; ADR86493.
XX
PT New purified or isolated Aspergillus fumigatus nucleic acid molecule encoding a gene product, useful for diagnosing and/or treating invasive fungal infections, such as Farmer's lung disease.
XX
PS Claim 3; SEQ ID NO 543; 16pp; English.
XX
CC The present invention relates to Aspergillus fumigatus genes that are essential and are potential targets for drug screening. The methods and compositions of the present invention are useful for diagnosing and/or treating invasive Aspergillus fumigatus infection, including the allergic forms of the disease, such as Farmer's lung disease. They can also be

CC used in various drug discovery purposes, such as expression of the
CC recombinant protein, hybridization assay and construction of nucleic acid
CC arrays. The present sequence represents an *Aspergillus fumigatus*
CC essential gene full length genomic sequence, used during diagnosis and
CC drug development in the invention. These genes share a high degree of
CC sequence conservation with known essential genes of candida albicans. The
CC sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format from WIPO.

XX Sequence 3443 BP; 823 A; 843 C; 807 G; 970 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 13; Length 3443;
Best Local Similarity 76.9%; Pred. No. 2.2e+03;

Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACUC 14
DB 1057 GTAGTGCACCTCG 1045

RESULT 38
AAx20500/c
ID AAx20500 standard; DNA; 14063 BP.

XX AAx20500;

XX 05-MAY-1999 (first entry)

DE Polynucleotide sequence from the genome of *Treponema pallidum*.

XX *Treponema pallidum* infection; syphilis; *Borrelia* infection; animal;
KM enzyme production; ds.

XX *Treponema pallidum*.

XX MO9859034-A2.

XX 30-DEC-1998.

XX 23-JUN-1998; 98WO-US013041.

XX 24-JUN-1997; 97US-0050667P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Fraser CM;

XX WPI; 1999-081273/07.

XX New isolated *Treponema pallidum* nucleic acids - used to develop products
PT for the detection, diagnosis, characterisation, prevention and therapy of
T. *pallidum* infections, particularly syphilis.

XX Claim 1; Page 178-186; 1150pp; English.

XX AAx20500-21243 represent polynucleotide sequences from the genome of
CC *Treponema pallidum*. The sequences can be used for detection, diagnosis,
CC characterisation, prevention and therapy for T. *pallidum* infections,
CC particularly syphilis. They can also be used for detecting diseases
CC related to *Borrelia* infections in animals, and for the production of
CC biosynthetic products such as enzymes

XX Sequence 14063 BP; 3225 A; 4086 C; 3507 G; 3225 T; 0 U; 20 Other;

Query Match 92.9%; Score 13; DB 2; Length 14063;
Best Local Similarity 76.9%; Pred. No. 2.4e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13
DB 5719 CGTACTGCACCTC 5707

RESULT 39
ADZ13310/c
ID ADZ13310 standard; DNA; 83493 BP.

XX ADZ13310;

XX 16-JUN-2005 (first entry)

XX Murine cancer-associated genomic DNA #71.

XX Diagnosis; DNA microarray; microarray; bclchip; cancer; neoplasm;

XX Cytostratic; gene; ds.

XX Mus sp.

XX MO2005031001-A2.

XX 23-SEP-2004; 2004MO-US031617.

XX 23-SEP-2003; 2003US-00669920.

XX (CHIR) CHIRON CORP.

XX Morris DW, Malandro MS;

XX WPI; 2005-273395/28.

XX Nucleic acid array useful for detecting cancer associated nucleic acid,
PT comprises two or more nucleic acid probes.

XX Disclosure; SEQ ID NO 830; 198pp; English.

XX The invention relates to a nucleic acid array for detecting a cancer
CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
CC The invention also relates to a peptide array comprising two or more
CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
CC that binds to a polypeptide, an isolated antibody or its fragment which
CC binds to a polypeptide, which is prepared by immunizing a host animal
CC with a composition comprising the polypeptide or its antigen binding
CC fragment and collecting cells from the host expressing antibodies against
CC the antigen or its antigen binding fragment, a composition comprising the
CC antibody and a carrier, a method of screening for anticancer activity, a
CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a
CC method of treating cancer and a method of inhibiting expression of a CA
CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
CC nucleic acids. The antibody is useful for detecting the presence or
CC absence of cancer cells in an individual which involves contacting cells
CC from the individual with the antibody and detecting a complex of a CA
CC protein from the cancer cells and the antibody, where the detection of
CC the complex correlates with the presence of cancer cells in the
CC individual. The composition is useful for inhibiting growth of cancer
CC cells in an individual or for delivering a therapeutic agent to cancer
CC cells in an individual. The invention is also useful for diagnosing
CC cancer, for treating cancer and for inhibiting expression of a CA gene in
CC a cell. This sequence represents murine cancer-associated genomic DNA of
CC the invention.

XX Sequence 83493 BP; 22528 A; 17868 C; 19019 G; 24033 T; 0 U; 45 Other;

Query Match 92.9%; Score 13; DB 14; Length 83493;
Best Local Similarity 76.9%; Pred. No. 2.6e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13
DB 36317 CGTACTGCACCTC 36305

RESULT 40
AB067196_6/c
Continuation (7 of 7) of AB067196 from base 600001 (Listeria innocua contig DNA sequence

WP	SequenceSplit	Fragment Name	Begin	End	Accession	Abg67196
WP	ABG67196_0	1	110000			
WP	ABG67196_1	100001	210000			
WP	ABG67196_2	200001	310000			
WP	ABG67196_3	300001	410000			
WP	ABG67196_4	400001	510000			
WP	ABG67196_5	500001	610000			
WP	ABG67196_6	600001	684707			

Query Match	92.9%;	Score 13;	DB 6;	Length 84707;
Best Local Similarity	76.9%;	Pred. No. 2.6e+03;		
Matches 10;	Conservative 3;	Mismatches 0;	Indels 0;	Gaps 0;

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QY      1 CGUACUGCACTUC 13
          ||::|::|::|::|
Db      46081 CGTACTGCACTC 46069

```

ABQ69245_26
Continuation (27 of 31) of ABQ69245 from base 2600001 (Listeria innocua DNA sequence #66)
MP Sequence split into 31 fragments LOCUS ABQ69245 Accession Abq69245
Fragment Name End Position

WP	ABQ69245_00	1	110000
WP	ABQ69245_01	100001	210000
WP	ABQ69245_02	200001	310000
WP	ABQ69245_03	300001	410000
WP	ABQ69245_04	400001	510000
WP	ABQ69245_05	500001	610000
WP	ABQ69245_06	600001	710000
WP	ABQ69245_07	700001	810000
WP	ABQ69245_08	800001	910000
WP	ABQ69245_09	900001	1010000
WP	ABQ69245_10	1000001	1110000
WP	ABQ69245_11	1100001	1210000
WP	ABQ69245_12	1200001	1310000
WP	ABQ69245_13	1300001	1410000
WP	ABQ69245_14	1400001	1510000
WP	ABQ69245_15	1500001	1610000
WP	ABQ69245_16	1600001	1710000
WP	ABQ69245_17	1700001	1810000
WP	ABQ69245_18	1800001	1910000
WP	ABQ69245_19	1900001	2010000
WP	ABQ69245_20	2000001	2110000
WP	ABQ69245_21	2100001	2210000
WP	ABQ69245_22	2200001	2310000
WP	ABQ69245_23	2300001	2410000
WP	ABQ69245_24	2400001	2510000
WP	ABQ69245_25	2500001	2610000
WP	ABQ69245_26	2600001	2710000
WP	ABQ69245_27	2700001	2810000
WP	ABQ69245_28	2800001	2910000
WP	ABQ69245_29	2900001	3010000
WP	ABQ69245_30	3000001	3011208

		92.9%	Score 13:	DB 6:	Length 110000;
		Best Local Similarity	76.9%	Pred. No.	2.7e+03;
		Matches	10;	Conservative	3; Mismatches 0; Indels 0;
QY	1 CGUACUGCAATCUC	13			
	:: :: :: ::				
Db	34732 CGTACTGCACTTC	34744			

WP	Fragment Name	Begin	End	LOCUS	Accession	Aeb39175	DNA	SEQ	ID	NO	3507
WP	AEB39175_00	1	110000								
WP	AEB39175_01	100001	210000								
WP	AEB39175_02	200001	310000								

WP	AEBS39175	03	300001	440000
WP	AEBS39175	04	400001	510000
WP	AEBS39175	05	500001	610000
WP	AEBS39175	06	600001	710000
WP	AEBS39175	07	700001	810000
WP	AEBS39175	08	800001	910000
WP	AEBS39175	09	900001	1010000
WP	AEBS39175	10	1000001	1110000
WP	AEBS39175	11	1100001	1210000
WP	AEBS39175	12	1200001	1310000
WP	AEBS39175	13	1300001	1410000
WP	AEBS39175	14	1400001	1510000
WP	AEBS39175	15	1500001	1610000
WP	AEBS39175	16	1600001	1710000
WP	AEBS39175	17	1700001	1810000
WP	AEBS39175	18	1800001	1910000
WP	AEBS39175	19	1900001	2010000
WP	AEBS39175	20	2000001	2110000
WP	AEBS39175	21	2100001	2210000
WP	AEBS39175	22	2200001	2310000
WP	AEBS39175	23	2300001	2410000
WP	AEBS39175	24	2400001	2510000
WP	AEBS39175	25	2500001	2610000
WP	AEBS39175	26	2600001	2710000
WP	AEBS39175	27	2700001	2810000
WP	AEBS39175	28	2800001	290000
WP	AEBS39175	29	2900001	3010000
WP	AEBS39175	30	3000001	3110000
WP	AEBS39175	31	3100001	3210000
WP	AEBS39175	32	3200001	3310000
WP	AEBS39175	33	3300001	3410000
WP	AEBS39175	34	3400001	3503610

Query Match	92.9%;	Score 13;	DB 14;	Length 110000;
Best Local Similarity	76.9%;	Pred. No. 2.7e+03;		
Matches 10; Conservative	3;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	CGUACUGCAACUC	13
Db	88966	CGTACTGCAACTC	88954

RESULT 43
ABE42401_12/c
Contribution (13 of 34) of ABE42401 from base 1200001 (L. pneumophila DNA SEQ ID NO 6733
MP Sequence split into 34 fragments LOCUS ABE42401 Accession Aeb42401

WP	Arrangement	Begin	End
WP	AEBA2401_00	1	110000
WP	AEBA2401_01	100001	210000
WP	AEBA2401_02	200001	310000
WP	AEBA2401_03	300001	410000
WP	AEBA2401_04	400001	510000
WP	AEBA2401_05	500001	610000
WP	AEBA2401_06	600001	710000
WP	AEBA2401_07	700001	810000
WP	AEBA2401_08	800001	910000
WP	AEBA2401_09	900001	1010000
WP	AEBA2401_10	1000001	1110000
WP	AEBA2401_11	1100001	1210000
WP	AEBA2401_12	1200001	1310000
WP	AEBA2401_13	1300001	1410000
WP	AEBA2401_14	1400001	1510000
WP	AEBA2401_15	1500001	1610000
WP	AEBA2401_16	1600001	1710000
WP	AEBA2401_17	1700001	1810000
WP	AEBA2401_18	1800001	1910000
WP	AEBA2401_19	1900001	2010000
WP	AEBA2401_20	2000001	2110000
WP	AEBA2401_21	2100001	2210000
WP	AEBA2401_22	2200001	2310000
WP	AEBA2401_23	2300001	2410000
WP	AEBA2401_24	2400001	2510000
WP	AEBA2401_25	2500001	2610000

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WP AEB42401_26 260001 2710000
PT AEB42401_27 2700001 2810000
WP AEB42401_28 2800001 2910000
PT AEB42401_29 2900001 3010000
WP AEB42401_30 3000001 3110000
PT AEB42401_31 3100001 3210000
WP AEB42401_32 3200001 3310000
PT AEB42401_33 3300001 345687

Query Match 92.9%; Score 13; DB 14; Length 110000;
Best Local Similarity 76.9%; Pred. No. 2.7e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUC 13
Db 98980 CGTACTGCAACTC 98968

RESULT 44
AEB42736_6/c
Continuation (7 of 8) of AEB42736 from base 600001 (L. pneumophila DNA SEQ ID NO 7068.)
WP Sequence split into 8 fragments LOCUS AEB42736 Accession Aeb42736
WP Fragment Name Begin End
WP AEB42736_0 1 110000
WP AEB42736_1 100001 210000
WP AEB42736_2 200001 310000
WP AEB42736_3 300001 410000
WP AEB42736_4 400001 510000
WP AEB42736_5 500001 610000
WP AEB42736_6 600001 710000
WP AEB42736_7 700001 740626

Query Match 92.9%; Score 13; DB 14; Length 110000;
Best Local Similarity 76.9%; Pred. No. 2.7e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUC 13
Db 60645 CGTACTGCAACTC 60633

RESULT 45
AEB35722/c
ID AEB35722 standard; DNA; 184368 BP.
XX
XX AEB35722;
AC
XX
XX AEB35722;
AC
XX
XX 08-SEP-2005 (first entry)
DT
XX
XX L. pneumophila DNA SEQ ID NO 54.
DE
XX
XX detection; infection; Antibacterial; Vaccine; ds; gene.
KM
XX
XX Legionella pneumophila.
OS
XX
XX WO2005049642-A2.
PN
XX
XX 02-JUN-2005.
PD
XX
XX 23-SEP-2004; 2004MO-IB003578.
PF
XX
XX 21-NOV-2003; 2003FR-00013687.
PR
XX
XX (INSP ) INST PASTEUR.
PA
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UTLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Buchrieser C, Tichit M, Etienne J, Ma L, Cazale C, Glaser P;
PI Ruanlok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
PI Jarraud S;
XX
XX WPI; 2005-388305/40.

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XX
XX New genome of Legionella pneumophila Paris strain and derived
PT polypeptides, useful for detection or identification of the strain and
PT for treatment and prevention of infections.
XX
XX Claim 1, SEQ ID NO 54; 660bp; English.
PS
XX
XX The invention relates to an isolated or purified nucleotide sequences (I)
CC from Legionella pneumophila Paris strain. (I), and their related
CC sequences or fragments, are useful as primers and probes for detection
CC and amplification, including differentiation between the Paris and
CC Philadelphia strains of Legionella pneumophila and to prepare recombinant
CC (hybrid) polypeptides (II). (II) are also useful for preparation of
CC specific antibodies (Ab), also used for detection/identification of
CC Legionella, and some (II), specifically those involved in synthesis of
CC surface proteins, are targets for identification of inhibitors. (II), or
CC vectors that contain (I), are useful as vaccines and immunogenic
CC compositions, for treatment and prevention of infections by L.
CC pneumophila. The present sequence represents a L. pneumophila DNA.
XX
XX Sequence 184368 BP; 57341 A; 33604 C; 36303 G; 57120 T; 0 U; 0 Other;
SQ

Query Match 92.9%; Score 13; DB 14; Length 184368;
Best Local Similarity 76.9%; Pred. No. 2.7e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUC 13
Db 119323 CGTACTGCAACTC 119311

RESULT 46
AEB39170
ID AEB39170 standard; DNA; 207461 BP.
XX
XX AEB39170;
AC
XX
XX 08-SEP-2005 (first entry)
DT
XX
XX L. pneumophila DNA SEQ ID NO 3502.
DE
XX
XX detection; infection; Antibacterial; Vaccine; ds; gene.
KM
XX
XX Legionella pneumophila.
OS
XX
XX WO2005049642-A2.
PN
XX
XX 02-JUN-2005.
PD
XX
XX 23-SEP-2004; 2004MO-IB003578.
PF
XX
XX 21-NOV-2003; 2003FR-00013687.
PR
XX
XX (INSP ) INST PASTEUR.
PA
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UTLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Buchrieser C, Tichit M, Etienne J, Ma L, Cazale C, Glaser P;
PI Ruanlok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
PI Jarraud S;
XX
XX WPI; 2005-388305/40.
XX
XX New genome of Legionella pneumophila Paris strain and derived
PT polypeptides, useful for detection or identification of the strain and
PT for treatment and prevention of infections.
XX
XX Example 9; SEQ ID NO 3502; 660bp; English.
XX
XX The invention relates to an isolated or purified nucleotide sequences (I)
CC from Legionella pneumophila Paris strain. (I), and their related
CC sequences or fragments, are useful as primers and probes for detection
CC

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CC and amplification, including differentiation between the Paris and
CC Philadelphia strains of Legionella pneumophila and to prepare recombinant
CC (hybrid) polypeptides (II). (II) are also useful for preparation of
CC specific antibodies (Ab), also used for detection/identification of
CC Legionella, and some (I), specifically those involved in synthesis of
CC surface proteins, are targets for identification of inhibitors. (II), or
CC vectors that contain (I) are useful as vaccines and immunogenic
CC compositions, for treatment and prevention of infections by L.
CC pneumophila. The present sequence represents a L. pneumophila DNA.
XX

Sequence 207461 BP; 66316 A; 40889 C; 36511 G; 63745 T; 0 U; 0 Other;
SQ

Query Match 92.9%; Score 13; DB 14; Length 207461;
Best Local Similarity 76.9%; Pred. No. 2.7e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13
DB 80862 CGTACTGCAATC 80874
||:|||||:|
|:|:|:|:|:|

RESULT 47
ADS37261
ID ADS37261 standard; DNA; 201 BP.
XX
AC ADS37261;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human autoimmune disease-related SNP context sequence - SEQ ID 2475.
XX
KW single nucleotide polymorphism detection; SNP detection;
KW rheumatoid arthritis; type 1 diabetes; multiple sclerosis;
KW systemic lupus erythematosus; inflammatory bowel disease; psoriasis;
KW thyroiditis; celiac disease; pernicious anaemia; asthma; vitiligo;
KW glomerulonephritis; Grave's disease; myocarditis; Sjogren's disease;
KW primary systemic vasculitis; ds.
XX
OS Homo sapiens.
XX
PN WO2004083403-A2.
XX
PD 30-SEP-2004.
XX
PF 18-MAR-2004; 2004WO-US008461.
XX
PR 18-MAR-2003; 2003US-0455444P.
XX
PT 25-APR-2003; 2003US-0465241P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Begovich AB, Alexander HC;
XX
DR WPI; 2004-728480/71.
XX
PT New isolated nucleic acid molecule comprises at least 8 contiguous
PT nucleotides where one of the nucleotides is a single nucleotide
PT polymorphism (SNP), useful for diagnosing or treating autoimmune
PT diseases, e.g. rheumatoid arthritis.
XX
PS Claim 16; SEQ ID NO 2475; 123bp; English.
XX
XX The invention comprises amino acid and coding sequences containing
CC genetic polymorphisms associated with an altered risk of developing an
CC autoimmune disease (e.g. rheumatoid arthritis). The invention further
CC comprises a method of identifying an individual that has an altered risk
CC of developing an autoimmune disease, comprising detecting a single
CC nucleotide polymorphism (SNP) in a nucleic acid of the invention. The DNA
CC and protein sequences of the invention are useful for diagnosing and
CC treating autoimmune diseases, such as: rheumatoid arthritis, type 1
CC diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory
CC bowel diseases, psoriasis, thyroiditis, celiac disease, pernicious
CC anaemia, asthma, vitiligo, glomerulonephritis, Grave's disease,
CC anemias, asthma, vitiligo, glomerulonephritis, Grave's disease,

CC myocarditis, Sjogren's disease, or primary systemic vasculitis. The
CC present DNA sequence represents a human autoimmune disease-related
CC genetic-based SNP context sequence of the invention. NOTE: The present
CC sequence is not shown in the specification, but has been retrieved from
CC the WIPO website.
XX

Sequence 201 BP; 59 A; 35 C; 45 G; 61 T; 0 U; 1 Other;
SQ

Query Match 90.0%; Score 12.6; DB 13; Length 201;
Best Local Similarity 76.9%; Pred. No. 3.1e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13
DB 99 CGTACTGCAATC 111
||:|||||:|
|:|:|:|:|:|

RESULT 48
ADS40621/C
ID ADS40621 standard; DNA; 201 BP.
XX
AC ADS40621;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human autoimmune disease-related SNP context sequence - SEQ ID 5835.
XX
KW single nucleotide polymorphism detection; SNP detection;
KW rheumatoid arthritis; type 1 diabetes; multiple sclerosis;
KW systemic lupus erythematosus; inflammatory bowel disease; psoriasis;
KW thyroiditis; celiac disease; pernicious anaemia; asthma; vitiligo;
KW glomerulonephritis; Grave's disease; myocarditis; Sjogren's disease;
KW primary systemic vasculitis; ds.
XX
OS Homo sapiens.
XX
PN WO2004083403-A2.
XX
PD 30-SEP-2004.
XX
PF 18-MAR-2004; 2004WO-US008461.
XX
PR 18-MAR-2003; 2003US-0455444P.
XX
PT 25-APR-2003; 2003US-0465241P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Begovich AB, Alexander HC;
XX
DR WPI; 2004-728480/71.
XX
PT New isolated nucleic acid molecule comprises at least 8 contiguous
PT nucleotides where one of the nucleotides is a single nucleotide
PT polymorphism (SNP), useful for diagnosing or treating autoimmune
PT diseases, e.g. rheumatoid arthritis.
XX
PS Claim 16; SEQ ID NO 5835; 123bp; English.
XX
XX The invention comprises amino acid and coding sequences containing
CC genetic polymorphisms associated with an altered risk of developing an
CC autoimmune disease (e.g. rheumatoid arthritis). The invention further
CC comprises a method of identifying an individual that has an altered risk
CC of developing an autoimmune disease, comprising detecting a single
CC nucleotide polymorphism (SNP) in a nucleic acid of the invention. The DNA
CC and protein sequences of the invention are useful for diagnosing and
CC treating autoimmune diseases, such as: rheumatoid arthritis, type 1
CC diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory
CC bowel diseases, psoriasis, thyroiditis, celiac disease, pernicious
CC anaemia, asthma, vitiligo, glomerulonephritis, Grave's disease,
CC myocarditis, Sjogren's disease, or primary systemic vasculitis. The
CC present DNA sequence represents a human autoimmune disease-related
CC genetic-based SNP context sequence of the invention. NOTE: The present
CC sequence is not shown in the specification, but has been retrieved from

CC the WIPO website.
 XX Sequence 201 BP; 61 A; 45 C; 35 G; 59 T; 0 U; 1 Other;
 SQ Query Match 90.0%; Score 12.6; DB 13; Length 201;
 Best Local Similarity 76.9%; Pred. No. 3.1e+03;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13
 ||:|||||:
 DB 103 CGVACTGCAACTC 91

RESULT 49
 AAA28522/c
 ID AAA28522 standard; CDNA; 2290 BP.
 XX
 AC AAA28522;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Human opioid growth factor receptor cDNA of spliced form A.
 XX
 KM OGR; opioid growth factor receptor; growth inhibitor; proliferative;
 KM cytostatic; vulnerary. gene therapy; antagonist; chromosome 20q13.3; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 34..2007
 FT /*tag= a
 XX
 PN WO200026340-A2.
 PD 11-MAY-2000.
 XX
 PF 02-NOV-1999; 99MO-US025802.
 XX
 PR 03-NOV-1998; 98US-0106879P.
 XX
 PA (PENN-) PENN STATE RES FOUND.
 XX
 PI Zagom IS, McLaughlin PJ, Verderame MF;
 XX
 DR WPI; 2000-365594/31.
 XX
 PT New cDNA encoding rat and human opioid growth factor receptors which
 PT modulate cell growth, useful for treating cancer.
 XX
 PS Claim 1; Page 77-78; 91pp; English.
 XX
 CC Primers generated from rat opioid growth factor receptor (OGR) cDNA were
 CC used to clone a fragment of the human OGR cDNA. The complete sequence of
 CC human OGR was assembled with a combination of 3' and 5' RACE. 5' RACE
 CC consistently yielded a single species of cDNA, while the 3' RACE revealed
 CC extensive alternative splicing. The alternate splice forms were missing
 CC the imperfect repeats or differed in the number of imperfect repeats. The
 CC human OGR gene chromosomal location was determined by FISH as 20q13.3.
 CC expression vector are useful for detecting expression or levels of an
 CC OGR in a tissue. OGR nucleic acids can be used to inhibit growth of
 CC cells in vitro. The antisense sequences and antibodies can be used to
 CC promote growth of cells in vitro. Cell growth can be promoted by
 CC interfering with the OGR ligand-receptor system, especially where a
 CC subject suffers from a tissue wound. Treating cancer comprises enhancing
 CC the function of the OGR ligand-receptor system in cancerous cells of a
 CC patient or administering the OGR nucleic acid to the patient

SQ Sequence 2290 BP; 470 A; 713 C; 807 G; 297 T; 0 U; 3 Other;
 Query Match 90.0%; Score 12.6; DB 3; Length 2290;
 Best Local Similarity 69.2%; Pred. No. 3.6e+03;
 Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13
 ||:|||||:
 DB 1969 CGTMTGCAACTC 1957

RESULT 50
 ADS36480/c
 ID ADS36480 standard; DNA; 29871 BP.
 XX
 AC ADS36480;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1694.
 XX
 KM single nucleotide polymorphism detection; SNP detection;
 KM rheumatoid arthritis; type 1 diabetes; multiple sclerosis;
 KM systemic lupus erythematosus; inflammatory bowel disease; psoriasis;
 KM chryoiditis; celiac disease; pernicious anaemia; asthma; vitiligo;
 KM glomerulonephritis; Grave's disease; myocarditis; Sjogren's disease;
 KM primary systemic vasculitis; de.
 XX
 OS Homo sapiens.
 XX
 PN WO2004083403-A2.
 PD 30-SEP-2004.
 XX
 PF 18-MAR-2004; 2004MO-US008461.
 XX
 PR 18-MAR-2003; 2003US-045544P.
 PR 25-APR-2003; 2003US-0465241P.
 XX
 PA (APPL-) APPLERA CORP.
 XX
 PI Cargill M, Begovich AB, Alexander HC;
 XX
 DR WPI; 2004-728480/71.
 XX
 PT New isolated nucleic acid molecule comprises at least 8 contiguous
 PT nucleotides where one of the nucleotides is a single nucleotide
 PT polymorphism (SNP), useful for diagnosing or treating autoimmune
 PT diseases, e.g. rheumatoid arthritis.
 XX
 PS Claim 16; SEQ ID NO 1694; 123pp; English.
 XX
 CC The invention comprises amino acid and coding sequences containing
 CC genetic polymorphisms associated with an altered risk of developing an
 CC autoimmune disease (e.g. rheumatoid arthritis). The invention further
 CC comprises a method of identifying an individual that has an altered risk
 CC of developing an autoimmune disease, comprising detecting a single
 CC nucleotide polymorphism (SNP) in a nucleic acid of the invention. The DNA
 CC and protein sequences of the invention are useful for diagnosing and
 CC treating autoimmune diseases, such as: rheumatoid arthritis, type 1
 CC diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory
 CC bowel diseases, psoriasis, thyroiditis, celiac disease, pernicious
 CC anaemia, asthma, vitiligo, glomerulonephritis, Grave's disease,
 CC myocardiitis, Sjogren's disease, or primary systemic vasculitis. The
 CC present nucleic acid represents a human autoimmune disease-related
 CC genomic DNA sequence of the invention. NOTE: The present sequence is not
 CC shown in the specification, but has been retrieved from the WIPO website.

SQ Sequence 29871 BP; 8723 A; 7387 C; 6374 G; 7338 T; 0 U; 49 Other;
 Query Match 90.0%; Score 12.6; DB 13; Length 29871;
 Best Local Similarity 76.9%; Pred. No. 4.2e+03;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13
 ||:|||||:
 DB 14198 CGVACTGCAACTC 14186

Thu Mar 23 15:50:24 2006

Search completed: March 18, 2006, 18:54:38
Job time : 344.346 secs

us-10-800-926-2.rng

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OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:35:00 ; Search time 711.308 Seconds
(without alignments)
1118.796 Million cell updates/sec

Title: US-10-800-926-2

Perfect score: 14
Sequence: 1 cguacugcaacug 14

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_scs:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hcg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
C 1	14	100.0	2832 13	SLMNPYR
C 2	14	100.0	10151 15	AF484941
C 3	14	100.0	11318 1	AE012045
C 4	14	100.0	14169 1	AE009858
C 5	14	100.0	96360 14	AP003867
C 6	14	100.0	99251 8	AL592045
C 7	14	100.0	101249 15	AP003884
C 8	14	100.0	110000 1	AE016853_08
C 9	14	100.0	110000 14	CP000058_08
C 10	14	100.0	110000 5	CR954209
C 11	14	100.0	110000 14	LMPLCR18_00
C 12	14	100.0	110000 15	AP008214_143
C 13	14	100.0	110000 15	AP008215_150
C 14	14	100.0	110000 15	CR382131_08
C 15	14	100.0	110000 15	CR382131_09
C 16	14	100.0	133106 15	AP004759
C 17	14	100.0	140409 14	AC044825
C 18	14	100.0	148848 15	AP005426

19	14	100.0	154950	15	AP005429	AP005429 Oryza sat
20	14	100.0	173867	5	BX088687	BX088687 zebrafish
21	14	100.0	188872	14	AC108605	AC108605 Rattus no
22	14	100.0	218764	14	AC103229	AC103229 Rattus no
23	14	100.0	230865	5	BX640547	BX640547 zebrafish
24	14	100.0	232180	14	AC021883	AC021883 Homo sapi
25	14	100.0	293350	1	BX294153	BX294153 Pirella
26	13	92.9	65	6	COS54118	COS54118 Sequence
27	13	92.9	100	6	AX988576	AX988576 Sequence
28	13	92.9	100	6	AX988577	AX988577 Sequence
29	13	92.9	186	9	AF069774	AF069774 Mus muscu
30	13	92.9	200	2	TRBPRTXNB	TRBPRTXNB
31	13	92.9	327	8	AF232912	AF232912 Macaca mu
32	13	92.9	398	8	AY011660	AY011660 Ateles fu
33	13	92.9	406	8	MACTCRAL	MACTCRAL
34	13	92.9	408	8	MACTCRAK	MACTCRAK
35	13	92.9	580	15	AK111239	AK111239 Oryza sat
36	13	92.9	615	1	AY136528	AY136528 Acridovora
37	13	92.9	620	10	BV502883	BV502883 qjy90e11.
38	13	92.9	693	10	BV507671	BV507671 gtf62a12.
39	13	92.9	742	10	BV635227	BV635227 S217P6390
40	13	92.9	768	10	BV530657	BV530657 G591P6179
41	13	92.9	773	10	BV530662	BV530662 G591P6179
42	13	92.9	774	10	BV530664	BV530664 G591P6179
43	13	92.9	939	5	D64054	D64054 Myxine glut
44	13	92.9	971	10	BV550217	BV550217 S215P6032
45	13	92.9	1197	6	E38273	E38273 Formate deh
46	13	92.9	1241	1	KFN344089	KFN344089 Klebsiell
47	13	92.9	1330	3	BSP308467	BSP308467 Enterobac
48	13	92.9	1347	3	AY985960	AY985960 Unculture
49	13	92.9	1356	3	AY985162	AY985162 Unculture
50	13	92.9	1357	3	AY986117	AY986117 Unculture
51	13	92.9	1433	5	CR761525	CR761525 Xenopus t
52	13	92.9	1541	3	AY013692	AY013692 Unculture
53	13	92.9	1720	6	AA405992	AA405992 Sequence
54	13	92.9	1720	6	AX356828	AX356828 Sequence
55	13	92.9	1945	6	CO053680	CO053680 Sequence
56	13	92.9	1945	6	CO068836	CO068836 Sequence
57	13	92.9	1945	6	CO095899	CO095899 Sequence
58	13	92.9	1945	6	CO134643	CO134643 Sequence
59	13	92.9	1945	6	CO173137	CO173137 Sequence
60	13	92.9	1945	6	CO202326	CO202326 Sequence
61	13	92.9	1945	6	CO217908	CO217908 Sequence
62	13	92.9	1945	6	CO256479	CO256479 Sequence
63	13	92.9	1945	6	CO293574	CO293574 Sequence
64	13	92.9	1945	6	CO330497	CO330497 Sequence
65	13	92.9	1985	2	TRR439686	TRR439686 Trypanoso
66	13	92.9	2000	6	AX595578	AX595578 Sequence
67	13	92.9	2000	6	AX819720	AX819720 Sequence
68	13	92.9	2000	6	AX830750	AX830750 Sequence
69	13	92.9	2301	2	TEBLK	TEBLK
70	13	92.9	2454	15	AY133724	AY133724 Arabidops
71	13	92.9	2490	9	RNU50717	RNU50717 Rattus norv
72	13	92.9	2559	9	AF388675	AF388675 Mus muscu
73	13	92.9	2580	1	AB051073	AB051073 Hyalomict
74	13	92.9	2695	15	YSCVPS33P	M34638 S.cerevisia
75	13	92.9	2866	9	RNU53368	US3368 Rattus norv
76	13	92.9	3002	9	RNU49049	U49049 Rattus norv
77	13	92.9	3176	14	AC019684	AC019684 Drosophi1
78	13	92.9	3288	2	AY920799	AY920799 Aequorea
79	13	92.9	3456	15	YSCSP1A	M34474 S.cerevisia
80	13	92.9	9669	15	NTR416576	AJ416576 Nicotiana
81	13	92.9	10339	1	AB001200	AB001200 Treponema
82	13	92.9	10849	1	AE011567	AE011567 Leptospir
83	13	92.9	12620	1	AF197465	AF197465 Pseudomon
84	13	92.9	17484	15	AB084950	AB084950 Nicotiana
85	13	92.9	19580	1	AJ786382	AJ786382 Streptomy
86	13	92.9	19791	1	D90850	D90850 E.coli geno
87	13	92.9	28740	8	AL158136	AL158136 Human DNA
88	13	92.9	30866	2	L09634	L09634 Caenorhabdi
89	13	92.9	34948	2	CARG33E23	AC084551 Caenorhab
90	13	92.9	39149	1	ECOHU49	U00008 centilome_4
91	13	92.9	39502	3	AY534910	AY534910 Unculture

92	13	92.9	40198	15	YSLC8084	U19729 Saccharomyc	165	13	92.9	160950	14	AC163250	AC163550 Loxodonta
93	13	92.9	42734	2	CEBY3	Z96047 Caenorhabdi	166	13	92.9	164301	14	AC018671	AC018671 Homo sapi
94	13	92.9	43586	4	OSIG00036	AL732335 Oryza sat	167	13	92.9	164925	18	AC098966	AC098966 Homo sapi
95	13	92.9	58623	14	AC101064	AC101064 Mus muscu	168	13	92.9	164925	14	AC087372	AC087372 Homo sapi
96	13	92.9	63105	14	AC120027	AC120027 Homo sapi	169	13	92.9	166117	14	CR855265	CR855265 Dario rer
97	13	92.9	63643	14	AC090923	AC090923 Homo sapi	170	13	92.9	167511	14	AC162049	AC162049 Bos tauru
98	13	92.9	66145	14	H0609A12	AL512544 Oryza sat	171	13	92.9	167812	14	AC125875	AC125875 Rattus no
99	13	92.9	66506	14	AC120028	AC120028 Homo sapi	172	13	92.9	167851	8	AC118660	AC118660 Homo sapi
100	13	92.9	68272	6	AC090171	AC090171 Homo sapi	173	13	92.9	168169	14	AC145953	AC145953 Pan trogl
101	13	92.9	84707	14	AX417037	AX417037 Sequence	174	13	92.9	168297	9	AC116801	AC116801 Mus muscu
102	13	92.9	88538	14	AC164461	AC164461 Bos tauru	175	13	92.9	168662	14	AC022241	AC022241 Homo sapi
103	13	92.9	89855	14	AC074220	AC074220 Mus muscu	176	13	92.9	168980	8	AC010165	AC010165 Homo sapi
104	13	92.9	98630	15	AC006535	AC006535 Genomic B	177	13	92.9	169453	8	AC096558	AC096558 Homo sapi
105	13	92.9	101104	1	CP000089_44	Contimnation (45 o	178	13	92.9	170260	8	BX908763	BX908763 Zebrafish
106	13	92.9	103273	8	AC139932	AC139932 Homo sapi	179	13	92.9	171072	8	CR805786	CR805786 Human chr
107	13	92.9	104321	15	AP006142	AP006142 Lotus cor	180	13	92.9	171973	14	AC013571	AC013571 Homo sapi
108	13	92.9	104712	8	AL3390786	AL3390786 Human DNA	181	13	92.9	172127	14	AC013572	AC013572 Homo sapi
109	13	92.9	107489	8	AL137804	AL137804 Human DNA	182	13	92.9	173384	8	PTB44823	PTB44823 Homo sapi
110	13	92.9	107819	15	AP004926	AP004926 Oryza sat	183	13	92.9	173916	14	AC007747	AC007747 Homo sapi
111	13	92.9	109022	15	AP004926	Contimnation (31 o	184	13	92.9	176357	14	CR85031	CR85031 Dario rer
112	13	92.9	110000	1	AE005174_30	Contimnation (32 o	185	13	92.9	182172	15	CR807YPC	CR807YPC Homo sapi
113	13	92.9	110000	1	AE005174_31	Contimnation (32 o	186	13	92.9	182172	15	CR807YPC	CR807YPC Homo sapi
114	13	92.9	110000	1	AE005674_23	Contimnation (24 o	187	13	92.9	183224	14	AC166615	AC166615 Oryctoarg
115	13	92.9	110000	1	CR628336_12	Contimnation (13 o	188	13	92.9	184518	8	AC099524	AC099524 Homo sapi
116	13	92.9	110000	1	CR628337_12	Contimnation (13 o	189	13	92.9	184558	14	AC020570	AC020570 Homo sapi
117	13	92.9	110000	1	U00096_22	Contimnation (23 o	190	13	92.9	185444	14	AC158419	AC158419 Homo sapi
118	13	92.9	110000	1	U00096_23	Contimnation (24 o	191	13	92.9	187787	9	AC121802	AC121802 Mus muscu
119	13	92.9	110000	1	AE017354_12	Contimnation (13 o	192	13	92.9	188131	14	AC161201	AC161201 Mus muscu
120	13	92.9	110000	1	AP006716_04	Contimnation (5 o	193	13	92.9	189722	14	AC164403	AC164403 Homo sapi
121	13	92.9	110000	1	AP008231_20	Contimnation (21 o	194	13	92.9	192065	14	AC148556	AC148556 Homo sapi
122	13	92.9	110000	1	BA000007_30	Contimnation (31 o	195	13	92.9	192617	14	AC123751	AC123751 Mus muscu
123	13	92.9	110000	1	BA000030_32	Contimnation (33 o	196	13	92.9	193101	14	AC009561	AC009561 Homo sapi
124	13	92.9	110000	1	BA000030_59	Contimnation (60 o	197	13	92.9	193579	9	AC130675	AC130675 Mus muscu
125	13	92.9	110000	1	CP000075_08	Contimnation (9 o	198	13	92.9	193900	14	AC165972	AC165972 Mus muscu
126	13	92.9	110000	14	AC020850_2	Contimnation (3 o	199	13	92.9	194520	8	AC148837	AC148837 Homo sapi
127	13	92.9	110000	14	CR954199_02	Contimnation (4 o	200	13	92.9	194551	14	AC092291	AC092291 Homo sapi
128	13	92.9	110000	14	CR954201_03	Contimnation (4 o	201	13	92.9	196164	5	BX119916	BX119916 Zebrafish
129	13	92.9	110000	14	CT005267_10	Contimnation (11 o	202	13	92.9	199047	9	AC103574	AC103574 Ratius no
130	13	92.9	110000	14	CT005267_11	Contimnation (12 o	203	13	92.9	207476	14	AC157524	AC157524 Mus muscu
131	13	92.9	110000	14	IMF1CHR32_04	Contimnation (5 o	204	13	92.9	208695	9	AL671478	AL671478 Mouse DNA
132	13	92.9	110000	15	AP008218_158	Contimnation (159	205	13	92.9	209121	5	CR889850	CR889850 Zebrafish
133	13	92.9	110000	15	AP008218_158	Contimnation (210	206	13	92.9	209587	9	AC158236	AC158236 Mus muscu
134	13	92.9	110000	15	AB017347_06	Contimnation (7 o	207	13	92.9	212870	14	AC156189	AC156189 Bos tauru
135	13	92.9	110000	15	AP008207_212	Contimnation (214	208	13	92.9	212870	14	AC020970	AC020970 Mus muscu
136	13	92.9	110000	15	AP008207_212	Contimnation (331	209	13	92.9	215999	14	AC102792	AC102792 Mus muscu
137	13	92.9	110000	15	AP008210_16	Contimnation (17 o	210	13	92.9	217642	14	AC115542	AC115542 Rattus no
138	13	92.9	110000	15	AP008210_16	Contimnation (17 o	211	13	92.9	219491	14	AC092256	AC092256 Mus muscu
139	13	92.9	113212	15	AC091527	AC091527 Trypanoso	212	13	92.9	220503	14	AC161192	AC161192 Bos tauru
140	13	92.9	114057	2	AF546189	AF546189 Contignou	213	13	92.9	220503	14	AC161192	AC161192 Bos tauru
141	13	92.9	116115	15	AC153108	AC153108 Loxodonta	214	13	92.9	220503	14	AC097956	AC097956 Rattus no
142	13	92.9	124175	14	AC163303	AC163303 Mus muscu	215	13	92.9	220503	14	AC156131	AC156131 Homo sapi
143	13	92.9	124175	14	AC129011	AC129011 Leishmani	216	13	92.9	227676	14	AC109506	AC109506 Mus muscu
144	13	92.9	125228	14	AC008842	AC008842 Homo sapi	217	13	92.9	229963	14	AC150456	AC150456 Callitric
145	13	92.9	131867	2	AY449460	AY449460 Oikopleur	218	13	92.9	231840	5	AL954746	AL954746 Zebrafish
146	13	92.9	131867	2	AY449460	AY449460 Homo sapi	219	13	92.9	234660	14	AC134709	AC134709 Rattus no
147	13	92.9	131891	8	AC008131	AC008131 Homo sapi	220	13	92.9	234660	14	AC160179	AC160179 Bos tauru
148	13	92.9	132678	1	AY596294	AY596294 Halloarcul	221	13	92.9	234660	14	AC095895	AC095895 Rattus no
149	13	92.9	134290	2	AC159439	AC159439 Trypanoso	222	13	92.9	237041	14	AC164273	AC164273 Bos tauru
150	13	92.9	134580	8	AC002526	AC002526 Human PAC	223	13	92.9	237041	14	AC148336	AC148336 Mus muscu
151	13	92.9	135578	8	AF064861	AF064861 Homo sapi	224	13	92.9	240475	14	AC099247	AC099247 Rattus no
152	13	92.9	140626	15	OS0N00057	OS0N00057 Oryza sat	225	13	92.9	243051	9	AC126217	AC126217 Rattus no
153	13	92.9	141424	14	AC162149	AC162149 Dasypus n	226	13	92.9	243468	14	AC103320	AC103320 Rattus no
154	13	92.9	142350	5	BX664625	BX664625 Zebrafish	227	13	92.9	244047	14	AC133427	AC133427 Rattus no
155	13	92.9	145796	15	AC130598	AC130598 Oryza sat	228	13	92.9	250323	14	AC119713	AC119713 Rattus no
156	13	92.9	147817	15	AP003267	AP003267 Oryza sat	229	13	92.9	255705	14	AC097750	AC097750 Rattus no
157	13	92.9	152714	8	BS000156	BS000156 Pan trogl	230	13	92.9	256019	8	AC016525	AC016525 Homo sapi
158	13	92.9	153617	8	AC012306	AC012306 Homo sapi	231	13	92.9	256719	9	AC154873	AC154873 Mus muscu
159	13	92.9	154066	8	HS24018	HS24018 Human DNA	232	13	92.9	258622	14	AC020877	AC020877 Mus muscu
160	13	92.9	154375	14	AC145837	AC145837 Pan trogl	233	13	92.9	258938	14	AC099416	AC099416 Mus muscu
161	13	92.9	157395	9	CNS07878	AL512355 Human chr	234	13	92.9	271275	14	AC135198	AC135198 Rattus no
162	13	92.9	158710	9	AC126539	AC126539 Mus muscu	235	13	92.9	295689	14	AB016985	AB016985 Shigella
163	13	92.9	159767	14	AC023529	AC023529 Homo sapi	236	13	92.9	296821	14	AC127127	AC127127 Rattus no
164	13	92.9	159767	14	AC023529	AC023529 Homo sapi	237	13	92.9	296821	14	AC127127	AC127127 Rattus no

C 238	13	92.9	301130	1	AB016763	AB016763	Beckrich	311	12.4	88.6	782	2	AV113559	AV113559 Drosophila
C 239	13	92.9	301132	1	AB017012	AB017012	Bacillus	312	12.4	88.6	785	10	BV663682	BV663682 S215P659
C 240	13	92.9	302101	1	AB016784	AB016784	Pseudomon	C 313	12.4	88.6	788	2	AP180708	AP180708 Aedes aeg
C 241	13	92.9	305050	1	AL596173	AL596173	Listeria	C 314	12.4	88.6	788	2	AP266757	AP266757 Aedes aeg
C 242	13	92.9	309502	14	AL512434	AL512434	Bos taurus	C 315	12.4	88.6	798	6	BD125095	BD125095 Primer fo
C 243	13	92.9	309626	8	AY332722	AY332722	Homo sapi	C 316	12.4	88.6	798	6	BD127034	BD127034 Primer fo
C 244	13	92.9	340000	8	HS21C079	HS21C079	Alu163279	C 317	12.4	88.6	798	6	CQ780386	CQ780386 Sequence
C 245	13	92.9	345630	14	AC098929	AC098929	Rattus no	C 318	12.4	88.6	798	6	CQ782325	CQ782325 Sequence
C 246	13	92.9	346027	14	AC128985	AC128985	Rattus no	C 319	12.4	88.6	812	10	BV545689	BV545689 Cml197f05
C 247	13	92.9	348313	1	CR378666	CR378666	Photobact	C 320	12.4	88.6	828	15	AP321883	AP321883 Neutropor
C 248	13	92.9	349697	1	BX842649	BX842649	Bellovib	C 321	12.4	88.6	831	1	ECORRPX	ECORRPX J05113 E.-coli rldo
C 249	13	92.9	349980	6	AX417036	AX417036	Sequence	C 322	12.4	88.6	831	1	AJ632066	AJ632066 Nosroc al
C 250	13	92.9	349980	6	AX417036	AX417036	Sequence	C 323	12.4	88.6	841	10	BV529365	BV529365 GS91P6248
C 251	12.6	90.0	201	6	CQ927442	CQ927442	Sequence	C 324	12.4	88.6	852	2	AY198134	AY198134 Aedes aeg
C 252	12.6	90.0	201	6	CQ930802	CQ930802	Sequence	C 325	12.4	88.6	862	2	MOSTRIP	MOSTRIP M781814 Aedes aeg
C 253	12.6	90.0	29871	6	CQ926631	CQ926631	Sequence	C 326	12.4	88.6	867	6	AR624404	AR624404 Sequence
C 254	12.6	90.0	321019	6	CQ926631	CQ926631	Sequence	C 327	12.4	88.6	883	8	SS1407	SS1407 decay acce1
C 255	12.4	88.6	40	6	BD133929	BD133929	Novel met	C 328	12.4	88.6	884	8	HSN331221	HSN331221 Homo sapi
C 256	12.4	88.6	100	6	AX988725	AX988725	Sequence	C 329	12.4	88.6	889	6	AX144281	AX144281 Sequence
C 257	12.4	88.6	100	6	AX988726	AX988726	Sequence	C 330	12.4	88.6	899	6	BD125006	BD125006 Primer fo
C 258	12.4	88.6	100	6	AX991571	AX991571	Sequence	C 331	12.4	88.6	906	6	BD126264	BD126264 Primer fo
C 259	12.4	88.6	128	6	BD131217	BD131217	Cytotoxic	C 332	12.4	88.6	906	6	CQ780297	CQ780297 Primer fo
C 260	12.4	88.6	128	6	AX003031	AX003031	Sequence	C 333	12.4	88.6	906	6	CQ781555	CQ781555 Sequence
C 261	12.4	88.6	140	6	AR522163	AR522163	Sequence	C 334	12.4	88.6	906	6	CQ782256	CQ782256 Sequence
C 262	12.4	88.6	283	6	CQ436183	CQ436183	Sequence	C 335	12.4	88.6	906	6	CQ782256	CQ782256 Sequence
C 263	12.4	88.6	287	15	AY022329	AY022329	Oryza sat	C 336	12.4	88.6	915	10	BV545222	BV545222 BY556b11
C 264	12.4	88.6	333	6	BD026046	BD026046	Sequence	C 337	12.4	88.6	925	1	AJ783702	AJ783702 Nodularia
C 265	12.4	88.6	333	6	AX886436	AX886436	Sequence	C 338	12.4	88.6	960	6	CQ582132	CQ582132 Sequence
C 266	12.4	88.6	346	1	FSP251394	FSP251394	Frankia s	C 339	12.4	88.6	969	6	CQ735117	CQ735117 Sequence
C 267	12.4	88.6	349	6	AR102510	AR102510	Sequence	C 340	12.4	88.6	1005	6	AR625940	AR625940 Sequence
C 268	12.4	88.6	355	9	MMRN45PR	MMRN45PR	Mouse rdna	C 341	12.4	88.6	1007	6	AR618675	AR618675 Sequence
C 269	12.4	88.6	359	10	BV005953	BV005953	ORF 377 S	C 342	12.4	88.6	1017	6	AR347554	AR347554 Sequence
C 270	12.4	88.6	366	6	E14891	E14891	Partial seq	C 343	12.4	88.6	1026	15	DD017765	DD017765 Silene la
C 271	12.4	88.6	399	6	BD108597	BD108597	EST and e	C 344	12.4	88.6	1028	6	CQ608220	CQ608220 Sequence
C 272	12.4	88.6	399	6	AR413044	AR413044	Sequence	C 345	12.4	88.6	1032	6	AX535312	AX535312 Sequence
C 273	12.4	88.6	399	6	AX969878	AX969878	Sequence	C 346	12.4	88.6	1035	6	AX574002	AX574002 Sequence
C 274	12.4	88.6	401	1	AB054942	AB054942	Pseudobac	C 347	12.4	88.6	1104	6	AR386154	AR386154 Sequence
C 275	12.4	88.6	421	11	AR452983	AR452983	Synthetic	C 348	12.4	88.6	1126	15	OSRDC22	OSRDC22
C 276	12.4	88.6	438	1	LGA87925	LGA87925	Lactococc	C 349	12.4	88.6	1144	6	AX770122	AX770122
C 277	12.4	88.6	438	6	AX354209	AX354209	Sequence	C 350	12.4	88.6	1163	15	AF289119	AF289119
C 278	12.4	88.6	449	1	AY702514	AY702514	Manneim	C 351	12.4	88.6	1185	15	AF289117	AF289117 Muscarl a
C 279	12.4	88.6	449	2	AU028367	AU028367	Aedes aegy	C 352	12.4	88.6	1194	15	BT019033	BT019033 Zea mays
C 280	12.4	88.6	480	5	AF139089	AF139089	Gymnotus	C 353	12.4	88.6	1195	6	AX772832	AX772832 Sequence
C 281	12.4	88.6	516	1	AY613943	AY613943	Xanthomon	C 354	12.4	88.6	1195	15	AK101344	AK101344 Oryza sat
C 282	12.4	88.6	535	6	BD124944	BD124944	Primer fo	C 355	12.4	88.6	1196	8	HSN332584	HSN332584 Homo sapi
C 283	12.4	88.6	535	6	BD126975	BD126975	Primer fo	C 356	12.4	88.6	1202	2	TCMU5422	TCMU5422 Trilobium
C 284	12.4	88.6	535	6	CQ780235	CQ780235	Sequence	C 357	12.4	88.6	1205	15	ZEU90266	ZEU90266 Zm12a elem
C 285	12.4	88.6	535	6	CQ782266	CQ782266	Sequence	C 358	12.4	88.6	1206	6	BD172008	BD172008 Mutant of
C 286	12.4	88.6	555	6	BD133927	BD133927	Novel met	C 359	12.4	88.6	1206	6	CQ800935	CQ800935 Sequence
C 287	12.4	88.6	558	6	E03074	E03074	DNA sequenc	C 360	12.4	88.6	1206	6	E14890	E14890 Mycobacteri
C 288	12.4	88.6	558	6	E54935	E54935	Vibrio para	C 361	12.4	88.6	1206	6	AR615673	AR615673 Sequence
C 289	12.4	88.6	567	15	AY586280	AY586280	Phycophth	C 362	12.4	88.6	1206	6	AX452067	AX452067 Sequence
C 290	12.4	88.6	572	6	RATRDNA1S	RATRDNA1S	Rattus nov	C 363	12.4	88.6	1230	2	ASU18347	ASU18347 Ascaris suu
C 291	12.4	88.6	597	6	AR500487	AR500487	Sequence	C 364	12.4	88.6	1238	2	AY071660	AY071660 Drosophila
C 292	12.4	88.6	597	6	AR515769	AR515769	Sequence	C 365	12.4	88.6	1246	2	TCMU5421	TCMU5421 Trilobium
C 293	12.4	88.6	625	9	RATTIMPRX	RATTIMPRX	Rat metallo	C 366	12.4	88.6	1248	15	AK061308	AK061308 Oryza sat
C 294	12.4	88.6	627	10	AF287295	AF287295	Drosophila	C 367	12.4	88.6	1256	15	AK106002	AK106002 Oryza sat
C 295	12.4	88.6	630	11	AY657581	AY657581	Synthetic	C 368	12.4	88.6	1257	15	AF425715	AF425715 Laguncula
C 296	12.4	88.6	645	6	CQ590925	CQ590925	Sequence	C 369	12.4	88.6	1257	15	AF425716	AF425716 Laguncula
C 297	12.4	88.6	646	1	AY328009	AY328009	Symbiont	C 370	12.4	88.6	1259	15	AK070917	AK070917 Oryza sat
C 298	12.4	88.6	648	6	BD126283	BD126283	Primer fo	C 371	12.4	88.6	1259	15	CPY16901	CPY16901 Limonium mo
C 299	12.4	88.6	648	6	CQ781574	CQ781574	Sequence	C 372	12.4	88.6	1271	2	AY089282	AY089282 Drosophila
C 300	12.4	88.6	664	10	BV566995	BV566995	tpa62b04	C 373	12.4	88.6	1275	1	AB106890	AB106890 Thiodacil
C 301	12.4	88.6	701	10	BV241019	BV241019	S234P6324	C 374	12.4	88.6	1279	15	GSP312254	GSP312254 Gonoliimo
C 302	12.4	88.6	715	1	AB064319	AB064319	Vibrio pa	C 375	12.4	88.6	1284	15	BT006584	BT006584 Arabidops
C 303	12.4	88.6	717	10	BV289200	BV289200	S232P6254	C 376	12.4	88.6	1284	15	AF507911	AF507911 Arabidops
C 304	12.4	88.6	737	6	AR506567	AR506567	Sequence	C 377	12.4	88.6	1287	6	AX961341	AX961341 Sequence
C 305	12.4	88.6	743	6	BD124964	BD124964	Primer fo	C 378	12.4	88.6	1287	6	AX961341	AX961341 Sequence
C 306	12.4	88.6	743	6	BD126374	BD126374	Primer fo	C 379	12.4	88.6	1292	15	AAAN312252	AAAN312252 Aegialiti
C 307	12.4	88.6	743	6	CQ780255	CQ780255	Sequence	C 380	12.4	88.6	1292	15	AAAN402918	AAAN402918 Aegialiti
C 308	12.4	88.6	743	6	CQ781665	CQ781665	Sequence	C 381	12.4	88.6	1293	15	LITE286365	LITE286365 Limonium
C 309	12.4	88.6	757	8	HSN333315	HSN333315	Homo sapi	C 382	12.4	88.6	1302	6	CQ964339	CQ964339 Sequence
C 310	12.4	88.6	759	10	BV552387	BV552387	S221P6090	C 383	12.4	88.6	1304	15	LMA286364	LMA286364 Limonium

384	12.4	88.6	1318	15	CPY16900	Y16900 Limonium s1	457	12.4	88.6	2370	6	AR384634	AR384634 Sequence
385	12.4	88.6	1319	15	DAF312253	AJ312253 Dyerophyt	c 458	12.4	88.6	2404	5	AF098788	AF098788 Gallus ga
386	12.4	88.6	1320	15	LGU286358	AJ286358 Limoniaet	c 459	12.4	88.6	2406	5	AX770134	AX770134 Sequence
387	12.4	88.6	1322	15	CPY16903	Y16903 Limonium de	460	12.4	88.6	2409	6	BD273957	BD273957 Sequence
388	12.4	88.6	1332	15	CPY16907	Y16907 Psylliostec	461	12.4	88.6	2409	6	AX005499	AX005499 Sequence
389	12.4	88.6	1334	15	CME286361	AJ286361 Ceratolim	462	12.4	88.6	2416	6	CS071123	CS071123 Sequence
390	12.4	88.6	1335	15	AF206789	AF206789 Limonium	c 463	12.4	88.6	2431	6	CO719959	CO719959 Sequence
391	12.4	88.6	1339	15	CPY16904	Y16904 Limonium vu	464	12.4	88.6	2451	6	BD273958	BD273958 Sequence
392	12.4	88.6	1330	15	LAX286362	Y16906 Plumbago ca	c 465	12.4	88.6	2451	6	AX005501	AX005501 Sequence
393	12.4	88.6	1331	15	CPY16906	Y16908 Armeria apl	c 466	12.4	88.6	2465	1	SAU439341	SAU439341 Sequence
394	12.4	88.6	1331	15	CPY16909	Y16908 Armeria apl	c 467	12.4	88.6	2485	15	Y12580339	Y12580339
395	12.4	88.6	1331	15	CPY16908	AJ286360 Ceratolim	c 468	12.4	88.6	2495	6	AR338781	AR338781 Sequence
396	12.4	88.6	1340	15	CME286360	AJ286360 Ceratolim	c 469	12.4	88.6	2520	6	BD127364	BD127364 Primer fo
c 397	12.4	88.6	1341	3	UBA301572	AJ301572 Unculture	c 470	12.4	88.6	2520	6	CO782887	CO782887 Sequence
398	12.4	88.6	1342	15	LDU286363	AJ286363 Limonium	c 471	12.4	88.6	2520	8	AK074923	AK074923 Homo sapi
399	12.4	88.6	1345	15	CFR286357	AJ286357 Ceratolim	c 472	12.4	88.6	2543	6	BD127330	BD127330 Primer fo
400	12.4	88.6	1358	15	HVO238879	AJ238879 Haloferax	c 473	12.4	88.6	2543	6	CO782820	CO782820 Sequence
401	12.4	88.6	1359	6	AR387715	AR387715 Sequence	c 474	12.4	88.6	2543	6	AK074858	AK074858 Homo sapi
402	12.4	88.6	1360	15	SIF286359	AJ286359 Saharant	c 475	12.4	88.6	2547	6	BD127344	BD127344 Primer fo
403	12.4	88.6	1362	1	AY654839	AY654839 Mucis bac	c 476	12.4	88.6	2547	6	CO782847	CO782847 Sequence
404	12.4	88.6	1371	15	AK064363	AK064363 Oryza sat	c 477	12.4	88.6	2547	6	AK074880	AK074880 Homo sapi
405	12.4	88.6	1371	15	AY128246	AY128246 Malaura t	c 478	12.4	88.6	2556	6	AX416615	AX416615 Sequence
406	12.4	88.6	1398	15	AERP39277	U32977 Aesculus pa	c 479	12.4	88.6	2563	6	BD127943	BD127943 Primer fo
407	12.4	88.6	1402	15	APU39277	U32977 Aesculus pa	c 480	12.4	88.6	2563	6	CO784000	CO784000 Sequence
408	12.4	88.6	1402	15	DSU39268	U32968 Dicteronia	c 481	12.4	88.6	2563	6	AK075013	AK075013 Homo sapi
409	12.4	88.6	1408	15	BH1402929	AJ402929 Billia hi	c 482	12.4	88.6	2578	1	DMENAVRC	DMENAVRC
410	12.4	88.6	1427	15	AY841666	AY841666 Xylopia f	c 483	12.4	88.6	2605	2	PSENAVR	PSENAVR
411	12.4	88.6	1428	15	AAZ97639	Z97639 Acantholimo	c 484	12.4	88.6	2622	6	AR387855	AR387855 Sequence
412	12.4	88.6	1428	15	ABZ97640	Z97640 Armeria bot	c 485	12.4	88.6	2622	6	CO577722	CO577722 Sequence
413	12.4	88.6	1428	15	LCZ97643	Z97643 Limonium ca	c 486	12.4	88.6	2645	6	AX777339	AX777339 Sequence
414	12.4	88.6	1428	15	LDZ97644	Z97644 Limonium de	c 487	12.4	88.6	2645	6	BT010011	BT010011 Drosophi
415	12.4	88.6	1428	15	LMZ97642	Z97642 Limoniastru	c 488	12.4	88.6	2680	2	CPU21667	CPU21667 Crytopsori
416	12.4	88.6	1428	15	LRZ97645	Z97645 Limonium ri	c 489	12.4	88.6	2757	2	AY060857	AY060857 Drosophi
417	12.4	88.6	1428	15	LSZ97646	Z97646 Limonium sp	c 490	12.4	88.6	2806	6	AX770124	AX770124 Sequence
418	12.4	88.6	1428	15	MTU403017	AJ403017 Malaura t	c 491	12.4	88.6	2852	6	CO590924	CO590924 Sequence
419	12.4	88.6	1428	15	AERP39277	U32977 Aesculus pa	c 492	12.4	88.6	2852	6	CO592322	CO592322 Sequence
420	12.4	88.6	1428	15	AF215532	AF215532 Grafient	c 493	12.4	88.6	2861	6	CO592322	CO592322 Sequence
421	12.4	88.6	1428	15	AF215533	AF215533 Meriania	c 494	12.4	88.6	2874	6	CO586236	CO586236 Sequence
422	12.4	88.6	1429	15	AF215530	AF215530 Adelobotr	c 495	12.4	88.6	3007	8	HOSAL8024	HOSAL8024 Homo sapien
423	12.4	88.6	1429	15	AF215531	AF215531 Adelobotr	c 496	12.4	88.6	3010	8	BC015009	BC015009 Homo sapi
424	12.4	88.6	1434	15	AF046930	AF046930 Rhinocall	c 497	12.4	88.6	3033	15	AY6858231	AY6858231 Neurospor
425	12.4	88.6	1449	15	AJ786659	AJ786659 Limonium	c 498	12.4	88.6	3095	4	AT618974	AT618974 Bos tauru
426	12.4	88.6	1449	15	AJ786659	AK11000 Oryza sat	c 499	12.4	88.6	3114	2	AT069524	AT069524 Drosophi
c 427	12.4	88.6	1449	15	BCOHTPY	L03720 B. coli hea	c 500	12.4	88.6	3148	6	CO608219	CO608219 Sequence
428	12.4	88.6	1513	15	RXCRBCID	M77702 Rheum x cul	c 501	12.4	88.6	3171	1	ECHTGA	ECHTGA
429	12.4	88.6	1513	15	CO875959	CO875959 Sequence	c 502	12.4	88.6	3219	15	AF236387	AF236387 Schizosac
430	12.4	88.6	1584	6	AX429129	AX429129 Sequence	c 503	12.4	88.6	3232	2	BT001403	BT001403 Drosophi
431	12.4	88.6	1584	6	AX429129	AX429129 Sequence	c 504	12.4	88.6	3237	15	AJ7861427	AJ7861427 Soritaria
432	12.4	88.6	1621	2	AF241364	AF241364 Drosophi	c 505	12.4	88.6	3244	6	CO582131	CO582131 Sequence
c 433	12.4	88.6	1709	2	BT001266	BT001266 Drosophi	506	12.4	88.6	3244	6	AX306038	AX306038 Sequence
c 434	12.4	88.6	1710	2	LBAPBGL	M20151 L. casei P-b	507	12.4	88.6	3244	9	MDU03457	MDU03457 Mus musculu
c 435	12.4	88.6	1723	2	AY118718	AY118718 Drosophi	508	12.4	88.6	3244	9	CO578429	CO578429 Sequence
c 436	12.4	88.6	1735	2	AF346487	AF346487 Acetobact	c 509	12.4	88.6	3398	6	CO580932	CO580932 Sequence
c 437	12.4	88.6	1735	8	AF052110	AF052110 Homo sapi	c 510	12.4	88.6	3472	6	CO580932	CO580932 Sequence
c 438	12.4	88.6	1739	1	AF031189	AF031189 Chironati	c 511	12.4	88.6	3490	6	CO584338	CO584338 Sequence
c 439	12.4	88.6	1739	15	AK110577	AK110577 Oryza sat	512	12.4	88.6	3490	15	AY945225	AY945225 Aspergill
c 440	12.4	88.6	1750	1	AB072394	AB072394 Mycobacte	c 513	12.4	88.6	3507	6	CO590031	CO590031 Sequence
c 441	12.4	88.6	1770	1	AY083508	AY083508 Rhodococc	c 514	12.4	88.6	3552	15	AK119852	AK119852 Oryza sat
c 442	12.4	88.6	1770	6	AX824488	AX824488 Sequence	c 515	12.4	88.6	3710	6	CO589272	CO589272 Sequence
c 443	12.4	88.6	1779	6	YSCLTG3	DI6304 Yeast LTG3	c 516	12.4	88.6	3712	2	DMPHOS3XI	DMPHOS3XI
444	12.4	88.6	1782	6	AX659988	AX659988 Sequence	c 517	12.4	88.6	3712	2	CO580305	CO580305 Sequence
c 445	12.4	88.6	1809	15	AY570722	AY570722 Ostreococ	c 518	12.4	88.6	3712	6	AX179644	AX179644 Sequence
c 446	12.4	88.6	1880	2	CAR290862	AJ290862 Clytus ar	c 519	12.4	88.6	4185	13	STRP08	STRP08
c 447	12.4	88.6	1915	15	AY093149	AY093149 Arabidops	c 520	12.4	88.6	4382	2	BT021440	BT021440 Drosophi
c 448	12.4	88.6	2003	8	HIMDAPC1	M64356 Human decay	c 521	12.4	88.6	4407	2	BT003173	BT003173 Drosophi
c 449	12.4	88.6	2059	15	THINDALA	Z22594 T. narizianu	c 522	12.4	88.6	4462	2	AF126720	AF126720 Mycobacte
c 450	12.4	88.6	2075	15	ARGSRMA	M11376 Arthrobacte	c 523	12.4	88.6	4462	1	AF126720	AF126720 Mycobacte
c 451	12.4	88.6	2133	15	AK120817	AK120817 Oryza sat	c 524	12.4	88.6	4525	6	BD183405	BD183405 Novel gen
c 452	12.4	88.6	2263	6	AX202076	AX202076 Sequence	c 525	12.4	88.6	4607	13	AY844284	AY844284 Lymenitria
c 453	12.4	88.6	2277	1	ECOSMBA	D13334 Sacchericha	c 526	12.4	88.6	4729	1	AF282898	AF282898 Burkholdia
c 454	12.4	88.6	2280	5	DRU41419	U41419 Dario terio	c 527	12.4	88.6	4845	1	AY541701	AY541701 Ralstonia
c 455	12.4	88.6	2326	5	AK121040	AK121040 Oryza sat	c 528	12.4	88.6	4993	1	PRU04052	PRU04052 Pseudomonas
c 456	12.4	88.6	2349	15	AY262750	AY262750 Kluyverom	c 529	12.4	88.6	5000	1	AF099015	AF099015 Streptomy
										5069	2	BT009939	BT009939 Drosophi

530	12.4	88.6	5188	6	COS86235	Sequence	COS86235	Sequence	C603	12.4	88.6	17982	14	AC013097	AC013097 Drosophila
C 531	12.4	88.6	5217	1	AF287482	Chlorobium	AF287482	Chlorobium	604	12.4	88.6	18149	15	AY884187	AY884187 Coccollobo
C 532	12.4	88.6	5229	1	LCIACCT	L. casei	L. casei	L. casei	605	12.4	88.6	18931	1	AF501263	AF501263 Brwnia c
C 533	12.4	88.6	5628	1	RCAPIC02F	Rhodobacter	RCAPIC02F	Rhodobacter	606	12.4	88.6	20000	15	SPBP88B6	SPBP88B6
C 534	12.4	88.6	5883	8	HS242780	Homo sapi	HS242780	Homo sapi	607	12.4	88.6	20029	1	AE008874	AE008874 Salmonella
C 535	12.4	88.6	6203	8	AR619416	Sequence	AR619416	Sequence	608	12.4	88.6	20472	7	AY746495	AY746495 Enterobac
C 536	12.4	88.6	6398	11	AB119528	AB119528	AB119528	AB119528	609	12.4	88.6	20644	5	CR788299	CR788299 Zebrafish
C 537	12.4	88.6	6600	8	AY438640	AY438640	AY438640	AY438640	610	12.4	88.6	21918	1	AE008853	AE008853 Salmonella
C 538	12.4	88.6	7004	7	LHNSB	LHNSB	LHNSB	LHNSB	611	12.4	88.6	22118	6	AY951618	AY951618 Sequence
C 539	12.4	88.6	7114	6	COS80304	COS80304	COS80304	COS80304	612	12.4	88.6	22118	9	MM4558RN	MM4558RN
C 540	12.4	88.6	7353	15	CNS09540	CNS09540	CNS09540	CNS09540	613	12.4	88.6	23223	14	AC005975	AC005975
C 541	12.4	88.6	7363	2	AY229969	AY229969	AY229969	AY229969	614	12.4	88.6	23650	1	AE008894	AE008894
C 542	12.4	88.6	7365	6	COS87408	COS87408	COS87408	COS87408	615	12.4	88.6	24000	1	AE004856	AE004856
C 543	12.4	88.6	7601	1	AB070454	AB070454	AB070454	AB070454	616	12.4	88.6	24105	15	AY884189	AY884189
C 544	12.4	88.6	7766	13	AB096204	AB096204	AB096204	AB096204	617	12.4	88.6	24720	1	AF632203	AF632203
C 545	12.4	88.6	7910	13	AB096201	AB096201	AB096201	AB096201	618	12.4	88.6	25656	14	AC020181	AC020181
C 546	12.4	88.6	7950	1	AF016298	AF016298	AF016298	AF016298	619	12.4	88.6	27521	1	AB112586	AB112586
C 547	12.4	88.6	7985	13	AB096202	AB096202	AB096202	AB096202	620	12.4	88.6	27546	13	ASP437059	ASP437059
C 548	12.4	88.6	8004	13	AB096203	AB096203	AB096203	AB096203	621	12.4	88.6	28432	6	COS76998	COS76998
C 549	12.4	88.6	8544	6	COS80214	COS80214	COS80214	COS80214	622	12.4	88.6	29659	5	CR354374	CR354374
C 550	12.4	88.6	8802	6	COS90030	COS90030	COS90030	COS90030	623	12.4	88.6	30000	13	BHV130XB	BHV130XB
C 551	12.4	88.6	9555	13	AF458647	AF458647	AF458647	AF458647	624	12.4	88.6	30228	14	AC020449	AC020449
C 552	12.4	88.6	10007	1	AE008951	AE008951	AE008951	AE008951	625	12.4	88.6	31068	1	AY603426	AY603426
C 553	12.4	88.6	10115	1	AE010419	AE010419	AE010419	AE010419	626	12.4	88.6	31129	9	AF441733	AF441733
C 554	12.4	88.6	10138	1	AE011927	AE011927	AE011927	AE011927	627	12.4	88.6	31505	14	AC015140	AC015140
C 555	12.4	88.6	10153	1	AE002089	AE002089	AE002089	AE002089	628	12.4	88.6	32800	1	AF293355	AF293355
C 556	12.4	88.6	10165	1	AE004715	AE004715	AE004715	AE004715	629	12.4	88.6	33064	14	AY394844	AY394844
C 557	12.4	88.6	10189	1	AE004715	AE004715	AE004715	AE004715	630	12.4	88.6	33064	14	AY338477	AY338477
C 558	12.4	88.6	10315	1	AE004650	AE004650	AE004650	AE004650	631	12.4	88.6	34100	2	DMC3081	DMC3081
C 559	12.4	88.6	10387	1	PAU97979	PAU97979	PAU97979	PAU97979	632	12.4	88.6	34305	2	CEW02812	CEW02812
C 560	12.4	88.6	10387	6	AX191733	AX191733	AX191733	AX191733	633	12.4	88.6	34676	14	AC013929	AC013929
C 561	12.4	88.6	10412	1	AE012064	AE012064	AE012064	AE012064	634	12.4	88.6	35336	1	MSGV367	MSGV367
C 562	12.4	88.6	10475	1	AE004937	AE004937	AE004937	AE004937	635	12.4	88.6	35540	1	AP389112	AP389112
C 563	12.4	88.6	10652	1	AE004194	AE004194	AE004194	AE004194	636	12.4	88.6	35591	15	AC151928	AC151928
C 564	12.4	88.6	10663	1	AE004194	AE004194	AE004194	AE004194	637	12.4	88.6	35807	15	CER113H5	CER113H5
C 565	12.4	88.6	10732	1	AE004274	AE004274	AE004274	AE004274	638	12.4	88.6	36804	15	CR382138_23	CR382138_23
C 566	12.4	88.6	10794	1	AE005749	AE005749	AE005749	AE005749	639	12.4	88.6	37440	1	AY280634	AY280634
C 567	12.4	88.6	10853	1	AE005749	AE005749	AE005749	AE005749	640	12.4	88.6	38065	1	MCB1450	MCB1450
C 568	12.4	88.6	10916	1	AE004781	AE004781	AE004781	AE004781	641	12.4	88.6	38620	14	AC166544	AC166544
C 569	12.4	88.6	10968	1	AF141883	AF141883	AF141883	AF141883	642	12.4	88.6	38916	1	MCB2548	MCB2548
C 570	12.4	88.6	11009	1	AE007898	AE007898	AE007898	AE007898	643	12.4	88.6	39419	2	CBRG01C7	CBRG01C7
C 571	12.4	88.6	11108	1	AE012151	AE012151	AE012151	AE012151	644	12.4	88.6	41984	2	CBRG42E09	CBRG42E09
C 572	12.4	88.6	11141	1	AE011690	AE011690	AE011690	AE011690	645	12.4	88.6	42051	8	AF129076	AF129076
C 573	12.4	88.6	11180	1	AE004733	AE004733	AE004733	AE004733	646	12.4	88.6	42430	2	CBRG44D18	CBRG44D18
C 574	12.4	88.6	11196	1	AE012055	AE012055	AE012055	AE012055	647	12.4	88.6	43339	1	STYSTMPI	STYSTMPI
C 575	12.4	88.6	11204	6	AX370213	AX370213	AX370213	AX370213	648	12.4	88.6	43741	8	AY851161	AY851161
C 576	12.4	88.6	11334	1	AE001186	AE001186	AE001186	AE001186	649	12.4	88.6	43829	14	AC018185	AC018185
C 577	12.4	88.6	11421	1	AE004505	AE004505	AE004505	AE004505	650	12.4	88.6	45055	6	AX574197	AX574197
C 578	12.4	88.6	11797	1	AE011603	AE011603	AE011603	AE011603	651	12.4	88.6	45633	14	AC091640	AC091640
C 579	12.4	88.6	12046	1	AE005017	AE005017	AE005017	AE005017	652	12.4	88.6	46607	14	AC013865	AC013865
C 580	12.4	88.6	12198	1	AE001953	AE001953	AE001953	AE001953	653	12.4	88.6	48352	13	AY225134	AY225134
C 581	12.4	88.6	12236	1	AE012147	AE012147	AE012147	AE012147	654	12.4	88.6	48553	2	DNBHTM4	DNBHTM4
C 582	12.4	88.6	12809	1	AE005787	AE005787	AE005787	AE005787	655	12.4	88.6	48827	8	AC016994	AC016994
C 583	12.4	88.6	12970	1	SPU04005	SPU04005	SPU04005	SPU04005	656	12.4	88.6	49349	8	AL451134	AL451134
C 584	12.4	88.6	13345	1	AE001977	AE001977	AE001977	AE001977	657	12.4	88.6	49534	7	AF396866	AF396866
C 585	12.4	88.6	13484	14	AC014236	AC014236	AC014236	AC014236	658	12.4	88.6	50000	6	AX535264	AX535264
C 586	12.4	88.6	13579	1	AE005061	AE005061	AE005061	AE005061	659	12.4	88.6	50000	6	AX535266	AX535266
C 587	12.4	88.6	13625	1	AE004366	AE004366	AE004366	AE004366	660	12.4	88.6	51711	1	CP000060	CP000060
C 588	12.4	88.6	14138	1	AE004766	AE004766	AE004766	AE004766	661	12.4	88.6	51808	5	AC104683	AC104683
C 589	12.4	88.6	14283	6	COS77721	COS77721	COS77721	COS77721	662	12.4	88.6	52250	14	AY500153	AY500153
C 590	12.4	88.6	14988	1	AB015053	AB015053	AB015053	AB015053	663	12.4	88.6	54841	14	AC091475	AC091475
C 591	12.4	88.6	15062	6	CQ62852	CQ62852	CQ62852	CQ62852	664	12.4	88.6	55903	14	AC091475	AC091475
C 592	12.4	88.6	15197	1	AC013889	AC013889	AC013889	AC013889	665	12.4	88.6	56268	14	AC091240	AC091240
C 593	12.4	88.6	15711	6	CQ608651	CQ608651	CQ608651	CQ608651	666	12.4	88.6	56999	14	AC008776	AC008776
C 594	12.4	88.6	16499	6	COS89271	COS89271	COS89271	COS89271	667	12.4	88.6	57789	14	AC0091570	AC0091570
C 595	12.4	88.6	16520	1	AE001105	AE001105	AE001105	AE001105	668	12.4	88.6	58756	14	AP006484_4	AP006484_4
C 596	12.4	88.6	16704	1	AE004876	AE004876	AE004876	AE004876	669	12.4	88.6	58866	14	AC114556	AC114556
C 597	12.4	88.6	16941	1	AE004749	AE004749	AE004749	AE004749	670	12.4	88.6	59237	14	AC091279	AC091279
C 598	12.4	88.6	17183	1	AE001986	AE001986	AE001986	AE001986	671	12.4	88.6	59816	1	AP333038	AP333038
C 599	12.4	88.6	17280	14	AC017852	AC017852	AC017852	AC017852	672	12.4	88.6	60573	14	AC018267	AC018267
C 600	12.4	88.6	17425	14	RSU17129	RSU17129	RSU17129	RSU17129	673	12.4	88.6	60671	14	AC017512	AC017512
C 601	12.4	88.6	17477	14	CR954205_8	CR954205_8	CR954205_8	CR954205_8	674	12.4	88.6	61490	14	AC025630	AC025630
C 602	12.4	88.6	17973	1	MSM238027	MSM238027	MSM238027	MSM238027	675	12.4	88.6	61796	14	AC020875	AC020875

c 676	12.4	88.6	61845	1	AY623658	AY623658 Aeromicro	c 749	12.4	88.6	110000	1	CP000091_08	Continuation (9 of
c 677	12.4	88.6	63851	14	AC165666	AC165666 Bos tauu	c 750	12.4	88.6	110000	1	CP000091_09	Continuation (10 o
c 678	12.4	88.6	63933	14	AC090570	AC090570 Homo sapi	c 751	12.4	88.6	110000	1	CP000091_10	Continuation (11 o
c 679	12.4	88.6	64027	14	AC018192	AC018192 Drosophi	c 752	12.4	88.6	110000	1	CR555306_21	Continuation (12 o
c 680	12.4	88.6	64283	14	AC105693_3	Continuation (4 of	c 753	12.4	88.6	110000	1	CR555306_24	Continuation (25 o
c 681	12.4	88.6	65005	14	AC091277	AC091277 Mus muscu	c 754	12.4	88.6	110000	1	CR555306_29	Continuation (40 o
c 682	12.4	88.6	65076	15	NCB13020	AL451015 Neurospor	c 755	12.4	88.6	110000	1	CR931997_05	Continuation (6 of
c 683	12.4	88.6	65144	14	AC090665	AC090665 Homo sapi	c 756	12.4	88.6	110000	1	CR931997_10	Continuation (11 o
c 684	12.4	88.6	66612	2	AE003597_3	Continuation (4 of	c 757	12.4	88.6	110000	1	CR931997_22	Continuation (23 o
c 685	12.4	88.6	66796	14	AC017435	AC017435 Drosophi	c 758	12.4	88.6	110000	1	U00096_07	U00096 Escherichia
c 686	12.4	88.6	67392	14	AC018284	AC018284 Drosophi	c 759	12.4	88.6	110000	1	U00096_01	Continuation (12 of
c 687	12.4	88.6	68301	14	AC131486	AC131486 Lytechinu	c 760	12.4	88.6	110000	1	AB013558_26	Continuation (127 o
c 688	12.4	88.6	68999	7	AF547430	AF547430 Mycobacte	c 761	12.4	88.6	110000	1	AB014295_15	Continuation (16 o
c 689	12.4	88.6	70843	14	AC147864	AC147864 Gopherus	c 762	12.4	88.6	110000	1	AB014295_16	Continuation (17 o
c 690	12.4	88.6	70966	14	AC079058	AC079058 Homo sapi	c 763	12.4	88.6	110000	1	AB014295_20	Continuation (21 o
c 691	12.4	88.6	71616	15	ATAC022287	AC042287 Arabidops	c 764	12.4	88.6	110000	1	AB014295_21	Continuation (22 o
c 692	12.4	88.6	72494	14	AC149499	AC149499 Xenopus t	c 765	12.4	88.6	110000	1	AB016824_1	Continuation (12 of
c 693	12.4	88.6	72698	15	AB007645	AB007645 Arabidops	c 766	12.4	88.6	110000	1	AB016853_05	Continuation (16 of
c 694	12.4	88.6	72704	6	AR619878	AR619878 Sequence	c 767	12.4	88.6	110000	1	AB016853_06	Continuation (17 of
c 695	12.4	88.6	73778	14	AC090743	AC090743 Homo sapi	c 768	12.4	88.6	110000	1	AB016853_25	Continuation (8 of
c 696	12.4	88.6	73803	15	NCB11822	AY120853 Synechoco	c 769	12.4	88.6	110000	1	AB016853_32	Continuation (26 o
c 697	12.4	88.6	74355	1	AY120853	AY120853 Synechoco	c 770	12.4	88.6	110000	1	AB016853_32	Continuation (33 o
c 698	12.4	88.6	74502	14	AC024300	AC024300 Homo sapi	c 771	12.4	88.6	110000	1	AB016853_34	Continuation (35 o
c 699	12.4	88.6	75335	15	BX842627	BX842627 Neurospor	c 772	12.4	88.6	110000	1	AB016853_46	Continuation (47 o
c 700	12.4	88.6	76269	15	AC006456	AC006456 Drosophi	c 773	12.4	88.6	110000	1	AB017220_38	Continuation (39 o
c 701	12.4	88.6	78124	15	BX842681	BX842681 Neurospor	c 774	12.4	88.6	110000	1	AB017220_42	Continuation (43 o
c 702	12.4	88.6	78962	14	AC040956	AC040956 Mus muscu	c 775	12.4	88.6	110000	1	AB017220_43	Continuation (44 o
c 703	12.4	88.6	80646	14	AC013962	AC013962 Drosophi	c 776	12.4	88.6	110000	1	AB017340_12	Continuation (13 o
c 704	12.4	88.6	82727	1	BC082K	D26562 Escherichia	c 777	12.4	88.6	110000	1	AB017340_13	Continuation (14 o
c 705	12.4	88.6	82855	14	AC009354	AC009354 Drosophi	c 778	12.4	88.6	110000	1	AP006618_05	Continuation (6 of
c 706	12.4	88.6	83433	14	AP006501_12	Continuation (13 o	c 779	12.4	88.6	110000	1	AP006618_05	Continuation (19 o
c 707	12.4	88.6	84011	14	AP002084	AP002084 Homo sapi	c 780	12.4	88.6	110000	1	AP006618_18	Continuation (19 o
c 708	12.4	88.6	84549	14	AC006243	AC006243 Drosophi	c 781	12.4	88.6	110000	1	AP006618_35	Continuation (36 o
c 709	12.4	88.6	87283	14	AC017652	AC017652 Drosophi	c 782	12.4	88.6	110000	1	AP006618_52	Continuation (53 o
c 710	12.4	88.6	87776	14	AP007309	AP007309 Lotus cor	c 783	12.4	88.6	110000	1	AP006840_14	Continuation (15 o
c 711	12.4	88.6	88378	15	AC133002	AC133002 Oryza sat	c 784	12.4	88.6	110000	1	AP006840_28	Continuation (16 o
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c 713	12.4	88.6	88672	14	AC014992	AC014992 Drosophi	c 786	12.4	88.6	110000	1	AP006878_10	Continuation (11 o
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c 719	12.4	88.6	91723	8	AC010903	AC010903 Homo sapi	c 792	12.4	88.6	110000	1	BA000007_01	Continuation (2 of
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c 722	12.4	88.6	95637	15	BX842594	BX842594 Neurospor	c 795	12.4	88.6	110000	1	BA000030_28	Continuation (29 o
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c 726	12.4	88.6	98053	15	AC149809	AC149809 Medicago	c 799	12.4	88.6	110000	1	BA000030_67	Continuation (68 o
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852	12.4	88.6	110000	1	CP000075_37	Continuation (38 o	c 925	12.4	88.6	110000	14	TANN1_05	Continuation (6 of
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854	12.4	88.6	110000	1	CP000075_44	Continuation (45 o	c 927	12.4	88.6	110000	15	AP008214_206	Continuation (207
855	12.4	88.6	110000	1	CP000075_48	Continuation (49 o	c 928	12.4	88.6	110000	15	AP008214_241	Continuation (242
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ALIGNMENTS

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RESULT 1
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LOCUS Spodoptera littoralis nuclear polyhedrosis virus gene encoding
DEFINITION ribonucleotide reductase.
ACCESSION X98924.1 GI:2244676
VERSION large subunit; ribonucleotide reductase.
KEYWORDS Spodoptera littoralis nucleopolyhedrovirus
SOURCE Spodoptera littoralis nucleopolyhedrovirus
ORGANISM Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.

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REFERENCE
AUTHORS Van Strien,E.A., Faktor,O., Hu,Z.H., Zuidema,D., Goldbach,R.W. and
Vlak,J.M.
TITLE Baculoviruses contain a gene for the large subunit of
ribonucleotide reductase
JOURNAL J. Gen. Virol. 78 (Pt 9), 2365-2377 (1997)
PUBMED 9292027
REFERENCE
2 (bases 1 to 2832)
AUTHORS Faktor,O.
TITLE Direct Submission
JOURNAL Submitted (01-JUL-1996) O. Faktor, The Hebrew University of
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P.O.Box 12, Rehovot 76100, ISRAEL
FEATURES
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DB 2028 CGTACTGCACTCG 2015

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RESULT 2
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ACCESSION AF484941
VERSION AF484941.1 GI:28628848
KEYWORDS Fusarium oxysporum
SOURCE Fusarium oxysporum
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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REFERENCE
AUTHORS Madrid,M.P., Di Pietro,A. and Roncero,M.I.G.
TITLE Class V chitin synthase determines pathogenesis in the vascular
wilt fungus Fusarium oxysporum by mediating resistance to plant
defense compounds
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 10151)
AUTHORS Madrid,M.P., Di Pietro,A. and Roncero,M.I.G.
TITLE Direct Submission
JOURNAL Submitted (18-FEB-2002) Departamento de Genetica, Universidad de

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FEATURES Cordoba, Campus de Rabanales, CS, Cordoba 14071, Spain
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ORIGIN
 Query Match 100.0%; Score 14; DB 15; Length 10151;
 Best Local Similarity 78.6%; Pred. No. 5.2e+03;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUCG 14
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 Db 3081 CGTACGCAACTCG 3068

RESULT 3
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 DEFINITION Xanthomonas axonopodis pv. citri str. 306, section 423 of 469 of
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REFERENCE
 AUTHORS
 1 (bases 1 to 11318)
 da Silva, A.C.R., Ferro, J.A., Reinach, F.C., Parah, C.S., Furlan, L.R.,
 Quaggio, R.B., Monteiro-Vitorello, C.B., Van Sluys, M.A., Almeida, N.F.,
 Jr., Alves, L.M.C., do Amaral, A.M., Bertolini, M.C., Camargo, L.B.A.,
 Camarotte, G., Cammaran, F., Cardoso, J., Chambergo, F., Ciapina, L.P.,
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 Katsuyama, A.M., Kishi, L.T., Leite, R.P., Jr., Lemos, E.G.M.,
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 Sena, J.A.D., Silva, C., de Souza, R.F., Spindola, L.A.F., Takita, M.A.,
 Tamura, R.B., Teixeira, E.C., Tezsa, R.I.D., Trindade dos Santos, M.,
 Truffi, D., Tsai, S.M., White, F.F., Seubal, J.C. and Kitajima, J.P.
 Comparison of the genomes of two Xanthomonas pathogens with
 differing host specificities
 Nature 417 (6887), 459-463 (2002)

TITLE
 JOURNAL
 PUBLISHED
 12024217
 2 (bases 1 to 11318)
 da Silva, A.C.R., Ferro, J.A., Reinach, F.C., Parah, C.S., Furlan, L.R.,
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 Direct Submission
 Submitted (28-NOV-2001) Departamento de Bioquímica, Universidade de
 Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900,
 Brazil

TITLE
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 Direct Submission
 Submitted (28-NOV-2001) Departamento de Bioquímica, Universidade de
 Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900,
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            and Miller,J.H.
TITLE       Direct Submersion
JOURNAL     Submitted (12-DEC-2001) Microbiology and Molecular Genetics,
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TITLE       Direct Submersion
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            University of California, Los Angeles, 405 Hilgard Ave, Los
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Query Match      100.0%; Score 14; DB 1; Length 14169;
Best Local Similarity 78.6%; Pred. No. 5e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGUACUGCAACUCG 14
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RESULT 5
AP003867/c      96360 bp      DNA      linear      HTG 21-MAR-2002
LOCUS      Oryza sativa (japonica cultivar-group) chromosome 8 clone
DEFINITION      OJ111_B02, *** SEQUENCING IN PROGRESS ***.
ACCESSION      AP003867
VERSION      AP003867.1 GI:14646800
KEYWORDS      HTG; HTGS_PHASE2.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
      Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
      Eriatoidae; Oryzaceae; Oryza.
REFERENCE      1
AUTHORS      Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLES      Oryza sativa nipponbare (OAS) genomic DNA, chromosome 8, BAC
      clone: OJ111_B02
JOURNAL      Published only in Database (2001)
REFERENCES      2 (bases 1 to 96360)
AUTHORS      Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLES      Direct Submission
JOURNAL      Submitted (09-JUL-2001) Takuji Sasaki, National Institute of
      Agrobiological Resources, Rice Genome Research Program, Kannondai
      2-1-2, Tsukuba, Ibaraki 305-8602, Japan
      (E-mail: tsasaki@db.affrc.go.jp, URL: http://ryp.dna.affrc.go.jp/,

```

```

COMMENT
Tel:81-298-38-7441, Fax:81-298-38-7468)
The nucleotide sequence of this BAC clone was generated by
combining Monardo and RGP-Japan sequencing data.
NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
  source
    1..96360
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="genomic DNA"
    /cultivar="Nipponbare"
    /db_xref="taxon:39947"
    /chromosome="8"
    /clone="OJ111_B02"

ORIGIN
Query Match      100.0%; Score 14; DB 14; Length 96360;
Best Local Similarity 78.6%; Pred. No. 4e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGUACUGCAACUCG 14
      ||:|||||:|
Db      15563 CGTACTGCAACTCG 15550

RESULT 6
AL592045
LOCUS      AL592045
DEFINITION      Human DNA sequence from clone RP11-275114 on chromosome 1 Contains
      the ACBD3 gene for acyl-Coenzyme A binding domain containing 3, the
      pseudogene and the MIXL1 gene for Mixl homeobox-like 1 (Xenopus
      laevis), complete sequence.
ACCESSION      AL592045
VERSION      AL592045.28 GI:25136611
KEYWORDS      HTG; ACBD3; MIXL1; RPL34.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
      Hominoidea; Homo.
      1 (bases 1 to 99251)
      Bellington, A.
      Direct Submission
      Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
      Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
      Clone requests: clonerequest@sanger.ac.uk
      On Nov 19, 2002 this sequence version replaced gi:25045216.
      The following abbreviations are used to associate primary accession
      numbers given in the feature table with their source databases:
      Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information
      on the WORMPEP database can be found at
      http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence
      was generated from part of bacterial clone contigs of human
      chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
      Group. Further information can be found at
      http://www.sanger.ac.uk/HGP/Chr1
      RP11-275114 is from the library RGC1-11.1 constructed by the group
      of Piefer de Jong. For further details see
      http://www.chori.org/bacpac/home.htm
      VECTOR: pBAC3.6
      ----- Genome Center
      Center: Wellcome Trust Sanger Institute
      Center code: SC
      Web site: http://www.sanger.ac.uk
      Contact: vegas@sanger.ac.uk

```

 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

FEATURES

```

source
    location/Qualifiers
    1..99251
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"
    /chromosome="1"
    /clone_RP11-275114
    /clone_11b="RP11-11.1"
    2000
    /note="Clone right_end: RP11-396C23"
    10958..11001
    /note="Single clone region. Sequence generated from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."
    14058..14160
    /note="Single clone region. Assembly confirmed by restriction digest data."
    15501..15567
    /note="Sequence confirmed by (AC044825 and AC021883) sequenced by W1BR and WUSC."
    15568..15675
    /note="Sequence from AC044825 and AC021883 sequenced by W1BR and WUSC."
    15676..15727
    /note="Sequence confirmed by (AC044825 and AC021883) sequenced by W1BR and WUSC."
    31351..31525,33698..33856,36956..37096,38026..38167,58557..58897)
    /gene="ACBD3"
    /locus_tag="RP11-275114.1-001"
    complement(join(16846..16988,24502..24786,26814..27000,31351..31525,33698..33856,36956..37096,38026..38167,58557..58897))
    /gene="ACBD3"
    /locus_tag="RP11-275114.1-001"
    /product="acyl-Coenzyme A binding domain containing 3"
    /note="match: ESTs: Em:AA148726.1 Em:AA209287.1 Em:AA367578.1 Em:AA653205.1 Em:AI435122.1 Em:AI636211.1 Em:AI638527.1 Em:AI818463.1 Em:AL044336.1 Em:AL559297.2 Em:AL56667.2 Em:AUD79552.1 Em:AM081459.1 Em:AW151467.1 Em:AW162925.1 Em:AM300205.1 Em:AM452221.1 Em:AW601227.1 Em:AW627762.1 Em:AW631077.1 Em:AW634088.1 Em:BB673355.1 Em:BF195876.1 Em:BF197451.1 Em:BF875919.1 Em:BF567039.1 Em:BF751083.1 Em:BF797451.1 Em:BG533826.1 Em:BG283448.1 Em:BG528440.1 Em:BG533826.1 Em:BG699935.1 Em:BG705952.1 Em:BG720109.1 Em:BG76473.1 Em:BJ325049.1 Em:BI48303.1 Em:BM601531.1 Em:BM60490.1 Em:BM975030.1 Em:BM979013.1 Em:BM979559.1 Em:BO003515.1 Em:BO020219.1 Em:BO293172.1 Em:BO431320.1 Em:BO431231.1 Em:BO853499.1 Em:BO941643.1 Em:CA394672.1 Em:CA418495.1 Em:CA441287.1 Em:CA771017.1 Em:CD556802.1 Em:CF138542.1 Em:CF594090.1 Em:W00483.1
    match: CDNA3: Em:AB043587.2 Em:AC025520.1 Em:AY150218.1 Em:BC039575.1 Em:BC045533.1 Em:BC060792.1"
    complement(16846)
    /gene="ACBD3"
    /locus_tag="RP11-275114.1-001"
    complement(16860..16865)
    /gene="ACBD3"
    /locus_tag="RP11-275114.1-001"
    complement(join(18777..18988,24502..24786,26814..27000,31351..31525,33698..33856,36956..37096,38026..38167,58557..58842))
    /gene="ACBD3"
  
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```

CDS
    join(20198..20235,26770..27238)
    /locus_tag="RP11-275114.4-001"
    /standard_name="OTTHUMP000003668"
    /note="match: Proteins: Tr:AAH0792 Tr:Q81ZC5 Tr:Q9H3P7 Tr:Q9H6U3"
    /codon_start=1
    /product="acyl-Coenzyme A binding domain containing 3"
    /protein_id="CAH71922.1"
    /db_xref="GI:55665957"
    /translation="MAATLNARLEVSVDGTLSPDPERPGAGAPLLPPLPPSP
    PGGKPGASGEPFPGAAAGAAERARLEQKGRFLELYGALAFREKOKAP
    HPTVEKRLVALHKQVLMGPNDPTCEVPFDVLGDRRERMAALGNMSEDMV
    FVKILNRCSKFTYTVASHKIEKGEKREERERERERERERERERERER
    EERLREERERERLEERLRLQEQKQALMALNSQTAQVQFOYAAQYQGVYEQOIL
    IROLQOHYQOYMOOLYOVOLAQOALQOAOVAVASSLPTSKVATVSNMSV
    NQAKTHDSSKELEPRAARALENGKESLPVYASPMTRPQIQPKKLOODAD
    SVITGRGEVTVRPTFHESSYLFWEATNTNYDIGRVTYETWDSPTAIVSHSES
    SDDBEEERENICEERAKKANKPLDIEIVPYRRDCEEVYAGSHQYPGAGVYLK
    DNSYELMRSGKVVYRVYTR"
    join(20170..20235,26770..27238)
    /locus_tag="RP11-275114.4-001"
    join(20170..20235,26770..27238)
    /locus_tag="RP11-275114.4-001"
    /product="novel protein"
    /note="match: ESTs: Em:AI682391.1 Em:AW511439.1 Em:BG219206.1"
    join(20198..20235,26770..27052)
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    /standard_name="OTTHUMP0000038761"
    /codon_start=1
    /product="novel protein"
    /protein_id="CAH71921.1"
    /db_xref="GI:55665956"
    /db_xref="UniProt/TREMBL:Q5VTI8"
    /translation="MLVNHGQEFKTRKTRIGSGQTHNQNPPEPFSASAAAGSSS
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    KASK"
    complement(join(26809..27000,33698..33799))
    /gene="ACBD3"
    /locus_tag="RP11-275114.1-002"
    complement(join(26809..27000,33698..33799))
    /gene="ACBD3"
    /locus_tag="RP11-275114.1-002"
    /product="acyl-Coenzyme A binding domain containing 3"
    /note="match: ESTs: Em:BE765013.1"
    27208..27213
    /locus_tag="RP11-275114.4-001"
    27238
    /locus_tag="RP11-275114.4-001"
    36677..36687
    /note="Sequence from AC044825 and AC021883 sequenced by W1BR and WUSC."
    36688..36728
    /note="Sequence confirmed by (AC044825 and AC021883) sequenced by W1BR and WUSC."
    44107..44146
    /note="Single clone region. Sequence generated from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."
    44107..44141
    /note="Sequence from uni-directional dGTP big dye terminator reads only."
    53593..53611
    /note="Single clone region. Assembly confirmed by restriction digest data."
    58694..58752
    /note="Sequence confirmed by (AC044825 and AC021883) sequenced by W1BR and WUSC."
    58989..59028
    /note="Sequence confirmed by (AC044825 and AC021883) sequenced by W1BR and WUSC."
    complement(61040..61388)
    /locus_tag="RP11-275114.2-001"
    /pseudo
  
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CDS complement(61040..61388)
 /locus_tag="RP11-275114.2-001"
 /note="match: proteins: Sw:P49207 Sw:Q29223 Sw:Q90Y75 Sw:Q9D1R9 Tr:AAH58118 Tr:AAI87001 Tr:Q7SZ79 Tr:Q7ZMJ7" /pseudo
 /product="ribosomal protein L34 (RPL34) pseudogene"
 /gene="RPL34"
 /note="Single clone region. Sequence generated from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."
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 /note="Single clone region. Assembly confirmed by restriction digest data."
 71371..71443
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 100.0%; Score 14; DB 8; Length 99251;
 Best Local Similarity 78.6%; Pred. No. 4e+03; Indels 0; Gaps 0;
 Matches 11; Conservative 3; Mismatches 0; Gaps 0;
 QY 1 CGUACUGCAACUCG 14
 ||:|||||:
 Db 89702 CGTACTGCAACTCG 89715
 RESULT 7
 AP003884/c 101249 bp DNA linear PLN 19-NOV-2003
 LOCUS Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 8,
 DEFINITION BAC clone:OJ1136_A10.
 ACCSSION AP003884
 VERSION AP003884.2 GI:22212582
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eriophytaceae; Oryzaceae; Oryza.
 1
 Sasaki, T., Matsumoto, T. and Yamamoto, K.
 Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, BAC
 clone:OJ1136_A10
 Published only in Database (2001)
 2 (Bases 1 to 101249)
 Sasaki, T., Matsumoto, T. and Yamamoto, K.
 Direct Submission
 Submitted (09-JUL-2001) Takuji Sasaki, National Institute of
 Agrobiological Sciences, Rice Genome Research Program; Kamondai
 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
 E-mail: tsasaki@nias.affrc.go.jp, URL: http://rsgp.dna.affrc.go.jp/
 Tel: 81-298-38-7441, Fax: 81-298-38-7468
 On Aug 12, 2002 this sequence version replaced gi:14646817.
 Genes were predicted from the integrated results of the following:
 GENSCAN (http://CCR-081.mt.edu/GENSCAN.html), RGENESH
 (http://www.sotiberry.com/), Genemark.hmm
 (http://opal.biology.gatech.edu/Genemark/), Glimmer
 (http://www.cigr.org/cdb/glimmer/glmr form.html), RiceHMM
 (http://rsgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor
 (http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4
 (http://glabin.cse.psu.edu/html/docs/sim4.html), gap2
 (http://www.cigr.org/software/glimmer/), BLASTN and BLASTX. The
 genomic sequence was searched against NCBI NonRedundant Protein
 database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA
 sequence database at RGP or DBJ. Protein homologues of the coding
 regions were searched against NCBI NonRedundant Protein database
 with BLASTP. ESTs represent the identified cDNA sequences using
 BLASTN with the corresponding DBJ accession no. and RGP clone ID.
 A gene with identity or significant homology to a protein is
 classified based on the protein name to indicate the homology level
 such as same name, 'putative-' and '-like protein'. A gene without
 significant homology to any protein but with full-length cDNA or

EST homology (covering almost the entire length of partial
 sequence) is classified as an 'unknown' protein. A gene predicted
 by two or more gene prediction programs is classified as a
 'hypothetical' protein according to IRGSP standard. A gene
 predicted by a single gene prediction program is also classified as
 a probable 'hypothetical' protein and is included as a
 miscellaneous feature of the sequence.
 The orientation of the sequence is from M13rev to -21M13 of the BAC
 clone. This sequence of OJ1136_A10 clone has an overlap with
 P0703C03 (DBJ: AP004637) clone at 5' end and with P0670E08 (DBJ:
 AP004759) at 3' end. The sequence was generated by combining
 Monanico and RGP-japan sequencing data. Detailed information on
 overlap and assembly quality together with annotation of this entry
 is available at http://rsgp.dna.affrc.go.jp/genomeSeq.html.
 Location/Qualifiers
 1..101249
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="genomic DNA"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /chromosome="8"
 /clone="OJ1136_A10"
 complement(4254..6577)
 /gene="OJ1136_A10.101"
 complement(join(<4254..4478,5437..5573,6496..6577))
 /gene="OJ1136_A10.101"
 /note="start and end point are not identified"
 complement(join(4254..4478,5437..5573,6496..6577))
 /gene="OJ1136_A10.101"
 /codon_start=1
 /product="membrane-associated protein-like"
 /protein_id="BAD01669.1"
 /db_xref="GI:38423960"
 /translation="MDSPTPYGLSPPLSLVLRNPECTKDDVDGSDVIGSGSAA
 RRRKLGSRGRRGTGQGDVENVANSPARDPDSPPMAALRPPGTEIDARQVVD
 RADHYHSRPGCAPPLAALDSDESGDGDADSDSDADNDPRASE"
 13728..15631
 /gene="OJ1136_A10.102"
 13728..15631
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 /note="probably inactive due to 3' exon missing in CDS
 probably inactive due to 5' exon missing in CDS
 pseudogene, maize retrotransposon Cintl1-1 polyprotein"
 /pseudo
 15787..16590
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 15810..16565
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 /note="containing full-length cDNA(s) : AK106729"
 /codon_start=1
 /product="unknown protein"
 /protein_id="BAD01670.1"
 /db_xref="GI:38423961"
 /translation="MWRLLRGHTITOLLILAPVLLQRTIRBAATTLAPPPTOTIS
 SWIGLURGGRRLLAAASALAILLLLSRSPRRRPHGVYIDAGSTRSRVHYAYR
 SPFAAARAAALPWTIMARTASAKAPGCCSPSPPIAAYVGRRCSSSLMGCGARH
 GNVRQGSRGRRVLMVGGGSGRGRRRGRKGRVRAAALVMAAIIITLPGV
 RSPFSFMAVAFSGARRSVNPLIATGLLR"
 complement(21188..23972)
 /gene="OJ1136_A10.104"
 complement(join(21188..22363,22784..23339,23555..23972))
 /gene="OJ1136_A10.104"
 /note="supported by full-length cDNA(s) : AK120478"
 complement(join(21565..22363,22784..23250))
 /gene="OJ1136_A10.104"
 /note="containing full-length cDNA(s) : AK120478"
 /codon_start=1
 /product="Nuclear inhibitor of Pp1-like"
 /protein_id="BAC22308.1"

AE016853_50 500001 511000
AE016853_51 510001 521000
AE016853_52 520001 531000
AE016853_53 530001 541000
AE016853_54 540001 551000
AE016853_55 550001 561000
AE016853_56 560001 571000
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AE016853_58 580001 591000
AE016853_59 590001 601000
AE016853_60 600001 611000
AE016853_61 610001 621000
AE016853_62 620001 631000
AE016853_63 630001 6397126
Continuation (9 of 64) of AE016853 from base 800001 (AE016853 *Pseudomonas syringae* pv. b

Query Match 100.0%; Score 14; DB 1; Length 110000;
Best Local Similarity 78.6%; Pred. No. 4e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACGCACTCG 14
Db 97428 CGTACTGCACTCG 97415

RESULT 9
CP000058_08/c
WPCOMMENT

Sequence split into 60 fragments LOCUS CP000058 Accession CP000058

Fragment Name	Begin	End
CP000058_00	1	11000
CP000058_01	10001	21000
CP000058_02	20001	31000
CP000058_03	30001	41000
CP000058_04	40001	51000
CP000058_05	50001	61000
CP000058_06	60001	71000
CP000058_07	70001	81000
CP000058_08	80001	91000
CP000058_09	90001	101000
CP000058_10	100001	111000
CP000058_11	110001	121000
CP000058_12	120001	131000
CP000058_13	130001	141000
CP000058_14	140001	151000
CP000058_15	150001	161000
CP000058_16	160001	171000
CP000058_17	170001	181000
CP000058_18	180001	191000
CP000058_19	190001	201000
CP000058_20	200001	211000
CP000058_21	210001	221000
CP000058_22	220001	231000
CP000058_23	230001	241000
CP000058_24	240001	251000
CP000058_25	250001	261000
CP000058_26	260001	271000
CP000058_27	270001	281000
CP000058_28	280001	291000
CP000058_29	290001	301000
CP000058_30	300001	311000
CP000058_31	310001	321000
CP000058_32	320001	331000
CP000058_33	330001	341000
CP000058_34	340001	351000
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CP000058_36	360001	371000
CP000058_37	370001	381000
CP000058_38	380001	391000
CP000058_39	390001	401000
CP000058_40	400001	411000
CP000058_41	410001	421000
CP000058_42	420001	431000

CP000058_43 430001 441000
CP000058_44 440001 451000
CP000058_45 450001 461000
CP000058_46 460001 471000
CP000058_47 470001 481000
CP000058_48 480001 491000
CP000058_49 490001 501000
CP000058_50 500001 511000
CP000058_51 510001 521000
CP000058_52 520001 531000
CP000058_53 530001 541000
CP000058_54 540001 551000
CP000058_55 550001 561000
CP000058_56 560001 571000
CP000058_57 570001 581000
CP000058_58 580001 591000
CP000058_59 590001 5928787
Continuation (9 of 60) of CP000058 from base 800001 (CP000058 *Pseudomonas syringae* pv. pt

Query Match 100.0%; Score 14; DB 1; Length 110000;
Best Local Similarity 78.6%; Pred. No. 4e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACGCACTCG 14
Db 69525 CGTACTGCACTCG 69512

RESULT 10
CR954209_5/c
WPCOMMENT

Sequence split into 7 fragments LOCUS CR954209 Accession CR954209

Fragment Name	Begin	End
CR954209_0	1	11000
CR954209_1	10001	21000
CR954209_2	20001	31000
CR954209_3	30001	41000
CR954209_4	40001	51000
CR954209_5	50001	61000
CR954209_6	60001	683751

Continuation (6 of 7) of CR954209 from base 500001 (CR954209 *Ostreococcus tauri* strain 07

Query Match 100.0%; Score 14; DB 1; Length 110000;
Best Local Similarity 78.6%; Pred. No. 4e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACGCACTCG 14
Db 64859 CGTACTGCACTCG 64846

RESULT 11
LMFLCHR18_00
WPCOMMENT

Sequence split into 11 fragments LOCUS LMFLCHR18 Accession AL499620

Fragment Name	Begin	End
LMFLCHR18_00	1	11000
LMFLCHR18_01	10001	21000
LMFLCHR18_02	20001	31000
LMFLCHR18_03	30001	41000
LMFLCHR18_04	40001	51000
LMFLCHR18_05	50001	61000
LMFLCHR18_06	60001	71000
LMFLCHR18_07	70001	81000
LMFLCHR18_08	80001	91000
LMFLCHR18_09	90001	101000
LMFLCHR18_10	100001	1091246

LOCUS LMFLCHR18 1091246 bp DNA linear HTG 16-DEC-2000
DEFINITION *Leishmania major* strain Friedlin chromosome 18, 19, 20, 22 clone
Chr. 18, Chr. 19, Chr. 20, Chr. 22, *** SEQUENCING IN PROGRESS ***, 722
unordered pieces.

ACCESSION AL499620
VERSION AL499620.1 GI:11877283

KEYWORDS HTG; HTGS PHASE1.
SOURCE Leishmania major
ORGANISM Leishmania major
REFERENCE Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
AUTHORS 1 (bases 1 to 1091246)
MURPHY, L., Quail, M., Harris, D., Rajandream, M., Ivens, A. and
Barrell, B.
TITLE Direct Submission
JOURNAL Submitted (15-DEC-2000) major Genome Sequencing Consortium, The
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 1SA, UK
COMMENT For more information about this sequence or the Leishmania Project,
see http://www.sanger.ac.uk/Projects/L_major/
CAVEATS: 1. the sequencing is still in progress
2. this submission represents 721 unordered contigs of size 0.5kb
or greater, separated by blocks of N
3. it is derived from whole chromosome shotgun plus cosmid and/or
PAC skims
4. the data are EXTREMELY preliminary
5. the sequence may contain E. coli, sequencing/cloning vector, or
be cross-contaminated with other Leishmania chromosomes IMPORTANT:
This sequence is unfinished and does not necessarily represent the
correct sequence. Work on the sequence is in progress and the
release of these data is based on the understanding that the
sequence will change as work continues.
THE ORDER OF CONTIGS IS NOT KNOWN.
THESE DATA ARE PRELIMINARY ONLY, and annotation will follow
shortly.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 722 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
844: contig of 844 bp in length
845
944: gap of 100 bp
945
1437: contig of 493 bp in length
1438
1537: gap of 100 bp
1538
2130: contig of 593 bp in length
2131
2230: gap of 100 bp in length
2231
2756: contig of 526 bp in length
2757
2856: gap of 100 bp
3395: contig of 539 bp in length
3396
3495: gap of 100 bp
3496
4076: contig of 581 bp in length
4077
4176: gap of 100 bp
4177
4743: contig of 567 bp in length
4744
4843: gap of 100 bp
4844
5371: contig of 528 bp in length
5372
5471: gap of 100 bp
5472
6050: contig of 579 bp in length
6051
6150: gap of 100 bp
6151
6686: contig of 536 bp in length
6687
6786: gap of 100 bp
6787
7314: contig of 528 bp in length
7315
7414: gap of 100 bp
7415
8143: contig of 729 bp in length
8144
8243: gap of 100 bp
8244
8825: contig of 582 bp in length
8826
8925: gap of 100 bp
8926
9508: contig of 583 bp in length
9509
9608: gap of 100 bp
9609
10117: contig of 509 bp in length
10118
10217: gap of 100 bp
10219
10784: contig of 567 bp in length
10785
10884: gap of 100 bp
10885
11476: contig of 592 bp in length
11477
11576: gap of 100 bp
11577
12074: contig of 498 bp in length

12075
12175
12713
12813
12814
13346
13347
13447
13985
14085
14086
15175
15176
15275
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34665
34665
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35318
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35882
35882
35883
35983
35983
36580
36580
36680
37590
12174: gap of 100 bp
12713: contig of 539 bp in length
12813: gap of 100 bp
12814: contig of 533 bp in length
13346: gap of 100 bp
13347: gap of 100 bp
13447: gap of 100 bp
13985: contig of 538 bp in length
14085: gap of 100 bp
14086: contig of 1090 bp in length
15175: gap of 100 bp
15176: gap of 100 bp
15275: contig of 584 bp in length
15858: gap of 100 bp
15859: gap of 100 bp
15959: contig of 553 bp in length
16512: gap of 100 bp
16511: gap of 100 bp
16612: contig of 553 bp in length
17165: gap of 100 bp
17265: contig of 960 bp in length
17266: gap of 100 bp
18225: gap of 100 bp
18325: contig of 591 bp in length
18915: contig of 591 bp in length
18916: gap of 100 bp
19016: contig of 558 bp in length
19573: gap of 100 bp
19574: gap of 100 bp
19674: contig of 512 bp in length
20186: gap of 100 bp
20286: gap of 100 bp
20876: contig of 591 bp in length
20976: gap of 100 bp
21549: contig of 573 bp in length
21649: gap of 100 bp
21650: gap of 100 bp
22180: contig of 531 bp in length
22280: gap of 100 bp
22850: contig of 570 bp in length
22950: gap of 100 bp
23529: contig of 579 bp in length
23629: gap of 100 bp
24147: contig of 518 bp in length
24148: gap of 100 bp
24247: gap of 100 bp
24794: contig of 547 bp in length
24795: gap of 100 bp
24895: contig of 519 bp in length
25413: gap of 100 bp
25513: gap of 100 bp
26090: contig of 577 bp in length
26091: gap of 100 bp
26191: gap of 100 bp
26731: contig of 541 bp in length
26732: gap of 100 bp
26831: gap of 100 bp
26832: contig of 736 bp in length
27567: gap of 100 bp
27568: gap of 100 bp
27668: contig of 589 bp in length
28256: gap of 100 bp
28257: gap of 100 bp
28356: gap of 100 bp
29020: contig of 664 bp in length
29120: gap of 100 bp
29813: contig of 693 bp in length
29913: gap of 100 bp
30451: contig of 538 bp in length
30551: gap of 100 bp
30552: contig of 565 bp in length
31116: gap of 100 bp
31117: gap of 100 bp
31216: gap of 100 bp
31870: contig of 654 bp in length
31871: gap of 100 bp
32527: contig of 557 bp in length
32627: gap of 100 bp
33180: contig of 553 bp in length
33280: gap of 100 bp
33281: gap of 100 bp
33800: contig of 620 bp in length
34000: gap of 100 bp
34000: gap of 100 bp
34564: contig of 564 bp in length
34664: gap of 100 bp
34665: contig of 554 bp in length
35318: gap of 100 bp
35319: gap of 100 bp
35882: contig of 564 bp in length
35883: gap of 100 bp
35982: gap of 100 bp
35983: contig of 597 bp in length
36579: gap of 100 bp
36580: gap of 100 bp
37589: contig of 910 bp in length
37689: gap of 100 bp

* 37690 38264: contig of 575 bp in length
* 38265 38364: gap of 100 bp
* 38365 38899: contig of 535 bp in length
* 38900 38999: gap of 100 bp
* 39000 39559: contig of 560 bp in length
* 39560 39659: gap of 100 bp
* 39660 40416: contig of 757 bp in length
* 40417 40516: gap of 100 bp
* 40517 41084: contig of 568 bp in length
* 41085 41185 42202: contig of 1018 bp in length
* 41185 42202: contig of 1018 bp in length
* 42203 42832: gap of 100 bp
* 42833 42932: contig of 530 bp in length
* 42933 43927: gap of 100 bp
* 43928 44027: contig of 995 bp in length
* 44028 44822: gap of 100 bp
* 44823 44922: contig of 795 bp in length
* 44923 45474: gap of 100 bp
* 45475 45574: gap of 552 bp in length
* 45575 46219: gap of 100 bp
* 46219 46318: contig of 644 bp in length
* 46319 47064: gap of 100 bp
* 47065 47164: contig of 746 bp in length
* 47165 47708: gap of 100 bp
* 47709 47809: contig of 544 bp in length
* 47809 48532: gap of 100 bp
* 48533 49129: contig of 724 bp in length
* 49130 49229: gap of 100 bp
* 49230 49787: contig of 497 bp in length
* 49788 49887: gap of 558 bp in length
* 49888 50455: gap of 100 bp
* 50456 50555: contig of 568 bp in length
* 50555: gap of 100 bp

Query Match 100.0%; Score 14; DB 14; Length 110000;
Best Local Similarity 78.6%; Pred. No. 4e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGUACUCGACATCG 14
DB 16121 CGTACTCGACATCG 16134

RESULT 12
AP008214_143/c
WPCOMMENT

Sequence split into 285 fragments LOCUS AP008214 Accession AP008214
Fragment Name Begin End
AP008214_000 1 110000
AP008214_001 100001 210000
AP008214_002 200001 310000
AP008214_003 300001 410000
AP008214_004 400001 510000
AP008214_005 500001 610000
AP008214_006 600001 710000
AP008214_007 700001 810000
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AP008214_010 1000001 1110000
AP008214_011 1100001 1210000
AP008214_012 1200001 1310000
AP008214_013 1300001 1410000
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AP008214_015 1500001 1610000
AP008214_016 1600001 1710000
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AP008214_020 2000001 2110000
AP008214_021 2100001 2210000
AP008214_022 2200001 2310000
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AP008214_030 3000001 3110000
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 AP008214_191 19100001 19210000
 AP008214_192 19200001 19310000
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 AP008214_194 19400001 19510000
 AP008214_195 19500001 19610000
 AP008214_196 19600001 19710000

Query Match 100.0%; Score 14; DB 15; Length 110000;
 Best Local Similarity 78.6%; Pred. No. 4e+03;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14
 Db 62186 CGUACUGCACTCG 62173

RESULT 13
 AP008215_150
 WPCOMMENT

Sequence split into 227 fragments LOCUS AP008215 Accession AP008215
 Fragment Name Begin End
 AP008215_000 1 110000
 AP008215_001 100001 210000
 AP008215_002 200001 310000
 AP008215_003 300001 410000
 AP008215_004 400001 510000
 AP008215_005 500001 610000
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 AP008215_020 2000001 2110000
 AP008215_021 2100001 2210000
 AP008215_022 2200001 2310000
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 AP008215_028 2800001 2910000
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 AP008215_030 3000001 3110000

AP008215_031 3100001 3210000
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AP008215_033 3300001 3410000
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AP008215_171 17100001 17210000
AP008215_172 17200001 17310000
AP008215_173 17300001 17410000
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AP008215_177 17700001 17810000
AP008215_178 17800001 17910000
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AP008215_180 18000001 18110000
AP008215_181 18100001 18210000
AP008215_182 18200001 18310000
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AP008215_189 18900001 19010000
AP008215_190 19000001 19110000
AP008215_191 19100001 19210000
AP008215_192 19200001 19310000
AP008215_193 19300001 19410000
AP008215_194 19400001 19510000
AP008215_195 19500001 19610000
AP008215_196 19600001 19710000

Query Match 100.0%; Score 14; DB 15; Length 110000;
Best Local Similarity 78.6%; Pred. No. 4e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACGCACTCG 14
DB 27463 CGTACTGCACTCG 27476

RESULT 14
CR382131_08
WPCOMMENT

Sequence split into 43 fragments LOCUS CR382131 Accession CR382131

Fragment Name	Begin	End
CR382131_00	1	110000
CR382131_01	100001	210000
CR382131_02	200001	310000
CR382131_03	300001	410000
CR382131_04	400001	510000
CR382131_05	500001	610000
CR382131_06	600001	710000
CR382131_07	700001	810000
CR382131_08	800001	910000
CR382131_09	900001	1010000
CR382131_10	1000001	1110000
CR382131_11	1100001	1210000
CR382131_12	1200001	1310000
CR382131_13	1300001	1410000
CR382131_14	1400001	1510000
CR382131_15	1500001	1610000
CR382131_16	1600001	1710000
CR382131_17	1700001	1810000
CR382131_18	1800001	1910000
CR382131_19	1900001	2010000
CR382131_20	2000001	2110000
CR382131_21	2100001	2210000
CR382131_22	2200001	2310000
CR382131_23	2300001	2410000
CR382131_24	2400001	2510000
CR382131_25	2500001	2610000
CR382131_26	2600001	2710000
CR382131_27	2700001	2810000
CR382131_28	2800001	2910000
CR382131_29	2900001	3010000
CR382131_30	3000001	3110000
CR382131_31	3100001	3210000
CR382131_32	3200001	3310000
CR382131_33	3300001	3410000
CR382131_34	3400001	3510000
CR382131_35	3500001	3610000
CR382131_36	3600001	3710000
CR382131_37	3700001	3810000

CR382131_38 3800001 3910000
CR382131_39 3900001 4010000
CR382131_40 4000001 4110000
CR382131_41 4100001 4210000
CR382131_42 4200001 4224103

Continuation (9 of 43) of CR382131 from base 800001 (CR382131 Yarrowia lipolytica chromo

QY 1 CGUACGCACTCG 14
DB 106773 CGTACTGCACTCG 106786

RESULT 15
CR382131_09
WPCOMMENT

Sequence split into 43 fragments LOCUS CR382131 Accession CR382131

Fragment Name	Begin	End
CR382131_00	1	110000
CR382131_01	100001	210000
CR382131_02	200001	310000
CR382131_03	300001	410000
CR382131_04	400001	510000
CR382131_05	500001	610000
CR382131_06	600001	710000
CR382131_07	700001	810000
CR382131_08	800001	910000
CR382131_09	900001	1010000
CR382131_10	1000001	1110000
CR382131_11	1100001	1210000
CR382131_12	1200001	1310000
CR382131_13	1300001	1410000
CR382131_14	1400001	1510000
CR382131_15	1500001	1610000
CR382131_16	1600001	1710000
CR382131_17	1700001	1810000
CR382131_18	1800001	1910000
CR382131_19	1900001	2010000
CR382131_20	2000001	2110000
CR382131_21	2100001	2210000
CR382131_22	2200001	2310000
CR382131_23	2300001	2410000
CR382131_24	2400001	2510000
CR382131_25	2500001	2610000
CR382131_26	2600001	2710000
CR382131_27	2700001	2810000
CR382131_28	2800001	2910000
CR382131_29	2900001	3010000
CR382131_30	3000001	3110000
CR382131_31	3100001	3210000
CR382131_32	3200001	3310000
CR382131_33	3300001	3410000
CR382131_34	3400001	3510000
CR382131_35	3500001	3610000
CR382131_36	3600001	3710000
CR382131_37	3700001	3810000
CR382131_38	3800001	3910000
CR382131_39	3900001	4010000
CR382131_40	4000001	4110000
CR382131_41	4100001	4210000
CR382131_42	4200001	4224103

Continuation (10 of 43) of CR382131 from base 900001 (CR382131 Yarrowia lipolytica chromo

Query Match 100.0%; Score 14; DB 15; Length 110000;
Best Local Similarity 78.6%; Pred. No. 4e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACGCACTCG 14
DB 6773 CGTACTGCACTCG 6786


```

* 2266 2365: gap of 100 bp
* 2366 3576: contig of 1211 bp in length
* 3577 4845: contig of 1169 bp in length
* 4846 7367: contig of 2422 bp in length
* 7368 8595: contig of 1128 bp in length
* 8596 10409: contig of 1714 bp in length
* 10410 10509: gap of 100 bp
* 10510 11838: contig of 1329 bp in length
* 11839 11938: gap of 100 bp
* 11939 13792: contig of 1854 bp in length
* 13793 13892: gap of 100 bp
* 13893 15478: contig of 1586 bp in length
* 15479 15578: gap of 100 bp
* 15579 17753: contig of 2175 bp in length
* 17754 17853: gap of 100 bp
* 17854 19331: contig of 1478 bp in length
* 19332 19431: gap of 100 bp
* 19432 21597: contig of 2166 bp in length
* 21598 21697: gap of 100 bp
* 21698 23136: contig of 1439 bp in length
* 23137 23236: gap of 100 bp
* 23237 25903: contig of 2667 bp in length
* 25904 26003: gap of 100 bp
* 26004 29751: contig of 3648 bp in length
* 29752 33001: contig of 3250 bp in length
* 33002 33101: gap of 100 bp
* 33102 35597: contig of 2496 bp in length
* 35598 37964: contig of 2267 bp in length
* 37965 38064: gap of 100 bp
* 38065 41070: contig of 3006 bp in length
* 41071 41170: gap of 100 bp
* 41171 43345: contig of 2175 bp in length
* 43346 46364: contig of 2919 bp in length
* 46365 46464: gap of 100 bp
* 46465 49323: contig of 2859 bp in length
* 49324 49423: gap of 100 bp
* 49424 52514: contig of 3091 bp in length
* 52515 56594: contig of 3980 bp in length
* 56595 60340: gap of 100 bp
* 60341 60440: gap of 100 bp
* 60441 64493: contig of 4053 bp in length
* 64494 66453: gap of 100 bp
* 66454 68745: contig of 4052 bp in length
* 68746 71501: contig of 2756 bp in length
* 71502 71601: gap of 100 bp
* 71602 74120: contig of 2519 bp in length
* 74121 78968: contig of 4748 bp in length
* 78969 79068: gap of 100 bp
* 79069 83734: contig of 4666 bp in length
* 83735 83834: gap of 100 bp
* 83835 89630: contig of 5696 bp in length
* 89631 94947: contig of 5317 bp in length
* 94948 95047: gap of 100 bp
* 95048 100827: contig of 5780 bp in length
* 100828 100927: gap of 100 bp
* 100928 105800: contig of 4873 bp in length
* 105801 114896: contig of 8996 bp in length
* 114897 114996: gap of 100 bp
* 114997 127117: contig of 12121 bp in length
* 127118 127217: gap of 100 bp

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FEATURES          * 127218 140409: contig of 13192 bp in length.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/map="1"
/clone="RP11-275I14"
/clone_1fb="RP11-11 Human Male BAC"
1..1156
/note="assembly_fragment"
gap
1157..1256
/estimated_length=100
misc_feature
1257..2265
/note="assembly_fragment"
2266..2365
/estimated_length=100
misc_feature
2366..3576
/note="assembly_fragment"
3577..3676
/estimated_length=100
gap
3677..4845
/note="assembly_fragment"
4846..4945
/estimated_length=100
misc_feature
4946..7367
/note="assembly_fragment"
7368..7467
/estimated_length=100
gap
7468..8595
/note="assembly_fragment"
8596..8695
/estimated_length=100
misc_feature
8696..10409
/note="assembly_fragment"
10410..10509
/estimated_length=100
gap
10510..11838
/note="assembly_fragment"
11839..11938
/estimated_length=100
gap
11939..13792
/note="assembly_fragment"
13793..13892
/estimated_length=100
misc_feature
13893..15478
/note="assembly_fragment"
15479..15578
/estimated_length=100
gap
15579..17753
/estimated_length=100
misc_feature

Query Match      100.0%; Score 14; DB 14; Length 140409;
Best Local Similarity 78.6%; Pred. No. 3.9e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGUACUGCAACUG 14
Db      14580 CGTACTGCACACTCG 14567

RESULT 18
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LOCUS         AP005426
DEFINITION    Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 9,
ACCESSION     AP005426
VERSION       AP005426.3 GI:50725953
KEYWORDS
SOURCE        Oryza sativa (japonica cultivar-group)
              Oryza sativa (japonica cultivar-group)
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

```


REFERENCE
AUTHORS
TITLE
JOURNAL
AUTHORS
TITLE
JOURNAL
COMMENT

1
Sasaki, T., Matsumoto, T. and Katayose, Y.
Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, PAC
clone: P0668D04
Published Only in Database (2002)

2 (bases 1 to 148848)
Sasaki, T., Matsumoto, T. and Katayose, Y.
Direct Submission
Submitted (12-JUN-2002) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kamoudai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasaki@nias.affrc.go.jp, URL: http://rsgp.dna.affrc.go.jp/
Tel: 81-298-38-7441, Fax: 81-298-38-7468)
On Jul 27, 2004 this sequence version replaced gi:42415348.
Genes were predicted from the integrated results of the following:
GENSCAN (http://CCR-081.mt.edu/GENSCAN.html), FGENESH
(http://www.softberry.com/), GeneMark.hmm
(http://opal.biology.gatech.edu/GeneMark/), GlimmerM
(http://www.tigr.org/tdb/glimmer/glimmer.html), RiceHMM
(http://rsgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor
(http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4
(http://globin.cse.psu.edu/hm1/docs/sim4.html), gap2
(http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The
genomic sequence was searched against NCBI NonRedundant Protein
database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA
sequence database at RGP or DDBJ. Protein homologues of the coding
regions were searched against NCBI NonRedundant Protein database
with BLASTP. ESTs represent the identified cDNA sequences using
BLASTN with the corresponding DDBJ accession no. and RGP clone ID.
Full-length cDNAs represent the identified cDNA sequences using
BLASTN with the corresponding DDBJ accession no.
A gene with identity or significant homology to a protein is
classified based on the protein name to indicate the homology level
such as same name, 'putative-' and '-like protein'. A gene without
significant homology to any protein but with full-length cDNA or
EST homology (covering almost the entire length of partial
sequence) is classified as an 'unknown' protein. A gene predicted
by two or more gene prediction programs is classified as a
'hypothetical' protein according to IRGSP standard. A gene
predicted by a single gene prediction program is also classified as a
probable 'hypothetical' protein and is included as a
miscellaneous feature of the sequence.
The orientation of the sequence is from 77 to 506 of the PAC clone.
This sequence of P0668D04 clone has an overlap with P0701P11 (DDBJ:
AF005429) clone at 5' end and with PJ1740.D06 (DDBJ: AF005579)
clone at 3' end. Detailed information on overlap and assembly
quality together with annotation of this entry is available at
http://rsgp.dna.affrc.go.jp/GenomeSeq.html.
Location/Qualifiers

FEATURES
source

1.148848
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/mol_type="genomic DNA"
/cultiivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="9"
/clone="P0668D04"
/gene="P0668D04.1"
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/gene="P0668D04.1"
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/note="start and end point are not identified"
complement (join(1984..2246,2295..2430))
/gene="P0668D04.1"
/note="predicted by GENSCAN etc."
/codon_start=1
/product="hypothetical protein"
/protein_id="BAD33481.1"
/db_xref="GI:50725954"
/translation="MDGRMDGRMTAMADVPFRERRELTREVS TORQAAVFPFA
TAARGHRRSPSPHPIHPRHTIPSTTAIGRINTVTGQRERERERKDKHPYKO
VRLMRKEPRRGQIWGLVFPFLKPRFRSRP"
2793..8340

gene
mRNA
CDS

mRNA
misc_feature
gene
misc_feature
gene
mRNA
misc_feature
gene
misc_feature
mRNA
gene
misc_feature
mRNA
gene
mRNA
CDS

/gene="P0668D04.2-2"
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/gene="P0668D04.2-2"
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2793..8340
/gene="P0668D04.2-2"
/note="contains full-length cDNA(s) : AK121336
non-coding transcript
probably inactive due to including stop codon(s) in CDS"
2802..9052
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2802..9052
/gene="P0668D04.2-1"
/note="contains full-length cDNA(s) : AK073292
non-coding transcript
probably inactive due to including stop codon(s) in CDS"
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join(<4775..7588,7705..7793,7901..>9051)
/gene="P0668D04.2-3"
/note="supported by full-length cDNA(s) : AK068557"
4775..9051
/gene="P0668D04.2-3"
/note="contains full-length cDNA(s) : AK068557, AK058417
non-coding transcript
probably inactive due to including stop codon(s) in CDS"
join(10309..10457,10655..10802,11395..11418)
/gene="P0668D04.3"
join(10309..10457,10655..10802,11395..11418)
/gene="P0668D04.3"
/note="hypothetical ORF
predicted by RiceHMM
this category is not included in IRGSP standard"
complement (join(13250..13596,14755..15107,15521..15709,
15814..15968,16099..16319))
/gene="P0668D04.4-1"
complement (join(13250..13596,14755..15107,15521..15709,
15814..15968,16099..16319))
/gene="P0668D04.4-1"
/note="supported by full-length cDNA(s) : AK067949"
complement (join(13269..13596,14755..15107,15521..15709,
15814..15968,16099..16318))
/gene="P0668D04.4-1"
/note="supported by full-length cDNA(s) : AK104860"
complement (join(13407..13596,14755..15107,15521..15709,
15814..15968,16099..16285))
/gene="P0668D04.4-1"
/note="contains EST(s) : AU086004 (S10974), D46355 (S10974)
contains full-length cDNA(s) : AK067949, AK104860"
/codon_start=1
/product="putative cinnamoyl CoA reductase"
/protein_id="BAD33482.1"
/db_xref="GI:50725955"
/translation="MTVVVVVADDAAAAAAQQOERLPPHGQVTCVGAAGYISML
VTLIERGTGTYGTRNPDPPRNATKALDQADRELYNCKADLLDYDSIRAAVDCGQ
VHTASPYTDPEQVBFPAVRCGTETVITGAABAGYKRVVTSIGATYMDPRKPDV
VVDSCWSDLEFCCKTKWYCYGKAVAOACCKAAGVGVDSLVVSPPLQPT
VVAASVHLIKLYDGSARKYANAVOAYVVDVDAARVAFVPAKASGRLCAERLYLR
EDVHVLIGLTPPEYVPTRCSDVNPVRQPYMSKKQLQDLAIHPIPSDSLYETVKS
LOEKHLPLVLSKEIPEELNGVPA"
complement (join(14414..15107,15521..15709,15814..15968,
16099..16313))
/gene="P0668D04.4-2"
complement (join(14414..15107,15521..15709,15814..15968,
16099..16313))
/gene="P0668D04.4-2"
/note="supported by full-length cDNA(s) : AK107198"
complement (join(14751..15107,15521..15709,15814..15968,
16099..16285))
/gene="P0668D04.4-2"
/note="contains EST(s) : AU086004 (S10974), D46355 (S10974)
contains full-length cDNA(s) : AK107198"
/codon_start=1

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/protein_id="BAD33483.1"
/db_xref="GI:50725956"
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VKLLRGVYKGTAVNPPDPKRAHFKADGADERVLCKADLDYDPSIRAAVDGCH
VFTTAPYVDDPEQOMEPARVGTREYIKAAAEKGTTRVFTSSICATYMDPRGQDV
VDSGCSIDLEFCRKTNTCYGNAVAESQCAAEKRGVDLVVSPVAVGGLDPT
VNAASHIILKYLDSAKCANAAVQAVYDVDAHAHVFAEPASGRHLCARVLAHR
EDVHLIGKLFPEYPPETR"
/complement(17951..19577)
/gene="P0668D04.5"
/complement(join<17951..18249,19523..>19577))
/gene="P0668D04.5"
/notes="start and end point are not identified"
/complement(join(17951..18249,19523..19577))
/gene="P0668D04.5"
/notes="predicted by GENSCAN etc."
/codon_start=1
/product="hypothetical protein"
/protein_id="BAD33484.1"
/db_xref="GI:50725957"
/translation="MDELILLAAITDGLIEHSICPGRPGPAARATGRDRASGRGP
GPRTPARSHARGADVDVQPPRTTHQWRRAAASGSEIRPERGADASRALGV
VASGVWERTTGLAS"
/21544..22077
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/join(<21544..21564,21810..21888,21992..>22077)
/gene="P0668D04.6"
/notes="start and end point are not identified"
/join(21544..21564,21810..21888,21992..22077))
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/notes="predicted by GeneMark.hmm etc."
/codon_start=1
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/protein_id="BAD33485.1"
/db_xref="GI:50725958"
/translation="MAQILIEAGCFGAGGRADDEROAGRAPAGVGAGAAATPGNAA
ATAGTAAAPRSGCGS"
/22537..23576
/gene="P0668D04.7"
/22537..23576
/gene="P0668D04.7"
/notes="probably inactive due to 5' exon missing in CDS
.pseudogene, En/Spm-related transposon protein"

Query Match 100.0%; Score 14; DB 15; Length 148848;
Best Local Similarity 78.6%; Pred. No. 3.8e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14
||:|||||:|
Db 19106 CGTACTGCACACTCG 19119

RESULT 19
AP005429 154950 bp DNA linear PLN 13-JUN-2004
LOCUS Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 9,
DEFINITION PAC clone: P0701F11.
ACCESSION AP005429
VERSION AP005429.3 GI:50252464
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erihartoideae; Oryzaceae; Oryza.
REFERENCE 1
AUTHORS Sasaki,T., Matsumoto,T. and Katayose,Y.
TITLE Oryza sativa nipponbare (GMS3) genomic DNA, chromosome 9, PAC
clone: P0701F11
JOURNAL Published only in Database (2002)
2 (bases 1 to 154950)

```

AUTHORS

Sasaki,T., Matsumoto,T. and Katayose,Y.
 Direct Submission
 Submitted (12-JUN-2002) Takuji Sasaki, National Institute of
 Agricultural Sciences, Rice Genome Research Program, Kannondai
 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
 (E-mail:tsasaki@nias.affrc.go.jp, url:http://rtp.dna.affrc.go.jp/,
 Tel:81-298-38-7441, Fax:81-298-38-7468)
 On Jul 12, 2004 this sequence version replaced gi:38347824.
 Genes were predicted from the integrated results of the following:
 GENSCAN (http://CCR-081.mtc.edu/GENSCAN.html), FGENESH
 (http://www.softberry.com/), GeneMark.hmm
 (http://opal.biology.gatech.edu/GeneMark/), Glimmer
 (http://www.tigr.org/tgd/glimmer/glmr_form.html), RiceHMM
 (http://rtp.dna.affrc.go.jp/RiceHMM/), SplicePredictor
 (http://bioinformatics.lasstate.edu/cgi-bin/sp.cgi), sim4
 (http://globin.cse.psu.edu/html/doc/sim4.html), GAP2
 (http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The
 genomic sequence was searched against NCBI NonRedundant Protein
 database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA
 sequence database at RGP or DBJ. Protein homologues of the coding
 regions were searched against NCBI NonRedundant Protein database
 with BLASTP. RSTs represent the identified cDNA sequences using
 BLASTN with the corresponding DBJ accession no. and RGP clone ID.
 Full-length cDNAs represent the identified cDNA sequences using
 BLASTN with the corresponding DBJ accession no.
 A gene with identical or significant homology to a protein is
 classified based on the protein name to indicate the homology level
 such as same name, 'putative-' and '-like protein'. A gene without
 significant homology to any protein but with full-length cDNA or
 RST homology (covering almost the entire length of partial
 sequence) is classified as an 'unknown' protein. A gene predicted
 by two or more gene prediction programs is classified as a
 'hypothetical' protein according to IRGSP standard. A gene
 predicted by a single gene prediction program is also classified as a
 probable 'hypothetical' protein and is included as a
 miscellaneous feature of the sequence.
 The orientation of the sequence is from SP6 to T7 of the PAC clone.
 This sequence of P0701F11 clone has an overlap with P001G10 (DBJ:
 AP005784) clone at 5' end and with P0668D04 (DBJ: AP005426) clone
 at 3' end. Detailed information on overlap and assembly quality
 together with annotation of this entry is available at
 http://rtp.dna.affrc.go.jp/genomeseq.html.

COMMENT

FEATURES

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  /db_xref="taxon:39947"
  /chromosome="9"
  /clone="P0701F11"
  /complement(7738..9684)
  /gene="P0701F11.1"
  /complement(join(7738..8259,8789..8911,9006..9338,
  9472..9684))
  /gene="P0701F11.1"
  /notes="supported by full-length cDNA(s): AK067834"
  /complement(join(7843..8259,8789..8911,9006..9338,
  9472..9555))
  /gene="P0701F11.1"
  /notes="contains full-length cDNA(s): AK067834"
  /codon_start=1
  /product="putative WIZZ"
  /protein_id="BAD28643.1"
  /db_xref="GI:50252465"
  /translation="MDDDGDSGSPDSDAAGILPLPSRSPAELEKTRAPMEENA
  RTRRLDAIHLAHQRLALPSLAPPPSPITARAISVSTSCAREDAAPVAAAAA
  STAPSRQOPPAEPAPRPVTRVADAADADANSMARVADGVTQMRKYGQKVRDN
  PYRAVFRCAFAPCPVYKQRCORCAEDSRSMVAATYGEHNHLSQTTFEFAVSGCTTS
  GAAAGSSSLPCLCSISINSGRITLDTLQNGSSISACGVAALAAVSGELVTVASPE
  LRRHIVERVQVLKDAEFAVTAVAAVDQIPHVPVH"
  /join(11245..11304,12099..12272,12615..12681,16273..16317,
  17030..17142,17983..18084)
  /gene="P0701F11.2"

gene
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  /cultivar="Nipponbare"
  /db_xref="taxon:39947"
  /chromosome="9"
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  9472..9684))
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  STAPSRQOPPAEPAPRPVTRVADAADADANSMARVADGVTQMRKYGQKVRDN
  PYRAVFRCAFAPCPVYKQRCORCAEDSRSMVAATYGEHNHLSQTTFEFAVSGCTTS
  GAAAGSSSLPCLCSISINSGRITLDTLQNGSSISACGVAALAAVSGELVTVASPE
  LRRHIVERVQVLKDAEFAVTAVAAVDQIPHVPVH"
  /join(11245..11304,12099..12272,12615..12681,16273..16317,
  17030..17142,17983..18084)
  /gene="P0701F11.2"

```

[illegible]

gene
 mRNA
 CDS
 gene
 mRNA
 CDS
 gene
 misc_feature
 gene
 1 CGUACUGCAACUCG 14
 Db 96909 C9TACTGCAACTCG 96922
 Query Match 100.0%; Score 14; DB 15; Length 154950;
 Best Local Similarity 78.6%; Pred. No. 3.8e+03;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Oy
 RESULT 20
 LOCUS BX088687
 DEFINITION Zebrafish DNA sequence from clone CH211-206114 in linkage group 7,
 complete sequence.
 VERSION BX088687
 SOURCE BX088687.6 GI:40994808
 ORGANISM HNG.
 Danio rerio (zebrafish)
 Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 173867)
 BIlwood, M.
 Direct Submission
 Submitted (15-JAN-2004) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 zfish-help@sanger.ac.uk Clone requests: clonesrequest@sanger.ac.uk
 On Jan 17, 2004 this sequence version replaced gi:37803616.
 ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: zfish-help@sanger.ac.uk

 COMMENT
 JOURNAL
 AUTHORS
 TITLE
 REFERENCE
 COMMENT

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: EMBL, SWISSPROT, TrEMBL, WP, Wormer, Wormer, information on the Wormer database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormer Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhifeng Bao and Sean Eddy, submitted), and those beginning 'dir' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_reio/fishmask.shtml CH211-206114 is from a CHORI-211 BAC library

FEATURES

source Location/Qualifiers

1. 173867
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-206114"
/clone_id="CHORI-211"

ORIGIN

Query Match 100.0%; Score 14; DB 5; Length 173867;
Best Local Similarity 78.6%; Pred. No. 3.7e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUG 14
||:|||||:
Db 73300 CGTACTGCAACTCG 73313

RESULT 21
AC108605/c
AC108605
DEFINITION
*** 2 unordered pieces.
AC108605 188872 bp DNA linear HTG 09-OCT-2002
Rattus norvegicus clone CH230-267P22, *** SEQUENCING IN PROGRESS
AC108605
VERSION
AC108605.4 GI:23195553
HTG; HTG_PHASE1; HTG_DRAFT; HTG_ENRICHED.
KEYWORDS
Rattus norvegicus (Norway rat)
SOURCE
Rattus norvegicus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Rattus.
1 (bases 1 to 188872)
Muzny, D., Marler, M., Metzger, M., Lee, A., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooke, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, R., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bismail, K., Blair, J., Blankenburg, K., Blych, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Butrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,

TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL

TITLE
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REFERENCE
AUTHORS
JOURNAL

Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregregorys, R., Gee, K., Gill, R., Grady, M., Guerrero, M., Guevara, W., Gunatirane, P., Healand, W., Hamill, C., Hamilton, C., Hamilton, K., Harrey, Y., Havlik, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodges, A., Hogues, M., Hollins, B., Howells, S., Hu, Y., Hume, J., Idelberg, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolyet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowals, C., Kraft, C.L., Ledow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Loshenshew, L., Louisedge, H., Lozano, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, B., Mangum, P., Martin, K., Martin, R., Martinez, B., Manwiny, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Mirza, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokoelameli, O., Okunolu, G., Olarpunagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Polidexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzo, M., Quirroz, J., Rachlin, B., Reeves, K., Regier, M.A., Reich, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Slisom, I., Sletter, C.D., Smajls, D., Sneed, A., Sodergren, R., Song, X.-Z., Sorrelle, R., Soza, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Uemami, K., Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczek, R., Wooden, H., Wolley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, J., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 188872)
Worley, K.C.
Direct Submission
Submitted (31-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 188872)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (09-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 19, 2002 this sequence version replaced gi:21737677.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Center: Baylor College of Medicine
Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

Project Information
Center project name: GPCC
Center clone name: CH230-267P22

Summary Statistics

Assembly program: Phrap; bases: 0.990339
Consensus quality: 177756 bases at least Q40
Consensus quality: 179112 bases at least Q30
Consensus quality: 179978 bases at least Q20
Estimated insert size: 191240; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1	185765:	contig of 185765 bp in length
*	185766	185865: gap of unknown length
*	185866	188872: contig of 3007 bp in length.

FEATURES

Bouice

misc_feature

misc_feature

misc_feature

misc_feature

ପ୍ରାର୍ଥନା

misc_feature

ORIGIN

	Query Match	100.0%	Score 14;	DB 14;	Length 188872;
	Best Local Similarity	78.6%	Pred. No. 3;	7e+03;	
	Matches	11;	Conservative	0;	Mismatches 0;
					Indels 0;
QY	1 CGUACUGCACTCG	14			
Db	60100 CGTACTGCNACTCG	60087			

RESULT 22

LOCUS	218764 bp	DNA	linear	HTG 13-MAY-2003
AC103229				
DEFINITION	Rattus norvegicus clone CH230-217018, WORKING DRAFT SEQUENCE.			

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISMS

REFERENCES

REFERENCE

AUTHORS

TITLE
JOURNAL
REFERENCE

JOURNAL

REFERENCE

JOURNAL

COMMENT

Allen, C., Allen, H., Alstbrooks, S., Amin, A., Anguiano, D., Anylabetsch, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bielawski, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bulay, C., Burch, P., Buttrill, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Cessar, H., Center, A., Chacra, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., L., Davis, C., Davy-Carroll, L., De Anda, C., Dedrich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Diya, K., Draper, H., Dugan-Bocsha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escoto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flisig, N., Forbes, L., Foster, M., Foster, P., Frazer, C.M., Gabbai, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebreyes, E., Geer, K., Giller, R., Grady, M., Guerra, M., Guenara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hernandez, J., Harvey, Y., Havlik, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladu, S. L., Hodgson, A., Hogues, M., Hollins, B., Howell, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, Z., Kowals, C., Kraft, C. L., Lebow, H., Levay, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Loreschne, L., Loulgesed, H., Lozada, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmood, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mathew, S., McLeod, M. P., McNeill, T. Z., Meenen, B., Mawhinney, S., McLeod, M. P., McNeill, T. Z., Meenen, B., Milosavljevic, A., Miner, G., Ming, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwackalameh, O., Okunnu, G., Olarinmugbon, A., Pal, S., Parke, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Plankoch, C., Plopper, F., Polndexter, A., Popovic, D., Primus, E., Pu, L., L., Puzo, M., Quiroz, F., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojals, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Saverly, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smales, D., Sneed, A., Sodergren, E., Song, X., Z., Sotelle, R., Sosa, J., Steinle, M., Thomas, R., Sutton, A., Svatek, A., Taber, P., Taylor, T., Taylor, T., Thomas, N., Tilton, S., Tingle, A., Trejos, Z., Uemari, K., Valas, R., Vera, V., Villaseca, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, P., Williams, G., Willson, R., Wlezyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, Y., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhuesen, A., Welles, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G., and Gibbs, R.A.

Direct Submissions

Unpublished

2 (bases 1 to 218764)

Worley, K.C.

Direct Submission

Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 218764)

Rat Genome Sequencing Consortium.

Direct Submissions

Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced g1:22856257.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgc.com.tmc.edu/projects/atlas/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome

shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Center project name: GUNO
Center clone name: CH230-217018

----- Summary Statistics
Assembly program: Atlas 3.0:

Consensus quality: 211841 bases at least Q40
Consensus quality: 213096 bases at least Q30
Consensus quality: 213870 bases at least Q20
Estimated insert size: 218571; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 218764: contig of 218764 bp in length.
Location/Qualifiers

FEATURES
source
1. 218764
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-217018"
1. 1339
/note="wgs_contig"

ORIGIN
misc_feature
/note="wgs_contig"

Query Match 100.0%; Score 14; DB 14; Length 218764;
Best Local Similarity 78.6%; Pred. No. 3.6e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUCG 14
||:|||||:|||||
Db 170317 CGTACTGCAACTCG 170304

RESULT 23
BX640547 230865 bp DNA linear VRT 29-JAN-2005
LOCUS Zebrafish DNA sequence from clone DKEX-4UJ1 in linkage group 14,
DEFINITION complete sequence.
ACCESSION BX640547
VERSION BX640547.35 GI:58331761
KEYWORDS HTG.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 230865)
Auger, K.
Direct Submission
Submitted (29-JAN-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfsh-help@sanger.ac.uk Clone requests: clonequest@sanger.ac.uk
On Jan 29, 2005 this sequence version replaced gi:57863663.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>

Contact: zfsh-help@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30)
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Bm: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPeP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep
Zebrafish pUC subclones occasionally display inconsistency over the
length of mononucleotide A/T runs and conserved TA repeats. Where
this is found the longest good quality representation will be
submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat
discovery system (Zhifeng Bao and Sean Rddy, submitted), and those
beginning 'dr' were identified by Rick Waterman (Stephen Johnson
lab, Mashu). For further information see
http://www.sanger.ac.uk/projects/D_rerio/fishmask.shtml DKEX-4UJ1
is from a Zebrafish BAC library
VECTOR: pindigoBAC-5.

FEATURES
source
1. 230865
Location/Qualifiers
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEX-4UJ1"
/clone_1fb="DanioKey"

ORIGIN

Query Match 100.0%; Score 14; DB 5; Length 230865;
Best Local Similarity 78.6%; Pred. No. 3.6e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUCG 14
||:|||||:|||||
Db 114950 CGTACTGCAACTCG 114963

RESULT 24
AC021883 232180 bp DNA linear HTG 25-AUG-2000
LOCUS Homo sapiens chromosome 1 clone RP11-588h15, *** SEQUENCING IN
DEFINITION PROGRESS ***, 40 unordered pieces.
ACCESSION AC021883
VERSION AC021883.4 GI:9910096
KEYWORDS HTG; HTGS PHASE1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Carcharia;
Homnidae; Homo.
1 (bases 1 to 232180)
Waterston, R.H.
The sequence of Homo sapiens clone
Unpublished
JOURNAL
TITLE
AUTHORS
REFERENCE
2 (bases 1 to 232180)
Waterston, R.H.
Direct Submission
Submitted (21-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

COMMENT

On Aug 25, 2000 this sequence version replaced gi:9838290.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 ----- Project Information -----
 Center project name: H_NH058H15
 ----- Summary Statistics -----
 Sequencing vector: M13, 86%
 Sequencing vector: plasmid, 14%
 Chemistry: Dye-terminator Big Dye, 14% of reads
 Assembly program: Phrap, version 0.990319
 Consensus quality: 211766 bases at least Q40
 Consensus quality: 217990 bases at least Q30
 Consensus quality: 221643 bases at least Q20
 Insert size: 181000; agarose-fp
 Insert size: 228280; sum-of-contigs
 Quality coverage: 6.35 in Q20 bases; agarose-fp
 Quality coverage: 4.69 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 40 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

```

1      1312: contig of 1312 bp in length
*      1313      1412: gap of unknown length
*      1413      2446: contig of 1034 bp in length
*      2447      2546: gap of unknown length
*      2547      3878: contig of 1332 bp in length
*      3879      3978: gap of unknown length
*      3979      5215: contig of 1237 bp in length
*      5216      5315: gap of unknown length
*      5316      6544: contig of 1229 bp in length
*      6545      6644: gap of unknown length
*      6645      7940: contig of 1296 bp in length
*      7941      8040: gap of unknown length
*      8041      9190: contig of 1150 bp in length
*      9191      9290: gap of unknown length
*      9291      10909: contig of 1619 bp in length
*      10910      11009: gap of unknown length
*      11010      12203: contig of 1194 bp in length
*      12204      12303: gap of unknown length
*      12304      13542: contig of 1239 bp in length
*      13543      13642: gap of unknown length
*      13643      14982: contig of 1340 bp in length
*      14983      15082: gap of unknown length
*      15083      16905: contig of 1823 bp in length
*      16906      17005: gap of unknown length
*      17006      18051: contig of 1046 bp in length
*      18052      18151: gap of unknown length
*      18152      19373: contig of 1222 bp in length
*      19374      19473: gap of unknown length
*      19474      20668: contig of 1195 bp in length
*      20669      20768: gap of unknown length
*      20769      22399: contig of 1631 bp in length
*      22400      22499: gap of unknown length
*      22500      24200: contig of 1701 bp in length
*      24201      24300: gap of unknown length
*      24301      25667: contig of 1367 bp in length
*      25668      25767: gap of unknown length
*      25768      27705: contig of 1938 bp in length
*      27706      27805: gap of unknown length
*      27806      29643: contig of 1838 bp in length
*      29644      29743: gap of unknown length
*      29744      31718: contig of 1975 bp in length
*      31719      31818: gap of unknown length
*      31819      33299: contig of 1481 bp in length

```

FEATURES

source

```

*      33300      33399: gap of unknown length
*      33400      35588: contig of 2189 bp in length
*      35589      35688: gap of unknown length
*      35689      37968: contig of 2280 bp in length
*      37969      38068: gap of unknown length
*      38069      40341: contig of 2273 bp in length
*      40342      40441: gap of unknown length
*      40442      42574: contig of 2133 bp in length
*      42575      42674: gap of unknown length
*      42675      44938: contig of 2264 bp in length
*      44939      45038: gap of unknown length
*      45039      50126: contig of 5088 bp in length
*      50127      50226: gap of unknown length
*      50227      52594: contig of 2368 bp in length
*      52595      52695: gap of unknown length
*      52695      57157: contig of 4462 bp in length
*      57157      57257: gap of unknown length
*      57257      61310: contig of 4054 bp in length
*      61311      61410: gap of unknown length
*      61411      65807: contig of 4397 bp in length
*      65808      65907: gap of unknown length
*      65908      70160: contig of 4253 bp in length
*      70161      70260: gap of unknown length
*      70261      76919: contig of 6659 bp in length
*      76920      77019: gap of unknown length
*      77020      85764: contig of 8745 bp in length
*      85765      85864: gap of unknown length
*      85865      106630: contig of 20766 bp in length
*      106631      134020: contig of 27290 bp in length
*      134021      134120: gap of unknown length
*      134121      165082: contig of 30962 bp in length
*      165083      165182: gap of unknown length
*      165183      196240: contig of 31058 bp in length
*      196241      232180: gap of unknown length
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Location/Qualifiers

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1413..2446 /note="assembly_name:Contig15"
2447..2546 /estimated_length=unknown
2547..3878 /note="assembly_name:Contig30"
3879..3978 /estimated_length=unknown
3979..5215 /note="assembly_name:Contig35"
5216..5315 /estimated_length=unknown
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6545..6644 /estimated_length=unknown
6645..7940 /note="assembly_name:Contig42"
7941..8040 /estimated_length=unknown
8041..9190 /note="assembly_name:Contig44"
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             /note="assembly_name:Contig152"
gap          13543. .13642
             /estimated_length=unknown
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gap          14583. .15082
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Best Local Similarity 78.6%; Pred. No. 3.6e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CGUACUGCAACUCG 14

Db 112822 CGTACTGCACACTCG 112809

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RESULT 25
BX294153/c      293350 bp   DNA      linear   BCT 17-APR-2005
LOCUS          Pirellula sp. strain 1 complete genome; segment 21/24.
DEFINITION     BX294153 BX119912
ACCESSION      BX294153.1 GI:32447383
VERSION        BX294153.1 GI:32447383
KEYWORDS       complete genome.
SOURCE          Rhodopirellula baltica SH 1
ORGANISM       Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
                Planctomycetaceae; Rhodopirellulalia.
REFERENCE      1 (bases 1 to 293350)
AUTHORS        Gloeckner,F.O., Kube,M., Bauer,M., Teeling,H., Lombardot,T.,
                Ludwig,W., Gade,D., Beck,A., Borzym,K., Heilmann,K., Rabus,R.,
                Schleener,H., Aumann,R. and Reinhardt,R.
TITLE          Complete genome sequence of the marine planctomycete Pirellula sp.
                strain 1
JOURNAL        Proc. Natl. Acad. Sci. U.S.A. 100 (14), 8298-8303 (2003)
PUBMED         12835416
REFERENCE      2 (bases 1 to 293350)
AUTHORS        Kube,M., Borzym,K., Heilmann,K., Klages,S., Marguardt,I.,
                Lohrack,S., Beck,A., Pawlik,R., Reinhardt,R., Gloeckner,F.O.,
                Bauer,M., Teeling,H., Lombardot,T., Ludwig,W., Gade,D., Rabus,R.,
                Schleener,H. and Aumann,R.
TITLE          Direct Submission
JOURNAL        Submitted (21-JAN-2003) Max Planck Institute for Molecular
                Genetics, ProScience Innestrasse 73, D-14195 Berlin, Germany Max
                Planck Institute for Marine Microbiology Celsiusstrasse 1, D-28359
                Bremen, Germany
COMMENT        This project was carried out by

```

FEATURES

source

gene

CDS

```

----- Summary Statistics -----
Sequencing vector: pUC19; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 7142841 bases at least Q40
Consensus quality: 7145138 bases at least Q30
Consensus quality: 7145484 bases at least Q20
Quality coverage: 8.03

-----
This sequence was finished as follows unless otherwise noted: all
regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid sequence; assembly was additionally confirmed by long
range PCR and cosmid end sequences.

-----
See http://www.micro-genomes.mpg.de/pirellula/ for more information
including minimal tiling path from a set of 220 cosmids out of
908. See the misc_feature tag below for the boundaries of the MTP
cosmids. ----- Annotation -----
Center: Max Planck Institute for Marine Microbiology
                Celsiusstrasse 1, D-28359 Bremen, Germany.
Center Code: MPI/M
Email: foggem@bremen.de
Phone: +49 (0)421 2028 938 Fax: +49 (0)421 2028 580

-----
Three different programs (Glimmer, Critica and Orpheus) were used
for ORF-prediction. A nonredundant list of ORFs was generated by
suitable parsing of the results.
Automated annotation was done with the software package Pedant Pro
(http://www.biomax.de). All ORF predictions and annotations were
manually corrected by considering all results of the different
tools applied. See http://www.regx.de for more information and
access to supplementary information.

----- Location/Qualifiers -----
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E=1e-07 gb:AA046412.1; AF096262.1 (AF096262) ER6 protein
[lycopersicon; E=1e-05 gb:AA04173.1; AB006246.3
(AB006246) conserved hypotheical; E=2e-05 CCG: MTH98;
CG00589 Universal stress protein Upa and related; E=1e-08
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/db_xref="UniProt/TREMBL:Q7UR82"
/translation="MRVLAVDSPYSQOAVFASHLPLRKPFDVLVAVPMVLD
TSGKMPNDPGSFLRTETRRERDAIDAVSDKSDHRSYVTHVPIQPSALIDVA
DSGADLVGAIHSAIRVILGVSVDYVAITHADSTTVAPPTSEADVPEPLQKIM
ALSGRPERMLTWLRRLKLRPNEVHLVRDPSYKQDLRQOASDAMQAOHROAQ

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gene
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SL11388; E=2e-05 gb:AGG20091.1; (AE005088) Vng1898c
Halobacterium sp. NRC-1; E=5e-05 swissprot:Q57951;
Y531_METUA HYPOTHEICAL PROTEIN M00531 -----; E=7e-04 COG:
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GLFSRAVILVSNASDIALPDVVALRVLVPCNEVILVVMETHPEYELHLKVAAYV
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(AF273214) Saar [Myxococcus xanthus]; E=3e-83
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REGULATOR; E=1e-81 gb:AAC28085.1; (AR100457) response
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/db_xref="InterPro:IPR003593"
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LMSHAKVAPTRFVPLVIGSGSVKAVARSVOOSDLADRFVTINCAPLAOLVIG
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[illegible]

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DEFINITION Sequence 39 from Patent EP1260592.
ACCESSION AX988576
VERSION AX988576.1 GI:40994900
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1
  AUTHORS Donner,H., Drescher,B., Huber,A. and Weber,J.
  TITLE Biochip
  JOURNAL Patent: EP 1260592-A 39 27-NOV-2002;
  MMG - Biotech AG (DE)
FEATURES
  source
    1..100
    /organism="Escherichia coli"
    /mol_type="unassigned DNA"
    /db_xref="taxon:562"
    /note="y0jh b2211 U00096 complement(2303128__2304774)"
ORIGIN
  Query Match          92.9%; Score 13; DB 6; Length 100;
  Best Local Similarity 76.9%; Pred. No. 3.1e+04;
  Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCACTCG 14
Db 14 GTACTGCACTCG 2

RESULT 28
AX988577/c
LOCUS AX988577 100 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 40 from Patent EP1260592.
ACCESSION AX988577
VERSION AX988577.1 GI:40994901
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1
  AUTHORS Donner,H., Drescher,B., Huber,A. and Weber,J.
  TITLE Biochip
  JOURNAL Patent: EP 1260592-A 40 27-NOV-2002;
  MMG - Biotech AG (DE)
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    /db_xref="taxon:562"
    /note="y0jh b2211 U00096 complement(2303128__2304774)"
ORIGIN
  Query Match          92.9%; Score 13; DB 6; Length 100;
  Best Local Similarity 76.9%; Pred. No. 3.1e+04;
  Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCACTCG 14
Db 52 GTACTGCACTCG 40

RESULT 29
AF069774
LOCUS AF069774 186 bp mRNA linear ROD 23-JUL-1998
DEFINITION Mus musculus chaplyn-110 mRNA, partial cds.
ACCESSION AF069774
VERSION AF069774.1 GI:3335542
KEYWORDS
SOURCE
ORGANISM
  Mus musculus (house mouse)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE
  1 (bases 1 to 186)
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Murioidea; Muridae; Murinae; Mus.
  AUTHORS Watanabe,M.
  TITLE Mouse chaplyn-110 partial cDNA
  JOURNAL Unpublished
  REFERENCE 2 (bases 1 to 186)
  Watanabe,M.
  AUTHORS
  JOURNAL Direct Submission
  Submitted (03-JUN-1998) Anatomy, Hokkaido University School of
  Medicine, N15W7, Kita-ku, Sapporo 060-8638, Japan
FEATURES
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ORIGIN
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  Best Local Similarity 76.9%; Pred. No. 2.9e+04;
  Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCACTCG 14
Db 146 GTACTGCACTCG 158

RESULT 30
TRBPRTNB/c
LOCUS TRBPRTNB 200 bp mRNA linear INV 18-JUL-1994
DEFINITION Trypanosoma brucei clone TBPk-A2 protein kinase mRNA, partial cds.
ACCESSION L10992
VERSION L10992.1 GI:310958
KEYWORDS
SOURCE
ORGANISM
  Trypanosoma brucei
  Trypanosoma brucei
  Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
  Trypanosoma.
  REFERENCES
    1 (bases 1 to 200)
    Hua,S.B. and Wang,C.C.
    Differential accumulation of a protein kinase homolog in
    Trypanosoma brucei
    J. Cell. Biochem. 54 (1), 20-31 (1994)
  JOURNAL PUBMED
  8126084
  COMMENT Original source text: Trypanosoma brucei strain TRU667 mRNA.
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ORIGIN APEIIGSRGHSYEDVWAFGV"

Query Match 92.9%; Score 13; DB 2; Length 200;
Best Local Similarity 76.9%; Pred. No. 2.9e+04;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13
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88 CGTACTGCAACTC 76

RESULT 31
AF232912 327 bp mRNA linear PRI 12-MAR-2000
LOCUS Macaca mulatta clone MNAV10-1 T-cell receptor alpha chain mRNA,
DEFINITION partial cds.
ACCESSION AF232912
VERSION AF232912.1 GI:7229664
KEYWORDS
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecoidea; Macaca.
REFERENCE 1 (bases 1 to 327)
AUTHORS Han, M., Nhu, Q., Folley, S. and Robinson, M.A.
JOURNAL Full Length cDNA of Rhesus Macaque TCR- α Genes
Unpublished
REFERENCE 2 (bases 1 to 327)
AUTHORS Han, M., Nhu, Q., Folley, S. and Robinson, M.A.
JOURNAL Direct Submission
Submitted (09-FEB-2000) Laboratory of Immunogenetics, NIAID, 12441
Parklawn Drive, Rockville, MD 20852, USA
FEATURES
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GLYLNG"

ORIGIN

Query Match 92.9%; Score 13; DB 8; Length 327;
Best Local Similarity 76.9%; Pred. No. 2.7e+04;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13
||:|||||:
116 CGTACTGCAACTC 128

RESULT 32
AY011660 398 bp DNA linear PRI 07-FEB-2001
LOCUS Ateles fusciceps cAMP responsive element moderator (CREM) gene,
DEFINITION partial cds.
ACCESSION AY011660
VERSION AY011660.1 GI:12699921
KEYWORDS
SOURCE Ateles fusciceps (brown-headed spider monkey)
ORGANISM Ateles fusciceps
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;
Cebidae; Ateleinae; Ateles.
REFERENCE 1 (bases 1 to 398)

AUTHORS Murphy, W.J., Bizirik, B., Johnson, W.B., Zhang, Y.P., Ryder, O.A. and O'Brien, S.J.
TITLE Molecular phylogenetics and the origins of placental mammals
JOURNAL Nature 409 (6820), 614-618 (2001)
PUBMED 11214319
REFERENCE 2 (bases 1 to 398)
AUTHORS Murphy, W.J., Bizirik, B., Johnson, W.B., Zhang, Y.P. and O'Brien, S.J.
JOURNAL Direct Submission
Submitted (01-NOV-2000) Laboratory of Genomic Diversity, National
Cancer Institute-FCRDC, P.O. Box B, Bldg. 560, Rm. 11-10,
Frederick, MD 21702, USA
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ORIGIN

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Best Local Similarity 76.9%; Pred. No. 2.7e+04;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACUC 14
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357 GYACTGCAACTCG 345

RESULT 33
MACTCRAAL 406 bp mRNA linear PRI 13-JAN-1995
LOCUS Macaca mulatta (clone VA1089) T-cell receptor alpha (TCR A) mRNA,
DEFINITION 5' end of cds.
ACCESSION L38870
VERSION L38870.1 GI:623116
KEYWORDS T-cell receptor alpha.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecoidea; Macaca.
REFERENCE 1 (bases 1 to 406)
AUTHORS Chen, Z.W.
JOURNAL Macaca mulatta TCR alpha chain sequences
Unpublished (1995)
COMMENT Original source text: Macaca mulatta cDNA to mRNA.
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1..406
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/gene="TCR A"
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Itcho, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
Kishikawa-Hirocane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ono, M., Osato, N.,
Ota, Y., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
Sasaki, D., Sato, K., Shibata, C., Shingawa, A., Shirai, T.,
Sogabe, Y., Tagami, M., Tagami, T., Taneda, Y., Tagawa, A., Takahashi, F.,
Takahara-Nakamura, S., Tanaka, I., Tomatsu, A., Toyota, T., Waki, K.,
Tasunishi, A., and Hayashizaki, Y.

```

location/Qualifiers
1..580
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="002-180-C10"

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ORIGIN

Query Match	92.9%	Score 13;	DB 15;	length 580;
Best Local Similarity	76.9%	Pred. No	2.6e+04;	
Matches 10;	Conservative	3;	Mismatches 0;	Indels 0;
			Gaps	0;

QY	2	GUACUGCAACTCG	14
		: : : : : :	
Db	181	GTACTGCAACTCG	193

RESULT 36	LOCUS	615 bp	DNA	linear	BCT 07-JAN-2003
AY136528	AY136528				
DEFINITION	Acidovorax sp. A-07-20 16S ribosomal RNA gene, partial sequence.				

```

/organism="Acidovorax sp. A-07-20"
/mol_type="genomic DNA"
/db_xref="taxon:208167"
/clone="A-07-20"
/country="Canada: Alert"
/notes="aerobic PAH enrichment culture at 7 deg C"
<1..>615
/product="16S ribosomal RNA"
rRNA

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ORIGIN

Query Match	92.9%	Score 13	DB 1	Length 615
Best Local Similarity	76.9%	Pred. No. 2.5e+04		
Matches 10	Conservative	3	Mismatches 0	Indels 0
			Gaps	0

QY 2 GUACUGCAACUGG 14
|:|:|:|:|:|:|:
Db 418 GTACTGCAACTCG 430

RESULT 37

SV502883/c	620 bp	DNA	linear	STS 07-APR-2005
LOCUS				
DEFINITION	g1y90ell.g1	Clnt Pan troglodytes	versus	sns genomic, sequence
				tagged site.
ACCESSION	SV502883			
VERSION	SV502883.1	GI:62346625		
KEYWORDS				
SOURCE	STS.			
ORGANISM	Pan troglodytes	versus		
	Pan troglodytes	versus		
	Pan troglodytes	versus		
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
	Hominidae; Pan.			
REFERENCE	1 (bases 1 to 620)			
AUTHORS	Mikkelsen,T.S., Hillier,W.L., Eichler,B.E., Zody,M.C. and			
	Jaffe,D.B.			
TITLE	Initial Sequence of the Chimpanzee Genome and Comparison with the			
JOURNAL	Human Genome			
COMMENT	Unpublished (2005)			

FEATURES
SOURCE

STS

Query Match

92.9%; Score 13; DB 10; Length 620;

than 100 NOS bases or with SNP rate > 0.01 were discarded. To exclude alignment between two copies of a single read, comparisons between two reads that share 95% of their genome alignments (>=95% bases of read A and >=95% bases of read B were placed at the same locus of human genome) were discarded.

FEATURES

source

1..742
/organism="Pan troglodytes troglodytes"
/mol_type="genomic DNA"
/sub_species="troglodytes"
/db_xref="taxon:37011"
/clone_1ib="Noemie"
<1..>742

ORIGIN

STS

Query Match 92.9%; Score 13; DB 10; Length 742;
Best Local Similarity 76.9%; Pred. No. 2.5e+04;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13
||:|||||:
Db 278 CGTACTGCAACTC 266

RESULT 40

BV530657

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BV530657 768 bp DNA linear STS 08-APR-2005
G591P617906R7.T0 Clint Pan troglodytes versu STS genomic, sequence tagged site.

BV530657 1 GI:62408441

SOURCE

Pan troglodytes versu

Pan troglodytes versu

Pan troglodytes versu

Pan troglodytes versu

Pan troglodytes versu

Pan troglodytes versu

Pan troglodytes versu

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Pan troglodytes versu

Pan troglodytes versu

Pan troglodytes versu

Pan troglodytes versu

Pan troglodytes versu

the read have Phred score >= 25), and the read must have at least 200 bp SNOS (30,25) bases. Reads not uniquely placed in the genome and read pairs whose two ends were not consistently placed were discarded. After above filtering, NOS (30,25) standard was applied to all pairs of overlapping reads to call NOS bases and SNPs. Alignments (between two reads) with less than 100 NOS bases or with SNP rate > 0.01 were discarded. To exclude alignment between two copies of a single read, comparisons between two reads that share 95% of their genome alignments (>=95% bases of read A and >=95% bases of read B were placed at the same locus of human genome) were discarded.

FEATURES

source

1..768
/organism="Pan troglodytes versu"
/mol_type="genomic DNA"
/sub_species="versu"
/db_xref="taxon:37012"
/clone_1ib="Clint"
<1..>768

ORIGIN

STS

Query Match 92.9%; Score 13; DB 10; Length 768;
Best Local Similarity 76.9%; Pred. No. 2.5e+04;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACUCG 14
||:|||||:
Db 701 GTACTGCAACTCG 713

RESULT 41

BV530662

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BV530662 773 bp DNA linear STS 08-APR-2005
G591P617904R12.T0 Clint Pan troglodytes versu STS genomic, sequence tagged site.

BV530662 1 GI:62408446

SOURCE

Pan troglodytes versu

Pan troglodytes versu

Pan troglodytes versu

Pan troglodytes versu

Pan troglodytes versu

Pan troglodytes versu

Pan troglodytes versu

Pan troglodytes versu

Pan troglodytes versu

Pan troglodytes versu

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Pan troglodytes versu

Pan troglodytes versu

Pan troglodytes versu

Pan troglodytes versu

Pan troglodytes versu

Pan troglodytes versu

Pan troglodytes versu

(Gon,Unknown Chimp). Common names: Pan troglodytes versus is the western chimp and Pan troglodytes troglodytes is the central chimp. To be included in chimpanzee SNP discovery, a read must be at least 500bp in length, at least 50% of its base calls must have Phred score >= 20, at least 30% of its base calls must satisfy SNOS(30,25) (single strand NOS, the base in question has Phred score >= 30, the surrounding 10 bases in the read have Phred score >= 25), and the read must have at least 200 bp SNOS(30,25) bases. Reads not uniquely placed in the genome and read pairs whose two ends were not consistently placed were discarded. After above filtering, NOS(30,25) standard was applied to all pairs of overlapping reads to call NOS bases and SNPs. Alignments (between two reads) with less than 100 NOS bases or with SNP rate > 0.01 were discarded. To exclude alignment between two copies of a single read, comparisons between two reads that share 95% of their genome alignments (>95% bases of read A and >95% bases of read B were placed at the same locus of human genome) were discarded.

FEATURES
source
1. .773
/organism="Pan troglodytes versus"
/mol_type="genomic DNA"
/sub_species="versus"
/db_xref="taxon:37012"
/clone_1fb="Clint"
<1. .>773

ORIGIN
STS

Query Match 92.9%; Score 13; DB 10; Length 773;
Best Local Similarity 76.9%; Pred. No. 2.5e+04;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACTGCAACG 14
Db 711 GTACTGCACTCG 723

RESULT 42
BV530664 774 bp DNA linear STS 08-APR-2005
LOCUS GS91P617902RB6.T0 Clint Pan troglodytes versus STS genomic, sequence tagged site.
ACCESSION BV530664
VERSION BV530664.1 GI:62408448
KEYWORDS STS.
SOURCE Pan troglodytes versus
ORGANISM Pan troglodytes versus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Pan.
1 (bases 1 to 774)
Uatte,D.B.
Initial Sequence of the Chimpanzee Genome and Comparison with the Human Genome
Unpublished (2005)

JOURNAL COMMENT
Contact: Michael C. Zody
Broad Institute of MIT and Harvard
320 Charles Street, Cambridge, MA 02141, USA
Tel: 6172580933
Fax: 6172580903
Email: mczody@broad.mit.edu
Primer A: No sequence submitted
Primer B: No sequence submitted
STS size: 774

Protocol:
23,021,928 chimpanzee whole genome shotgun reads were aligned to the Human genome NCBI Build 34 (hg16, July 2003). Chimp WGS reads were from 9 donors, including Clint (Pan troglodytes versus), 3 other Pan troglodytes versus chimps (Donald,Karlén,Yvonne), 3 Pan troglodytes troglodytes chimps (Noemie,Masuku,Clara) and 2 chimps of unknown origin (Gon,Unknown Chimp). Common names: Pan troglodytes versus is the western chimp and Pan troglodytes troglodytes is the central chimp. To be included in chimpanzee SNP discovery, a read must be at least 500bp in length, at least 50% of its base calls must have Phred score >= 20, at least 30% of its base calls must satisfy SNOS(30,25) (single strand NOS, the base in question has Phred score >= 30, the surrounding 10 bases in the read have Phred score >= 25), and the read must have at least 200 bp SNOS(30,25) bases. Reads not uniquely placed in the genome and read pairs whose two ends were not consistently placed were discarded. After above filtering, NOS(30,25) standard was applied to all pairs of overlapping reads to call NOS bases and SNPs. Alignments (between two reads) with less than 100 NOS bases or with SNP rate > 0.01 were discarded. To exclude alignment between two copies of a single read, comparisons between two reads that share 95% of their genome alignments (>95% bases of read A and >95% bases of read B were placed at the same locus of human genome) were discarded.

FEATURES
source
1. .774
/organism="Pan troglodytes versus"
/mol_type="genomic DNA"
/sub_species="versus"
/db_xref="taxon:37012"
/clone_1fb="Clint"
<1. .>774

ORIGIN
STS

Query Match 92.9%; Score 13; DB 10; Length 774;
Best Local Similarity 76.9%; Pred. No. 2.5e+04;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACTGCAACG 14
Db 707 GTACTGCACTCG 719

RESULT 43
D64054 939 bp mRNA linear VRT 01-FEB-2000
LOCUS Myxine glutinosa mRNA for IMPX of hagfish, complete cds.
DEFINITION D64054
ACCESSION D64054.1 GI:1405320
VERSION D64054.1 GI:1405320
KEYWORDS low molecular mass polypeptide, IMPX.
SOURCE Myxine glutinosa (Atlantic hagfish)
ORGANISM Myxine glutinosa
Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes; Myxiniidae; Myxiniinae; Myxine.

JOURNAL COMMENT
Contact: Michael C. Zody
Broad Institute of MIT and Harvard
320 Charles Street, Cambridge, MA 02141, USA
Tel: 6172580933
Fax: 6172580903
Email: mczody@broad.mit.edu
Primer A: No sequence submitted
Primer B: No sequence submitted
STS size: 774

AUTHORS Kasahara, M.
TITLE Direct Submission
JOURNAL Submitted (04-SEP-1995) Masanori Kasahara, Hokkaido University School of Medicine, Biochemistry, Kita 15 Nishi 7, Sapporo, Hokkaido 060, Japan (Tel:011-706-5047, Fax:011-717-5286)
FEATURES Location/Qualifiers
 source
 1.939
 /organism="Myxine glutinosa"
 /mol_type="mRNA"
 /db_xref="taxon:7769"
 /clone="HF2-1-1"
 /issue_type="Liver blood cell"
 /clone_lib="Uni-ZAP XR"
 1.12
 5'UTR
 CDS
 13..834
 /codon_start=1
 /product="LMPX of hagfish"
 /protein_id="BA10931.1"
 /db_xref="GI:1405321"
 /translation="MALAVCGVREIARLPLEHREGRGELQALGSLHQSFAIP
 KGLDPEFLKPRASGESDYKIEFHHTTTLAFKFDHGVVAVDSRATGASYASQTVK
 KYEINPYLGTAGAACDMWERVLNHRITELRNRLSVAAASFLANMYOY
 KKGSLMGTMICGMDRGPGLYVDEGRRLSGMFAVSGSTYAVGVDSNRPMT
 PEAYDLGRRALCHATHRDAYSQVNVLYHMOOSGWIKYVSQNDVSELQKFEEN"
 223..831
 /product="mature LMPX of hagfish"
 835..939
 919..924
ORIGIN
 3'UTR
 polyA_signal
 919..924
Query Match 92.9%; Score 13; DB 5; Length 939;
Best Local Similarity 76.9%; Pred. No. 2.4e+04;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 2 GUACUGCAACUCG 14
 ||:|||||:
 ||:|||||:
Db 813 GTRCTGCACTCG 801
RESULT 44
LOCUS BV550217 971 bp DNA linear STS 09-APR-2005
DEFINITION S21SF60320MD6.T0 Clara Pan troglodytes troglodytes STS genomic,
 sequence tagged site.
ACCESSION BV550217
VERSION BV550217
KEYWORDS STS.
SOURCE Pan troglodytes troglodytes
ORGANISM Pan troglodytes troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominoidea; Pan.
REFERENCE 1 (bases 1 to 971)
AUTHORS Mikkelson, T.S., Hillier, W.L., Bichler, E.E., Zody, M.C. and
 Jaffe, D.B.
TITLE Initial Sequence of the Chimpanzee Genome and Comparison with the
 Human Genome
JOURNAL Unpublished (2005)
COMMENT Contact: Michael C. Zody
 Broad Institute of MIT and Harvard
 320 Charles Street, Cambridge, MA 02141, USA
 Tel: 6172580933
 Fax: 6172580903
 Email: mczody@broad.mit.edu
 Primer A: No sequence submitted
 Primer B: No sequence submitted
 STS size: 971
 Protocol:
 23,021,928 chimpanzee whole genome shotgun reads were aligned to
 the Human genome NCBI
 Build 34 (hg16, July 2003). Chimp WGS reads were from 9 donors,
 including Clint (Pan

troglodytes verus), 3 other Pan troglodytes verus chimps
 (Donald, Karlien, Yvonne), 3 Pan
 troglodytes troglodytes chimps (Noemie, Masuku, Clara) and 2 chimps
 of unknown origin
 (Gon, Unknown Chimp). Common names: Pan troglodytes verus is the
 western chimp and Pan
 troglodytes troglodytes is the central chimp. To be included in
 chimpanzee SNP discovery, a
 read must be at least 500bp in length, at least 50% of its base
 calls must have Phred
 score >= 20, at least 30% of its base calls must satisfy
 SNOS(30,25) (single strand NOS, the
 base in question has Phred score >= 30, the surrounding 10 bases in
 the read have Phred
 score >= 25), and the read must have at least 200 bp SNOS(30,25)
 bases. Reads not uniquely
 placed in the genome and read pairs whose two ends were not
 consistently placed were
 discarded. After above filtering, NOS(30,25) standard was applied
 to all pairs of
 overlapping reads to call NOS bases and SNPs. Alignments (between
 two reads) with less
 than 100 NOS bases or with SNP rate > 0.01 were discarded. To
 exclude alignment between two
 copies of a single read, comparisons between two reads that share
 95% of their genome
 alignments (>=95% bases of read A and >=95% bases of read B were
 placed at the same locus
 of human genome) were discarded.
LOCATION/Qualifiers
 1..971
 /organism="Pan troglodytes troglodytes"
 /mol_type="genomic DNA"
 /sub_species="troglodytes"
 /db_xref="taxon:37011"
 /clone_lib="Clara"
 <1..>971
ORIGIN
 STS
Query Match 92.9%; Score 13; DB 10; Length 971;
Best Local Similarity 76.9%; Pred. No. 2.4e+04;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 2 GUACUGCAACUCG 14
 ||:|||||:
 ||:|||||:
Db 718 GTRCTGCACTCG 730
RESULT 45
LOCUS E38273 1197 bp DNA linear PAT 31-JAN-2002
DEFINITION Formate dehydrogenase gene, recombinant vector containing the same,
 transformant containing the vector and process for producing
 formate dehydrogenase by using the transformant.
ACCESSION E38273
VERSION E38273.1 GI:18626965
KEYWORDS JP 2000245471-A/1.
SOURCE Hypomicrobium sp.
ORGANISM Hypomicrobium sp.
 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 Hypomicrobiales; Hypomicrobium.
REFERENCE 1 (bases 1 to 1197)
AUTHORS Mitsunaga, T., Tanaka, Y., Yoshida, T. and Watanabe, K.
TITLE Formate dehydrogenase gene, recombinant vector containing the same,
 transformant containing the vector and process for producing
 formate dehydrogenase by using the transformant
JOURNAL Patent: JP 2000245471-A 1 12-SEP-2000;
COMMENT UNITIKA LTD
 OS Hypomicrobium sp.
 PN JP 2000245471-A/1
 PD 12-SEP-2000
 PR 01-MAR-1999 JP 1999052548

PI TOSHIRO MITSUNAGA, YASUHIRO TANAKA, TOYOKAZU YOSHIDA, PI
KATSUMI MATANABE
PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/02, PC
C12N15/00, C12N5/00
CC
FH Key Location/Qualifiers
FT Source 1. .1197
FT /organism="Hyphomicrobium sp.".
Location/Qualifiers
1. .1197
/organism="Hyphomicrobium sp."
/mol_type="genomic DNA"
/db_xref="taxon:82"

ORIGIN
Query Match 92.9%; Score 13; DB 6; Length 1197;
Best Local Similarity 76.9%; Pred. No. 2.4e+04; Mismatches 0; Gaps 0;
Matches 10; Conservative 3; Indels 0;

QY 1 CGUACUGCAACUC 13
|||:|||||:
Db 431 CGTACTGCAACTC 443

RESULT 46 1241 bp DNA linear BCT 15-APR-2005
LOCUS Klebsiella pneumoniae ompK36 gene, strain 103624.
KPN344089
AJ344089
AJ344089.2 GI:21912942
ompK36 gene; OmpK36 protein; porin.
Klebsiella pneumoniae
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.

REFERENCE
AUTHORS Crowley, B., Benedi, V.J. and Domenech-Sanchez, A.
TITLE Expression of SHV-2 beta-lactamase and of reduced amounts of OmpK36
porin in Klebsiella pneumoniae results in increased resistance to
cephalosporins and carbapenems
JOURNAL Antimicrob. Agents Chemother. 46 (11), 3679-3682 (2002)
PUBMED 12384391

REFERENCE
AUTHORS Domenech-Sanchez, A.
TITLE Direct Submission
JOURNAL Submitted (09-AUG-2001) Domenech-Sanchez A., Biologia, Area de
Microbiologia, Universitat de les Illes Balears and IMEDDA
(CSIC-UIB), Carretera de Valldemossa, km 7,5; Palma de Mallorca,
07071, SPAIN

REMARK
REFERENCE 3 (bases 1 to 1241)
AUTHORS Domenech-Sanchez, A.
TITLE Direct Submission
JOURNAL Submitted (15-JUL-2002) Domenech-Sanchez A., Biologia, Area de
Microbiologia, Universitat de les Illes Balears and IMEDDA
(CSIC-UIB), Carretera de Valldemossa, km 7,5; Palma de Mallorca,
07071, SPAIN

COMMENT
FEATURES
source
On Jul 20, 2002 this sequence version replaced gi:15149830.
Location/Qualifiers

1. .1241
/organism="Klebsiella pneumoniae"
/mol_type="genomic DNA"
/isolate="103624"
/db_xref="taxon:573"
/country="United Kingdom"
117. .1235
/gene="ompK36"
117. .1235
/gene="ompK36"
/function="porin"
/codon_start=11
/transl_table=11
/product="OmpK36 protein"

/protein_id="CAC50885.1"
/db_xref="GI:15149831"
/db_xref="GOA:093K39"
/db_xref="InterPro:IPR001702"
/db_xref="InterPro:IPR001897"
/db_xref="InterPro:IPR003229"
/db_xref="UniProt/TREMBL:Q93K39"
/translation="MKVKVLSILVPLALVAGAAANAALYNNKDGNTLDYGIKDLHYF
SDKSGDQGTVMR/VGVKGETOINDLTGYGMEYNOANNTSSSDQAMTRLAPAGL
KRGDAGSPDYGNNVGVVYDVTSMVDLPFGDGTYSNPLQSRANGVATYRNDPFG
LYDGLNPLQYGRKNGSISGSETSPNNRGLKONGGPGFGLTYDIDYDGSAGPAY
CNSKNGQDNRLDKRGDGNALRTYTGALTANNITLATOYTITNATRPSGSGSDSI
SGFANKAQNFEVVAQYQDFGLRPSVAALQSGKQIEGDDDLKYVDVGVATYVFNK
NMSTVYDKINLIDENDPFRSAGISTDVALGLVYGF"
117. .179
/gene="ompK36"
180. .1232
/gene="ompK36"
/product="mature OmpK36 protein"
/function="porin"

ORIGIN

Query Match 92.9%; Score 13; DB 1; Length 1241;
Best Local Similarity 76.9%; Pred. No. 2.4e+04; Mismatches 0; Gaps 0;
Matches 10; Conservative 3; Indels 0;

QY 1 CGUACUGCAACUC 13
|||:|||||:
Db 766 CGTACTGCAACTC 778

RESULT 47 1330 bp DNA linear BCT 06-JUN-2003
LOCUS Enterobacter sp. 22 partial 16S rRNA gene, isolate 22.
ESP308467
AJ308467
AJ308467.1 GI:15551737
16S ribosomal RNA; 16S rRNA gene.
Enterobacter sp. 22
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Enterobacter.

REFERENCE
AUTHORS Soutourina, O.A., Semenova, E.A., Parfenova, V.V., Danchin, A. and
Bertin, P.
TITLE Control of bacterial motility by environmental factors in polarly
flagellated and peritrichous bacteria isolated from Lake Baikal
JOURNAL Appl. Environ. Microbiol. 67 (9), 3852-3859 (2001)
PUBMED 11525977

REFERENCE
AUTHORS Soutourina, O.A.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-2001) Soutourina O.A., Biochimie et genetique
moleculaire, Pasteur Institute, Institut Pasteur, 28, rue du Dr.
Roux, 75724 Paris cedex 15, FRANCE

FEATURES
source
1. .1330
/organism="Enterobacter sp. 22"
/mol_type="genomic DNA"
/isolate="22"
/db_xref="taxon:151779"
/country="Russia:Lake Baikal"
1. .1330
/gene="16S rRNA"
1. .1330
/gene="16S rRNA"
/product="16S ribosomal RNA"

ORIGIN

Query Match 92.9%; Score 13; DB 1; Length 1330;
Best Local Similarity 76.9%; Pred. No. 2.3e+04; Mismatches 0; Gaps 0;
Matches 10; Conservative 3; Indels 0;

QY 2 GUACUGCACTCG 14
 Db 1250 GTACTGCACTCG 1262

RESULT 48
 AY985960
 LOCUS 1347 bp DNA linear ENV 25-APR-2005
 DEFINITION Uncultured bacterium clone D259 16S ribosomal RNA gene, partial
 sequence.

ACCESSION AY985960
 VERSION AY985960.1 GI:62765450
 KEYWORDS ENV.
 SOURCE uncultured bacterium
 ORGANISM Bacteria; environmental samples.

REFERENCE 1 (bases 1 to 1347)
 Eckburg, P.B., Bik, E.M., Bernstein, C.N., Purdom, E., Dethlefsen, L., Sargent, M., Gill, S.R., Nelson, K.E. and Relman, D.A.
 Diversity of the human intestinal microbial flora

TITLE Unpublished
 JOURNAL (bases 1 to 1347)
 Eckburg, P.B., Bik, E.M., Bernstein, C.N., Purdom, E., Dethlefsen, L., Sargent, M., Gill, S.R., Nelson, K.E. and Relman, D.A.
 Direct Submission

TITLE Submitted (28-MAR-2005) Division of Infectious Diseases & Geographic Medicine, Stanford University School of Medicine, 300 Pasteur Drive, Palo Alto, CA 94305, USA
 JOURNAL location/Qualifiers

FEATURES
 source 1.1347
 /organism="uncultured bacterium"
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REFERENCE 1 (bases 1 to 1356)
 Eckburg, P.B., Bik, E.M., Bernstein, C.N., Purdom, E., Dethlefsen, L., Sargent, M., Gill, S.R., Nelson, K.E. and Relman, D.A.
 Diversity of the human intestinal microbial flora

TITLE Unpublished
 JOURNAL (bases 1 to 1356)
 Eckburg, P.B., Bik, E.M., Bernstein, C.N., Purdom, E., Dethlefsen, L., Sargent, M., Gill, S.R., Nelson, K.E. and Relman, D.A.
 Direct Submission

TITLE Submitted (28-MAR-2005) Division of Infectious Diseases & Geographic Medicine, Stanford University School of Medicine, 300 Pasteur Drive, Palo Alto, CA 94305, USA
 JOURNAL location/Qualifiers

FEATURES

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 KEYWORDS ENV.
 SOURCE uncultured bacterium
 ORGANISM Bacteria; environmental samples.

REFERENCE 1 (bases 1 to 1357)
 Eckburg, P.B., Bik, E.M., Bernstein, C.N., Purdom, E., Dethlefsen, L., Sargent, M., Gill, S.R., Nelson, K.E. and Relman, D.A.
 Diversity of the human intestinal microbial flora

TITLE Unpublished
 JOURNAL (bases 1 to 1357)
 Eckburg, P.B., Bik, E.M., Bernstein, C.N., Purdom, E., Dethlefsen, L., Sargent, M., Gill, S.R., Nelson, K.E. and Relman, D.A.
 Direct Submission

TITLE Submitted (28-MAR-2005) Division of Infectious Diseases & Geographic Medicine, Stanford University School of Medicine, 300 Pasteur Drive, Palo Alto, CA 94305, USA
 JOURNAL location/Qualifiers

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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189	12.4	68.9	563	6	US-09-925-065A-918343	Sequence 918343,
190	12.4	68.9	563	6	US-09-925-065A-918344	Sequence 918344,
191	12.4	68.9	563	6	US-09-925-065A-918345	Sequence 918345,
192	12.4	68.9	563	6	US-09-925-065A-945084	Sequence 945084,
193	12.4	68.9	571	6	US-09-925-065A-920327	Sequence 920327,
194	12.4	68.9	571	6	US-09-925-065A-920328	Sequence 920328,
195	12.4	68.9	573	6	US-09-925-065A-93567	Sequence 93567,
196	12.4	68.9	580	6	US-09-925-065A-958466	Sequence 958466,
197	12.4	68.9	580	6	US-09-925-065A-958467	Sequence 958467,
198	12.4	68.9	581	6	US-09-925-065A-17051	Sequence 17051, A
199	12.4	68.9	600	12	US-11-136-527-7877	Sequence 7877, Ap
200	12.4	68.9	604	6	US-09-925-065A-473855	Sequence 473855,
201	12.4	68.9	604	6	US-09-925-065A-473856	Sequence 473856,
202	12.4	68.9	605	6	US-09-925-065A-859285	Sequence 859285,
203	12.4	68.9	606	6	US-09-925-065A-926510	Sequence 926510,
204	12.4	68.9	610	6	US-09-925-065A-945162	Sequence 945162,
205	12.4	68.9	610	6	US-09-925-065A-927605	Sequence 927605,
206	12.4	68.9	612	6	US-09-925-065A-926508	Sequence 926508,
207	12.4	68.9	612	6	US-09-925-065A-926509	Sequence 926509,
208	12.4	68.9	616	6	US-09-925-065A-932891	Sequence 932891,
209	12.4	68.9	629	6	US-09-925-065A-923734	Sequence 923734,
210	12.4	68.9	629	6	US-09-925-065A-901337	Sequence 901337,
211	12.4	68.9	631	6	US-09-925-065A-771833	Sequence 771833,
212	12.4	68.9	631	6	US-09-925-065A-771834	Sequence 771834,
213	12.4	68.9	632	6	US-09-925-065A-332575	Sequence 332575,
214	12.4	68.9	639	6	US-09-925-065A-947700	Sequence 947700,
215	12.4	68.9	639	6	US-09-925-065A-947701	Sequence 947701,
216	12.4	68.9	664	6	US-09-925-065A-953551	Sequence 953551,
217	12.4	68.9	707	6	US-09-925-065A-921419	Sequence 921419,
218	12.4	68.9	707	6	US-09-925-065A-946535	Sequence 946535,
219	12.4	68.9	714	6	US-09-925-065A-947645	Sequence 947645,
220	12.4	68.9	717	7	US-10-932-182A-1376	Sequence 1376, Ap
221	12.4	68.9	717	7	US-10-932-182A-1376	Sequence 1376, Ap
222	12.4	68.9	754	6	US-09-925-065A-924221	Sequence 924221,
223	12.4	68.9	754	6	US-09-925-065A-924222	Sequence 924222,
224	12.4	68.9	754	6	US-09-925-065A-924223	Sequence 924223,
225	12.4	68.9	792	6	US-09-925-065A-932474	Sequence 932474,
226	12.4	68.9	792	6	US-09-925-065A-92475	Sequence 92475,
227	12.4	68.9	807	6	US-10-467-657-7277	Sequence 7277, Ap
228	12.4	68.9	961	12	US-11-112-908-447	Sequence 447, App
229	12.4	68.9	1082	8	US-10-750-185-66314	Sequence 66314, A
230	12.4	68.9	1082	8	US-10-750-623-66314	Sequence 66314, A
231	12.4	68.9	1122	8	US-10-467-657-3785	Sequence 3785, Ap
232	12.4	68.9	1205	6	US-09-925-065A-94114	Sequence 94114, A
233	12.4	68.9	1205	6	US-09-925-065A-94115	Sequence 94115, A
234	12.4	68.9	1205	6	US-09-925-065A-94116	Sequence 94116, A
235	12.4	68.9	1258	8	US-10-750-185-40257	Sequence 40257, A
236	12.4	68.9	1258	8	US-10-750-623-40257	Sequence 40257, A
237	12.4	68.9	1271	8	US-10-750-185-28597	Sequence 28597, A
238	12.4	68.9	1271	8	US-10-750-623-28597	Sequence 28597, A
239	12.4	68.9	1279	8	US-10-750-185-44120	Sequence 44120, A

C 240	12.4	68.9	1279	8	US-10-750-623-44120	Sequence 44120, A	C 313	12.2	67.8	201	12	US-11-124-367A-21677	Sequence 21677, A
C 241	12.4	68.9	1290	7	US-11-096-568A-1839	Sequence 7839, Ap	C 314	12.2	67.8	201	12	US-11-124-367A-21679	Sequence 21679, A
C 242	12.4	68.9	1416	7	US-10-932-182A-3167	Sequence 3167, Ap	C 315	12.2	67.8	201	12	US-11-124-367A-21763	Sequence 21763, A
C 243	12.4	68.9	1416	7	US-10-932-182A-3167	Sequence 3167, Ap	C 316	12.2	67.8	201	12	US-11-124-367A-21767	Sequence 21767, A
C 244	12.4	68.9	1450	6	US-09-925-065A-683380	Sequence 683380, A	C 317	12.2	67.8	318	8	US-10-467-657-2957	Sequence 2957, Ap
C 245	12.4	68.9	1450	6	US-09-925-065A-683381	Sequence 683381, A	C 318	12.2	67.8	318	8	US-10-467-657-5709	Sequence 5709, Ap
C 246	12.4	68.9	1450	6	US-09-925-065A-683382	Sequence 683382, A	C 319	12.2	67.8	324	8	US-10-467-657-5107	Sequence 5107, Ap
C 247	12.4	68.9	1552	9	US-11-096-568A-12907	Sequence 12907, A	C 320	12.2	67.8	408	8	US-10-467-657-6107	Sequence 6107, Ap
C 248	12.4	68.9	1643	6	US-09-925-065A-61338	Sequence 61329, A	C 321	12.2	67.8	409	6	US-09-925-065A-487612	Sequence 487612, A
C 249	12.4	68.9	1643	6	US-09-925-065A-61339	Sequence 61329, A	C 322	12.2	67.8	409	6	US-09-925-065A-845068	Sequence 845068, A
C 250	12.4	68.9	1643	6	US-09-925-065A-148208	Sequence 548208, A	C 323	12.2	67.8	405	6	US-09-925-065A-289024	Sequence 289024, A
C 251	12.4	68.9	1643	6	US-09-925-065A-171827	Sequence 71827, A	C 324	12.2	67.8	456	6	US-09-925-065A-653177	Sequence 653177, A
C 252	12.4	68.9	1678	6	US-09-925-065A-70558	Sequence 70558, A	C 325	12.2	67.8	459	6	US-09-925-065A-507827	Sequence 507827, A
C 253	12.4	68.9	1678	6	US-09-925-065A-70559	Sequence 70559, A	C 326	12.2	67.8	459	6	US-09-925-065A-507827	Sequence 507827, A
C 254	12.4	68.9	1678	6	US-09-925-065A-705560	Sequence 70560, A	C 327	12.2	67.8	459	6	US-09-925-065A-501535	Sequence 501535, A
C 255	12.4	68.9	1698	8	US-10-467-657-3301	Sequence 3301, Ap	C 328	12.2	67.8	475	6	US-10-467-657-4359	Sequence 4359, Ap
C 256	12.4	68.9	1725	8	US-10-821-234-772	Sequence 772, Ap	C 329	12.2	67.8	480	6	US-09-925-065A-142400	Sequence 142400, A
C 257	12.4	68.9	1864	9	US-11-096-568A-22131	Sequence 22131, A	C 330	12.2	67.8	480	6	US-09-925-065A-500711	Sequence 500711, A
C 258	12.4	68.9	2004	8	US-10-750-185-43381	Sequence 43381, A	C 331	12.2	67.8	494	6	US-09-925-065A-153216	Sequence 153216, A
C 259	12.4	68.9	2004	8	US-10-750-623-43381	Sequence 43381, A	C 332	12.2	67.8	494	6	US-09-925-065A-153217	Sequence 153217, A
C 260	12.4	68.9	2005	9	US-11-072-512-175	Sequence 175, App	C 333	12.2	67.8	497	6	US-09-925-065A-153218	Sequence 153218, A
C 261	12.4	68.9	2319	12	US-11-024-959-162	Sequence 162, App	C 334	12.2	67.8	497	6	US-09-925-065A-843463	Sequence 843463, A
C 262	12.4	68.9	2534	6	US-09-925-065A-76182	Sequence 76182, A	C 335	12.2	67.8	488	6	US-09-925-065A-729563	Sequence 729563, A
C 263	12.4	68.9	2537	6	US-09-925-065A-715287	Sequence 715287, A	C 336	12.2	67.8	488	6	US-09-925-065A-729564	Sequence 729564, A
C 264	12.4	68.9	2537	6	US-09-925-065A-715288	Sequence 715288, A	C 337	12.2	67.8	503	6	US-09-925-065A-315416	Sequence 315416, A
C 265													

C 386	12.2	67.8	565	6	US-09-925-065A-44354	Sequence 44354, A	459	12.2	67.8	623	6	US-09-925-065A-932768	Sequence 932768, A
C 387	12.2	67.8	572	6	US-09-925-065A-439809	Sequence 439809, A	460	12.2	67.8	624	6	US-09-925-065A-47568	Sequence 47568, A
C 388	12.2	67.8	574	6	US-09-925-065A-723379	Sequence 723379, A	461	12.2	67.8	625	6	US-09-925-065A-472411	Sequence 472411, A
C 389	12.2	67.8	575	6	US-09-925-065A-723380	Sequence 723380, A	462	12.2	67.8	626	6	US-09-925-065A-723411	Sequence 723411, A
C 390	12.2	67.8	576	6	US-09-925-065A-135033	Sequence 135033, A	463	12.2	67.8	629	6	US-09-925-065A-355953	Sequence 355953, A
C 391	12.2	67.8	578	6	US-09-925-065A-563330	Sequence 563330, A	464	12.2	67.8	629	6	US-09-925-065A-355954	Sequence 355954, A
C 392	12.2	67.8	578	6	US-09-925-065A-563331	Sequence 563331, A	465	12.2	67.8	629	6	US-09-925-065A-355954	Sequence 355954, A
C 393	12.2	67.8	579	6	US-09-925-065A-609039	Sequence 609039, A	466	12.2	67.8	630	6	US-09-925-065A-355954	Sequence 355954, A
C 394	12.2	67.8	579	6	US-09-925-065A-784522	Sequence 784522, A	467	12.2	67.8	631	6	US-09-925-065A-355954	Sequence 355954, A
C 395	12.2	67.8	579	6	US-09-925-065A-784522	Sequence 784522, A	468	12.2	67.8	631	6	US-09-925-065A-355954	Sequence 355954, A
C 396	12.2	67.8	580	6	US-09-925-065A-923112	Sequence 923112, A	469	12.2	67.8	631	6	US-09-925-065A-355954	Sequence 355954, A
C 397	12.2	67.8	580	6	US-09-925-065A-923112	Sequence 923112, A	470	12.2	67.8	631	6	US-09-925-065A-355954	Sequence 355954, A
C 398	12.2	67.8	580	6	US-09-925-065A-947283	Sequence 947283, A	471	12.2	67.8	632	6	US-09-925-065A-355954	Sequence 355954, A
C 399	12.2	67.8	580	12	US-11-128-061-2309	Sequence 2309, Ap	472	12.2	67.8	632	6	US-09-925-065A-355954	Sequence 355954, A
C 400	12.2	67.8	580	12	US-11-128-061-2309	Sequence 2309, Ap	473	12.2	67.8	633	6	US-09-925-065A-355954	Sequence 355954, A
C 401	12.2	67.8	580	12	US-11-128-049-2309	Sequence 2309, Ap	474	12.2	67.8	633	6	US-09-925-065A-355954	Sequence 355954, A
C 402	12.2	67.8	580	12	US-11-128-049-2309	Sequence 2309, Ap	475	12.2	67.8	633	6	US-09-925-065A-355954	Sequence 355954, A
C 403	12.2	67.8	581	6	US-09-925-065A-927721	Sequence 927721, A	476	12.2	67.8	633	6	US-09-925-065A-355954	Sequence 355954, A
C 404	12.2	67.8	581	6	US-09-925-065A-927723	Sequence 927723, A	477	12.2	67.8	633	6	US-09-925-065A-355954	Sequence 355954, A
C 405	12.2	67.8	581	6	US-09-925-065A-949460	Sequence 949460, A	478	12.2	67.8	638	6	US-09-925-065A-355954	Sequence 355954, A
C 406	12.2	67.8	582	6	US-09-925-065A-507033	Sequence 507033, A	479	12.2	67.8	639	6	US-09-925-065A-355954	Sequence 355954, A
C 407	12.2	67.8	582	6	US-09-925-065A-507034	Sequence 507034, A	480	12.2	67.8	640	6	US-09-925-065A-355954	Sequence 355954, A
C 408	12.2	67.8	585	6	US-09-925-065A-255688	Sequence 255688, A	481	12.2	67.8	641	6	US-09-925-065A-355954	Sequence 355954, A
C 409	12.2	67.8	587	6	US-09-925-065A-302641	Sequence 302641, A	482	12.2	67.8	642	6	US-09-925-065A-355954	Sequence 355954, A
C 410	12.2	67.8	588	6	US-09-925-065A-97391	Sequence 97391, A	483	12.2	67.8	650	6	US-09-925-065A-355954	Sequence 355954, A
C 411	12.2	67.8	588	6	US-09-925-065A-428270	Sequence 428270, A	484	12.2	67.8	650	6	US-09-925-065A-355954	Sequence 355954, A
C 412	12.2	67.8	588	6	US-09-925-065A-428271	Sequence 428271, A	485	12.2	67.8	651	6	US-09-925-065A-355954	Sequence 355954, A
C 413	12.2	67.8	588	6	US-09-925-065A-619345	Sequence 619345, A	486	12.2	67.8	654	6	US-09-925-065A-355954	Sequence 355954, A
C 414	12.2	67.8	588	6	US-09-925-065A-768327	Sequence 768327, A	487	12.2	67.8	654	6	US-09-925-065A-355954	Sequence 355954, A
C 415	12.2	67.8	588	6	US-09-925-065A-833964	Sequence 833964, A	488	12.2	67.8	654	6	US-09-925-065A-355954	Sequence 355954, A
C 416	12.2	67.8	588	6	US-10-467-657-1157	Sequence 1157, Ap	489	12.2	67.8	656	6	US-09-925-065A-355954	Sequence 355954, A
C 417	12.2	67.8	590	6	US-09-925-065A-24297	Sequence 24297, A	490	12.2	67.8	657	6	US-09-925-065A-355954	Sequence 355954, A
C 418	12.2	67.8	590	6	US-09-925-065A-542989	Sequence 542989, A	491	12.2	67.8	659	6	US-09-925-065A-355954	Sequence 355954, A
C 419	12.2	67.8	590	6	US-09-925-065A-931196	Sequence 931196, A	492	12.2	67.8	669	6	US-09-925-065A-355954	Sequence 355954, A
C 420	12.2	67.8	593	6	US-09-925-065A-382018	Sequence 382018, A	493	12.2	67.8	674	6	US-09-925-065A-355954	Sequence 355954, A
C 421	12.2	67.8	593	6	US-09-925-065A-382020	Sequence 382020, A	494	12.2	67.8	674	6	US-09-925-065A-355954	Sequence 355954, A
C 422	12.2	67.8	593	6	US-09-925-065A-344121	Sequence 344121, A	495	12.2	67.8	674	6	US-09-925-065A-355954	Sequence 355954, A
C 423	12.2	67.8	593	6	US-09-925-065A-862191	Sequence 862191, A	496	12.2	67.8	681	6	US-09-925-065A-355954	Sequence 355954, A
C 424	12.2	67.8	593	6	US-09-925-065A-930553	Sequence 930553, A	497	12.2	67.8	682	6	US-09-925-065A-355954	Sequence 355954, A
C 425	12.2	67.8	594	6	US-09-925-065A-659312	Sequence 659312, A	498	12.2	67.8	683	6	US-09-925-065A-355954	Sequence 355954, A
C 426	12.2	67.8	594	6	US-09-925-065A-692719	Sequence 692719, A	499	12.2	67.8	689	6	US-09-925-065A-355954	Sequence 355954, A
C 427	12.2	67.8	594	6	US-09-925-065A-807601	Sequence 807601, A	500	12.2	67.8	702	6	US-09-925-065A-355954	Sequence 355954, A
C 428	12.2	67.8	595	6	US-09-925-065A-275903	Sequence 275903, A	501	12.2	67.8	702	6	US-09-925-065A-355954	Sequence 355954, A
C 429	12.2	67.8	595	6	US-09-925-065A-923244	Sequence 923244, A	502	12.2	67.8	704	6	US-09-925-065A-355954	Sequence 355954, A
C 430	12.2	67.8	596	6	US-09-925-065A-863531	Sequence 863531, A	503	12.2	67.8	705	6	US-09-925-065A-355954	Sequence 355954, A
C 431	12.2	67.8	600	6	US-09-925-065A-489929	Sequence 489929, A	504	12.2	67.8	745	6	US-09-925-065A-355954	Sequence 355954, A
C 432	12.2	67.8	600	8	US-10-750-185-3305	Sequence 3305, Ap	505	12.2	67.8	745	6	US-09-925-065A-355954	Sequence 355954, A
C 433	12.2	67.8	600	8	US-10-750-185-3305	Sequence 3305, Ap	506	12.2	67.8	757	6	US-09-925-065A-355954	Sequence 355954, A
C 434	12.2	67.8	600	8	US-10-750-623-3305	Sequence 3305, Ap	507	12.2	67.8	759	6	US-09-925-065A-355954	Sequence 355954, A
C 435	12.2	67.8	600	8	US-10-750-623-3305	Sequence 3305, Ap	508	12.2	67.8	759	6	US-09-925-065A-355954	Sequence 355954, A
C 436	12.2	67.8	600	12	US-11-136-527-6714	Sequence 6714, Ap	509	12.2	67.8	759	6	US-09-925-065A-355954	Sequence 355954, A
C 437	12.2	67.8	601	6	US-09-925-065A-740118	Sequence 740118, A	510	12.2	67.8	773	6	US-09-925-065A-355954	Sequence 355954, A
C 438	12.2	67.8	602	6	US-09-925-065A-557356	Sequence 557356, A	511	12.2	67.8	773	6	US-09-925-065A-355954	Sequence 355954, A
C 439	12.2	67.8	602	6	US-09-925-065A-652794	Sequence 652794, A	512	12.2	67.8	778	6	US-09-925-065A-355954	Sequence 355954, A
C 440	12.2	67.8	604	6	US-09-925-065A-729702	Sequence 729702, A	513	12.2	67.8	794	8	US-10-750-185-46100	Sequence 64100, A
C 441	12.2	67.8	604	6	US-09-925-065A-729703	Sequence 729703, A	514	12.2	67.8	794	8	US-10-750-185-46100	Sequence 64100, A
C 442	12.2	67.8	605	6	US-09-925-065A-774604	Sequence 774604, A	515	12.2	67.8	803	12	US-11-055-822-905	Sequence 905, Ap
C 443	12.2	67.8	605	6	US-09-925-065A-775868	Sequence 775868, A	516	12.2	67.8	825	8	US-10-467-657-2387	Sequence 2387, Ap
C 444	12.2	67.8	605	6	US-09-925-065A-837463	Sequence 837463, A	517	12.2	67.8	827	6	US-09-925-065A-355954	Sequence 355954, A
C 445	12.2	67.8	606	6	US-09-925-065A-492027	Sequence 492027, A	518	12.2	67.8	827	6	US-09-925-065A-355954	Sequence 355954, A
C 446	12.2	67.8	606	6	US-09-925-065A-812530	Sequence 812530, A	519	12.2	67.8	827	6	US-09-925-065A-355954	Sequence 355954, A
C 447	12.2	67.8	606	6	US-09-925-065A-844630	Sequence 844630, A	520	12.2	67.8	834	7	US-10-932-182A-3518	Sequence 3518, Ap
C 448	12.2	67.8	607	6	US-09-925-065A-220430	Sequence 220430, A	521	12.2	67.8	834	7	US-10-932-182A-3518	Sequence 3518, Ap
C 449	12.2	67.8	608	6	US-09-925-065A-355952	Sequence 355952, A	522	12.2	67.8	840	6	US-09-925-065A-355954	Sequence 355954, A
C 450	12.2	67.8	609	6	US-09-925-065A-865668	Sequence 865668, A	523	12.2	67.8	852	8	US-10-467-657-2387	Sequence 2387, Ap
C 451	12.2	67.8	610	6	US-09-925-065A-294410	Sequence 294410, A	524	12.2	67.8	875	6	US-09-925-065A-355954	Sequence 355954, A
C 452	12.2	67.8	610	6	US-09-925-065A-609038	Sequence 609038, A	525	12.2	67.8	896	6	US-09-925-065A-355954	Sequence 355954, A
C 453	12.2	67.8	611	6	US-09-925-065A-668820	Sequence 668820, A	526	12.2	67.8	903	6	US-09-925-065A-355954	Sequence 355954, A
C 454	12.2	67.8	612	6	US-09-925-065A-124180	Sequence 124180, A	527	12.2	67.8	937	6	US-09-925-065A-355954	Sequence 355954, A
C 455	12.2	67.8	616	6	US-09-925-065A-753581	Sequence 753581, A	528	12.2	67.8	938	6	US-09-925-065A-355954	Sequence 355954, A
C 456	12.2	67.8	617	6	US-09-925-065A-758114	Sequence 758114, A	529	12.2	67.8	987	8	US-10-750-185-48214	Sequence 48214, A
C 457	12.2	67.8	621	6	US-09-925-065A-840121	Sequence 840121, A	530	12.2	67.8	987	8	US-10-750-185-48214	Sequence 48214, A
C 458	12.2	67.8	623	6	US-09-925-065A-8120	Sequence 8120, Ap	531	12.2	67.8	990	7	US-10-932-182A-303	Sequence 303, Ap


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C 970 11.8 65.6 937 9 US-11-040-830-104 Sequence 104, App
C 971 11.8 65.6 991 8 US-10-750-185-55325 Sequence 5535, A
C 972 11.8 65.6 991 8 US-10-750-623-55325 Sequence 5535, A
C 973 11.8 65.6 1005 12 US-11-128-061-3370 Sequence 3370, Ap
C 974 11.8 65.6 1005 12 US-11-128-049-3370 Sequence 3370, Ap
C 975 11.8 65.6 1035 9 US-10-517-696-42 Sequence 42, Appl
C 976 11.8 65.6 1035 9 US-11-096-568A-18135 Sequence 18135, A
C 977 11.8 65.6 1045 6 US-09-925-065A-40400 Sequence 40400, A
C 978 11.8 65.6 1045 6 US-09-925-065A-40401 Sequence 40401, A
C 979 11.8 65.6 1045 6 US-09-925-065A-40402 Sequence 40402, A
C 980 11.8 65.6 1047 7 US-10-932-182A-3148 Sequence 3148, Ap
C 981 11.8 65.6 1047 7 US-10-932-182A-3148 Sequence 3148, Ap
C 982 11.8 65.6 1060 6 US-09-925-065A-37956 Sequence 37956, A
C 983 11.8 65.6 1060 6 US-09-925-065A-37957 Sequence 37957, A
C 984 11.8 65.6 1061 6 US-09-925-065A-37958 Sequence 37958, A
C 985 11.8 65.6 1061 6 US-09-925-065A-722772 Sequence 722772,
C 986 11.8 65.6 1061 6 US-09-925-065A-722773 Sequence 722773,
C 987 11.8 65.6 1077 7 US-10-932-182A-2575 Sequence 2575, Ap
C 988 11.8 65.6 1077 7 US-10-932-182A-2575 Sequence 2575, Ap
C 989 11.8 65.6 1092 9 US-11-096-568A-16872 Sequence 16872, A
C 990 11.8 65.6 1093 6 US-09-925-065A-80602 Sequence 80602, A
C 991 11.8 65.6 1093 6 US-09-925-065A-80603 Sequence 80603, A
C 992 11.8 65.6 1113 7 US-10-932-182A-76635 Sequence 76635, A
C 993 11.8 65.6 1113 7 US-10-932-182A-76635 Sequence 76635, A
C 994 11.8 65.6 1124 6 US-09-925-065A-713519 Sequence 713519,
C 995 11.8 65.6 1149 7 US-10-330-773-270 Sequence 270, Appl
C 996 11.8 65.6 1164 12 US-11-137-465-24 Sequence 24, Appl
C 997 11.8 65.6 1182 12 US-11-144-236-7 Sequence 7, Appl
C 998 11.8 65.6 1191 9 US-11-096-568A-19966 Sequence 19966, A
C1000 11.8 65.6 1199 9 US-11-245-147-81 Sequence 81, Appl
```

ALIGNMENTS

```
RESULT 1
US-10-619-279-60/c
; Sequence 60, Application US/10619279
; Publication No. US20050267057A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7023/HCL
; CURRENT APPLICATION NUMBER: US/10/619,279
; PRIOR FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 08/960,774
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-619-279-60
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Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 88.9%; Pred. No.1.2;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 AGAGGUGCGCAGCGGUA 18
Db 18 AGAGGUGCGCAGCGGUA 1
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```
RESULT 2
US-11-127-654-4/c
; Sequence 4, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; FILE REFERENCE: C1039, 70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-4
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Query Match 100.0%; Score 18; DB 12; Length 18;
Best Local Similarity 88.9%; Pred. No.1.2;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 AGAGGUGCGCAGCGGUA 18
Db 18 AGAGGUGCGCAGCGGUA 1
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RESULT 3
US-10-497-591A-41/c
; Sequence 41, Application US/10497591A
; Publication No. US20050250716A1
; GENERAL INFORMATION:
; APPLICANT: SCHMIDT, MALTE
; APPLICANT: SCHLACK, CAROLA
; APPLICANT: EGYED, ALENA
; APPLICANT: LINGNAU, KAREN
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGODEOXYNUCLEOTIDES
; FILE REFERENCE: SONN:045US
; CURRENT APPLICATION NUMBER: US/10/497,591A
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: PCT/EP02/13791
; PRIOR FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: A 1924/2001
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
; NAME/KEY: modified base
; LOCATION: (5)..(11)
; OTHER INFORMATION: n = inosine or uracil
US-10-497-591A-41
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Query Match 83.3%; Score 15; DB 8; Length 18;
Best Local Similarity 72.2%; Pred. No. 57;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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Qy 1 AGAGGUGCGCAGCGGUA 18
Db 18 AGAGGUGCGCAGCGGUA 1
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DB 18 AGAGGTGCGCANGNGGTA 1

RESULT 4
US-10-310-914A-990315/C
; Sequence 990315, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 990315
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-990315

Query Match 83.3%; Score 15; DB 8; Length 22;
Best Local Similarity 93.3%; Pred. No. 57;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCGG 16
DB 19 GAGGTCGCGACGCGG 5

RESULT 5
US-10-981-334-21
; Sequence 21, Application US/10981334
; Publication No. US20060008816A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Yi-Ping et al.
; TITLE OF INVENTION: PROMOTER, PROMOTER CONTROL ELEMENTS, AND COMBINATIONS, AND USES
; FILE REFERENCE: 2750-1581PUS2
; CURRENT APPLICATION NUMBER: US/10/981,334
; CURRENT FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 935
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Promoter and/or promoter control element identified from
US-10-981-334-21

Query Match 83.3%; Score 15; DB 7; Length 935;
Best Local Similarity 86.7%; Pred. No. 52;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGGUGCGACGCGGU 17
DB 864 AGGGTCGCGACGCGGT 878

RESULT 6
US-11-091-883-330/C
; Sequence 330, Application US/11091883
; Publication No. US20060024693A1
; GENERAL INFORMATION:
; APPLICANT: CIBELLI, JOSE
; APPLICANT: FERNANDEZ, EMILIO O.
; APPLICANT: JORDAO DE MEGALHAES, GUILHERME
; APPLICANT: KOCABAS, ARIF
; APPLICANT: CROSBY, JAVIER A.

;; TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH
;; TITLE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEBORN
;; FILE REFERENCE: 53942US
;; CURRENT APPLICATION NUMBER: US/11/091,883
;; CURRENT FILING DATE: 2005-03-29
;; PRIOR APPLICATION NUMBER: 60/556,875
;; PRIOR FILING DATE: 2004-03-29
;; NUMBER OF SEQ ID NOS: 513
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 330
;; LENGTH: 2162
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: modified base
;; LOCATION: (909)..(909)
;; OTHER INFORMATION: a, c, g, or t
;; FEATURE:
;; NAME/KEY: modified base
;; LOCATION: (1400)..(1400)
;; OTHER INFORMATION: a, c, g, or t
;; FEATURE:
;; NAME/KEY: modified base
;; LOCATION: (2051)..(2053)
;; OTHER INFORMATION: a, c, g, or t
;; FEATURE:
;; NAME/KEY: modified base
;; LOCATION: (2056)..(2056)
;; OTHER INFORMATION: a, c, g, or t
;; FEATURE:
;; NAME/KEY: modified base
;; LOCATION: (2072)..(2074)
;; OTHER INFORMATION: a, c, g, or t
US-11-091-883-330

Query Match 83.3%; Score 15; DB 12; Length 2162;
Best Local Similarity 93.3%; Pred. No. 51;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCGG 16
DB 2035 GAGGTCGCGACGCGG 2021

RESULT 7
US-10-750-185-55765
; Sequence 55765, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR IMPROVING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55765
; LENGTH: 2106
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-55765

Query Match 82.2%; Score 14.8; DB 8; Length 2106;
Best Local Similarity 77.8%; Pred. No. 66;

Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGAGGUCGACGCGGUA 18
|||||:|||||:
Db 831 AGAGGCTCGCATCGGTA 848

RESULT 8
US-10-750-623-55765
; Sequence 55765, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55765
; LENGTH: 2106
; TYPE: DNA
; ORGANISM: Bovine 19866881318594
US-10-750-623-55765

Query Match 82.2%; Score 14.8; DB 8; Length 2106;
Best Local Similarity 77.8%; Pred. No. 66;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAGGUCGACGCGGUA 18
|||||:|||||:
Db 831 AGAGGCTCGCATCGGTA 848

RESULT 9
US-10-750-185-37497/c
; Sequence 37497, Application US/10750185
; Publication No. US200502603A1
; GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37497
; LENGTH: 1411
; TYPE: DNA
; ORGANISM: Bovine 19866881318594
US-10-750-185-37497

Query Match 80.0%; Score 14.4; DB 8; Length 1411;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AGAGGUCGACGCGG 16

Db 655 AGAGGGCGCACGCGG 640
|||||:|||||:
|||||:|||||:

RESULT 10
US-10-750-623-37497/c
; Sequence 37497, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37497
; LENGTH: 1411
; TYPE: DNA
; ORGANISM: Bovine 19866881318594
US-10-750-623-37497

Query Match 80.0%; Score 14.4; DB 8; Length 1411;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUCGACGCGG 16
|||||:|||||:
Db 655 AGAGGGCGCACGCGG 640

RESULT 11
US-11-121-849-531952
; Sequence 531952, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded se
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 531952
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-531952

Query Match 77.8%; Score 14; DB 12; Length 25;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUCGACGCGG 15
|||||:|||||:
Db 12 GAGGCTCGCACGCG 25

RESULT 12
US-10-750-185-4096/c
; Sequence 4096, Application US/10750185
; Publication No. US200502603A1

GENERAL INFORMATION:
APPLICANT: MMT GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: M11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4096
LENGTH: 600
TYPE: DNA
ORGANISM: Bovine MMBT19288
US-10-750-185-4096

Query Match 77.8%; Score 14; DB 8; Length 600;
Best Local Similarity 87.5%; Pred. No. 1.9e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCAGCGCG 16
DB 307 AGAGGGGCGACCGCG 292

RESULT 13
US-10-750-623-4096/c
Sequence 4096, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MMT GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: M11100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4096
LENGTH: 600
TYPE: DNA
ORGANISM: Bovine MMBT19288
US-10-750-623-4096

Query Match 77.8%; Score 14; DB 8; Length 600;
Best Local Similarity 87.5%; Pred. No. 1.9e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCAGCGCG 16
DB 307 AGAGGGGCGACCGCG 292

RESULT 14
US-09-925-065A-552179/c
Sequence 552179, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 552179
LENGTH: 1454
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-552179

Query Match 77.8%; Score 14; DB 6; Length 1454;
Best Local Similarity 92.9%; Pred. No. 1.9e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGUGCAGCGCG 16
DB 422 AGGTCGACCGCG 409

RESULT 15
US-09-925-065A-649799
Sequence 649799, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 649799
LENGTH: 414
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-649799

Query Match 76.7%; Score 13.8; DB 6; Length 414;
Best Local Similarity 76.5%; Pred. No. 2.5e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGGUGCAGCGGUA 18
DB 292 GAGGTGCGACCGCAGTA 308

RESULT 16
US-09-925-065A-99074/c
Sequence 99074, Application US/09925065A
Publication No. US20040181048A1


```
RESULT 20
US-11-096-568A-18587/c
; Sequence 18587, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nicholas et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; PRIOR FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 18587
; LENGTH: 1490
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1490)
; OTHER INFORMATION: Ceres Seq. ID no. 12365955
US-11-096-568A-18587

Query Match          76.7%; Score 13.8; DB 9; Length 1490;
Best Local Similarity 76.5%; Pred. No. 2.4e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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```
QY 1 AGAGGUGCGACCGCGU 17
    |||||:|||||:
Db 876 AGCGGTCGACGCGGT 860
```

```
RESULT 21
US-09-925-065A-709998
; Sequence 70998, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70998
; LENGTH: 1492
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-709998
```

```
QY 1 AGAGGUGCGACCGCGU 17
    |||||:|||||:
Db 451 AGAGGTCGACGCGGT 467

Query Match          76.7%; Score 13.8; DB 6; Length 1492;
Best Local Similarity 76.5%; Pred. No. 2.4e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
RESULT 22
US-10-240-708-20
```

```
; Sequence 20, Application US/10240708
; Publication No. US20050282157A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIERSENROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/240,708
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 20
; LENGTH: 6866
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-708-20
```

```
Query Match          76.7%; Score 13.8; DB 8; Length 6866;
Best Local Similarity 76.5%; Pred. No. 2.3e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 AGAGGUGCGACCGCGU 17
    |||||:|||||:
Db 4008 ATAGGTCGACGCGGT 4024
```

```
RESULT 23
US-09-925-065A-74944
; Sequence 74944, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74944
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-74944
```

```
QY 1 AGAGGUGCGACCGCGU 17
    |||||:|||||:
Db 74.4%; Score 13.4; DB 6; Length 566;
Best Local Similarity 76.5%; Pred. No. 4.2e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

Db 273 AGAGGCGCAGCGCGT 289

RESULT 24
US-09-925-065A-46507

/ Sequence 46507, Application US/09925065A
/ Publication No. US20040181048A1

/ GENERAL INFORMATION:

/ APPLICANT: Wang, David G.

/ TITLE OF INVENTION: Identification and Mapping of Single

/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

/ FILE REFERENCE: 108827.135

/ CURRENT APPLICATION NUMBER: US/09/925,065A

/ PRIOR FILING DATE: 2001-08-08

/ PRIOR APPLICATION NUMBER: US 60/243,096

/ PRIOR FILING DATE: 2000-10-24

/ PRIOR APPLICATION NUMBER: US 60/252,147

/ PRIOR FILING DATE: 2000-11-20

/ PRIOR APPLICATION NUMBER: US 60/250,092

/ PRIOR FILING DATE: 2000-11-30

/ PRIOR APPLICATION NUMBER: US 60/261,766

/ PRIOR FILING DATE: 2001-01-16

/ PRIOR APPLICATION NUMBER: US 60/289,846

/ PRIOR FILING DATE: 2001-05-09

/ NUMBER OF SEQ ID NOS: 957086

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 46507

/ LENGTH: 580

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ US-09-925-065A-46507

Query Match 74.4%; Score 13.4; DB 6; Length 580;
Best Local Similarity 93.3%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGUCCAGCGCG 16
Db 123 GAGGGCGCAGCGCG 137

RESULT 25
US-09-925-065A-299863/c

/ Sequence 299863, Application US/09925065A

/ Publication No. US20040181048A1

/ GENERAL INFORMATION:

/ APPLICANT: Wang, David G.

/ TITLE OF INVENTION: Identification and Mapping of Single

/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

/ FILE REFERENCE: 108827.135

/ CURRENT APPLICATION NUMBER: US/09/925,065A

/ PRIOR FILING DATE: 2001-08-08

/ PRIOR APPLICATION NUMBER: US 60/243,096

/ PRIOR FILING DATE: 2000-10-24

/ PRIOR APPLICATION NUMBER: US 60/252,147

/ PRIOR FILING DATE: 2000-11-20

/ PRIOR APPLICATION NUMBER: US 60/250,092

/ PRIOR FILING DATE: 2000-11-30

/ PRIOR APPLICATION NUMBER: US 60/261,766

/ PRIOR FILING DATE: 2001-01-16

/ PRIOR APPLICATION NUMBER: US 60/289,846

/ PRIOR FILING DATE: 2001-05-09

/ NUMBER OF SEQ ID NOS: 957086

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 299863

/ LENGTH: 589

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ US-09-925-065A-299863

Query Match 74.4%; Score 13.4; DB 6; Length 589;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;

Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGGGUCCAGCGCGU 17
Db 528 AGGGTCGACCTCGGT 514

RESULT 26
US-09-925-065A-47629

/ Sequence 47629, Application US/09925065A

/ Publication No. US20040181048A1

/ GENERAL INFORMATION:

/ APPLICANT: Wang, David G.

/ TITLE OF INVENTION: Identification and Mapping of Single

/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

/ FILE REFERENCE: 108827.135

/ CURRENT APPLICATION NUMBER: US/09/925,065A

/ PRIOR FILING DATE: 2001-08-08

/ PRIOR APPLICATION NUMBER: US 60/243,096

/ PRIOR FILING DATE: 2000-10-24

/ PRIOR APPLICATION NUMBER: US 60/252,147

/ PRIOR FILING DATE: 2000-11-20

/ PRIOR APPLICATION NUMBER: US 60/250,092

/ PRIOR FILING DATE: 2000-11-30

/ PRIOR APPLICATION NUMBER: US 60/261,766

/ PRIOR FILING DATE: 2001-01-16

/ PRIOR APPLICATION NUMBER: US 60/289,846

/ PRIOR FILING DATE: 2001-05-09

/ NUMBER OF SEQ ID NOS: 957086

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 47629

/ LENGTH: 605

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ US-09-925-065A-47629

Query Match 74.4%; Score 13.4; DB 6; Length 605;
Best Local Similarity 93.3%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGUCCAGCGCG 16
Db 123 GAGGGCGCAGCGCG 137

RESULT 27
US-11-136-527-1781/c

/ Sequence 1781, Application US/11136527

/ Publication No. US20050287570A1

/ GENERAL INFORMATION:

/ APPLICANT: Wyeth

/ APPLICANT: Mounts, William M

/ TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

/ FILE REFERENCE: 031896-041000 (AM101086)

/ CURRENT APPLICATION NUMBER: US/11/136,527

/ PRIOR FILING DATE: 2005-05-25

/ PRIOR APPLICATION NUMBER: US 60/574,294

/ PRIOR FILING DATE: 2005-05-26

/ NUMBER OF SEQ ID NOS: 362830

/ SOFTWARE: Patentin version 3.2

/ SEQ ID NO 1781

/ LENGTH: 1185

/ TYPE: DNA

/ ORGANISM: Rattus norvegicus

/ US-11-136-527-1781

Query Match 74.4%; Score 13.4; DB 12; Length 1185;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGGGUCCAGCGCGU 17
Db 907 AGGGTCGACCGCGTT 893

RESULT 28

US-10-750-185-62892/c
; Sequence 62892, Application US/10750185
; Publication No. US2005026063A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62892
; LENGTH: 1213
; TYPE: DNA
; ORGANISM: Bovine 19866880761026
US-10-750-185-62892

Query Match 74.4%; Score 13.4; DB 8; Length 1213;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGGUGCGACGCGGUA 18
|||:|||||:
Db 775 GGGTGCACGCGGTA 761

RESULT 29

US-10-750-623-62892/c
; Sequence 62892, Application US/10750623
; Publication No. US2005028753A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62892
; LENGTH: 1213
; TYPE: DNA
; ORGANISM: Bovine 19866880761026
US-10-750-623-62892

Query Match 74.4%; Score 13.4; DB 8; Length 1213;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGGUGCGACGCGGUA 18
|||:|||||:
Db 775 GGGTGCACGCGGTA 761

RESULT 30

US-11-171-701-1/c

; Sequence 1, Application US/11171701
; Publication No. US20060008879A1
; GENERAL INFORMATION:
; APPLICANT: Ocani, Suzanne
; APPLICANT: Blinkovsky, Alexander
; APPLICANT: Ge, Haiyan
; APPLICANT: Harris, Paul
; APPLICANT: Yaver, Debbie
; TITLE OF INVENTION: Polypeptides Having Alpha-Glucosidase Activity And
; TITLE OF INVENTION: Polynucleotides Encoding Same
; FILE REFERENCE: 10655.200-US
; CURRENT APPLICATION NUMBER: US/11/171,701
; CURRENT FILING DATE: 2005-06-29
; PRIOR APPLICATION NUMBER: 60/585,336
; PRIOR FILING DATE: 2005-06-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 2954
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-11-171-701-1

Query Match 74.4%; Score 13.4; DB 12; Length 2954;
Best Local Similarity 86.7%; Pred. No. 4e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCGG 16
|||:|||||:
Db 2741 GAGGTCGCGCGCGG 2727

RESULT 31

US-10-912-971-1/c
; Sequence 1, Application US/10912971
; Publication No. US20060029546A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, et al.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR IDENTIFYING ANTI-SCHIZOPHRENIC AGENTS
; FILE REFERENCE: 30847/40237
; CURRENT APPLICATION NUMBER: US/10/912,971
; CURRENT FILING DATE: 2004-08-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 4663
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-912-971-1

Query Match 74.4%; Score 13.4; DB 7; Length 4663;
Best Local Similarity 86.7%; Pred. No. 4e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGGUGCGACGCGGUA 18
|||:|||||:
Db 1164 GGGTGCACGCGGCA 1150

RESULT 32

US-11-082-154A-118/c
; Sequence 118, Application US/11082154A
; Publication No. US20060024820A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Siena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan

;; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
;; FILE REFERENCE: 17084-022003 (420C)
;; CURRENT APPLICATION NUMBER: US/11/082,154A
;; CURRENT FILING DATE: 2005-03-15
;; PRIOR APPLICATION NUMBER: 60/294,758
;; PRIOR FILING DATE: 2001-05-30
;; PRIOR APPLICATION NUMBER: 60/366,891
;; PRIOR FILING DATE: 2002-03-21
;; PRIOR APPLICATION NUMBER: US 10/161,403
;; PRIOR FILING DATE: 2002-05-30
;; NUMBER OF SEQ ID NOS: 129
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 118
;; LENGTH: 17384
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: pFK61 Plasmid
US-11-082-154A-118

Query Match 74.4%; Score 13.4; DB 12; Length 17384;
Best Local Similarity 93.3%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGGUCCGACGCG 15
DB 7580 AGAGGACGACGCG 7566

RESULT 33
US-11-082-154A-18/C
;; Sequence 18, Application US/11082154A
;; Publication No. US20060024820A1
;; GENERAL INFORMATION:
;; APPLICANT: Perkins, Edward
;; APPLICANT: Lindenbaum, Michael
;; APPLICANT: Greene, Amy
;; APPLICANT: Leung, Josephine
;; APPLICANT: Fleming, Elena
;; APPLICANT: Stewart, Sandra
;; APPLICANT: Shellard, Joan
;; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
;; FILE REFERENCE: 17084-022003 (420C)
;; CURRENT APPLICATION NUMBER: US/11/082,154A
;; CURRENT FILING DATE: 2005-03-15
;; PRIOR APPLICATION NUMBER: 60/294,758
;; PRIOR FILING DATE: 2001-05-30
;; PRIOR APPLICATION NUMBER: 60/366,891
;; PRIOR FILING DATE: 2002-03-21
;; PRIOR APPLICATION NUMBER: US 10/161,403
;; PRIOR FILING DATE: 2002-05-30
;; NUMBER OF SEQ ID NOS: 129
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 18
;; LENGTH: 22118
;; TYPE: DNA
;; ORGANISM: Mus musculus
;; PUBLICATION INFORMATION:
;; DATABASE ACCESSION NUMBER: GenBank X82564
;; DATABASE ENTRY DATE: 1996-04-09
US-11-082-154A-18

Query Match 74.4%; Score 13.4; DB 12; Length 22118;
Best Local Similarity 93.3%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGGUCCGACGCG 15
DB 7580 AGAGGACGACGCG 7566

RESULT 34

US-10-933-982-106785
;; Sequence 106785, Application US/10933982
;; Publication No. US20060051769A1
;; GENERAL INFORMATION:
;; APPLICANT: Barts, Jennifer
;; TITLE OF INVENTION: Methods of Genetic Analysis of E. coli
;; FILE REFERENCE: 3700
;; CURRENT APPLICATION NUMBER: US/10/933,982
;; CURRENT FILING DATE: 2004-09-03
;; NUMBER OF SEQ ID NOS: 224976
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 106785
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: E. coli
US-10-933-982-106785

Query Match 73.3%; Score 13.2; DB 7; Length 25;
Best Local Similarity 72.2%; Pred. No. 5.8e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGGUCCGACGCGUA 18
DB 3 ATATGCTCGACGCTGTA 20

RESULT 35
US-11-121-849-355753
;; Sequence 355753, Application US/11121849
;; Publication No. US20050272080A1
;; GENERAL INFORMATION:
;; APPLICANT: John Palma
;; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded ss
;; FILE REFERENCE: 3684.1
;; CURRENT APPLICATION NUMBER: US/11/121,849
;; CURRENT FILING DATE: 2005-05-03
;; PRIOR APPLICATION NUMBER: 60/567,949
;; PRIOR FILING DATE: 2004-05-03
;; NUMBER OF SEQ ID NOS: 673904
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 355753
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-11-121-849-355753

Query Match 73.3%; Score 13.2; DB 12; Length 25;
Best Local Similarity 77.8%; Pred. No. 5.8e+02;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGGUCCGACGCGUA 18
DB 5 AGAGGTAAGTCTGCGGCA 22

RESULT 36
US-09-925-065A-290316
;; Sequence 290316, Application US/09925065A
;; Publication No. US20040181048A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single
;; FILE REFERENCE: 108927.135
;; CURRENT APPLICATION NUMBER: US/09/925,065A
;; CURRENT FILING DATE: 2001-08-08
;; PRIOR APPLICATION NUMBER: US 60/243,096
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: US 60/252,147
;; PRIOR FILING DATE: 2000-11-20
;; PRIOR APPLICATION NUMBER: US 60/250,092
;; PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 290316
LENGTH: 479
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-290316

Query Match 73.3%; Score 13.2; DB 6; Length 479;
Best Local Similarity 72.2%; Pred. No. 5.4e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGUA 18
DB 224 AGAGGCTGCGACGAGCTA 241

RESULT 37

US-09-925-065A-354563
Sequence 354563, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
Nucleotide Polymorphisms in the Human Genome
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 354563
LENGTH: 514
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-354563

Query Match 73.3%; Score 13.2; DB 6; Length 514;
Best Local Similarity 72.2%; Pred. No. 5.4e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGUA 18
DB 330 AGAGGCTGCGTGGCAGTA 347

RESULT 38

US-09-925-065A-143833
Sequence 143833, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
Nucleotide Polymorphisms in the Human Genome
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 143833
LENGTH: 526
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-143833

Query Match 73.3%; Score 13.2; DB 6; Length 526;
Best Local Similarity 77.8%; Pred. No. 5.4e+02;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGUA 18
DB 35 AGAGGCTGCGACGAGCTA 52

RESULT 39

US-09-925-065A-143834
Sequence 143834, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
Nucleotide Polymorphisms in the Human Genome
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 143834
LENGTH: 526
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-143834

Query Match 73.3%; Score 13.2; DB 6; Length 526;
Best Local Similarity 77.8%; Pred. No. 5.4e+02;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGUA 18
DB 35 AGAGGCTGCGACGAGCTA 52

RESULT 40

US-10-475-075-758
Sequence 758, Application US/10475075
Publication No. US20060053498A1
GENERAL INFORMATION:
APPLICANT: Benjamin, Stephanie
APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Mline Edwards, Jean-Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Giordano, Jean-Yves
TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins

```
FILE REFERENCE: G-081US03PCT
CURRENT APPLICATION NUMBER: US/10/475,075
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: PCT/IB01/00914
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 918
SOFTWARE: Patent.pm
SEQ ID NO 758
TYPE: DNA
LENGTH: 543
ORGANISM: Homo sapiens
US-10-475-075-758

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 6; Length 543;
Pred. No. 5.4e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUCGACCGGUA 18
Db 285 AAAGGTCCTCCACGCGTA 302

RESULT 41
US-09-925-065A-742789/C
Sequence 742789, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 742789
LENGTH: 548
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-742789

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 6; Length 548;
Pred. No. 5.4e+02;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUCGACCGGUA 18
Db 173 ACAGGGCCGACACGCGTA 156

RESULT 42
US-09-925-065A-505693/C
Sequence 505693, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
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PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 505693
LENGTH: 550
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-505693

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 6; Length 550;
Pred. No. 5.4e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUCGACCGGUA 18
Db 292 AGAGGTCCTCCACGCGTA 275

RESULT 43
US-09-925-065A-839454
Sequence 839454, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 839454
LENGTH: 584
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-839454

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 6; Length 584;
Pred. No. 5.4e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUCGACCGGUA 18
Db 14 AGAGGTCCTCCACTGTA 31

RESULT 44
US-09-925-065A-847993/C
Sequence 847993, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
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; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 847993
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-847993

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 6; Length 585;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACCGCGUA 18
DB 574 AGAGGCTCTCCTTGTA 557

RESULT 45
US-09-925-065A-516742
; Sequence 516742, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827,135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 516742
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-516742

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 6; Length 594;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACCGCGUA 18
DB 429 AGAGGCTGCGACCTTGTA 446

RESULT 46
US-09-925-065A-516743
; Sequence 516743, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
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; FILE REFERENCE: 108827,135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 516743
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-516743

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 6; Length 594;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACCGCGUA 18
DB 429 AGAGGCTGCGACCTTGTA 446

RESULT 47
US-09-925-065A-516744
; Sequence 516744, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827,135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 516744
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-516744

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 6; Length 594;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACCGCGUA 18
DB 429 AGAGGCTGCGACCTTGTA 446

RESULT 48
US-09-925-065A-151923
; Sequence 151923, Application US/09925065A
; Publication No. US20040181048A1
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; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151923
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-151923

```

```

Query Match          73.3%; Score 13.2; DB 6; Length 603;
Best Local Similarity 72.2%; Pred. No. 5.4e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      1 AGAGGUGCGACGCGGUA 18
Db      492 AGAGGUGCGACGCGGUA 509

```

```

RESULT 49
US-09-925-065A-841497
; Sequence 841497, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 841497
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-841497

```

```

Query Match          73.3%; Score 13.2; DB 6; Length 625;
Best Local Similarity 72.2%; Pred. No. 5.4e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      1 AGAGGUGCGACGCGGUA 18
Db      457 AGAGGUGCGACGCGGUA 474

```

RESULT 50

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US-09-925-065A-821405
; Sequence 821405, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 821405
; LENGTH: 629
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-821405

```

```

Query Match          73.3%; Score 13.2; DB 6; Length 629;
Best Local Similarity 72.2%; Pred. No. 5.4e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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```

QY      1 AGAGGUGCGACGCGGUA 18
Db      461 AGAGGUGCGACGCGGUA 478

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Search completed: March 19, 2006, 05:42:21
Job time : 1217.62 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:35:47 ; Search time 2695.85 Seconds
(without alignments)
55.214 Million cell updates/sec

Title: US-10-800-926-1

Sequence: 1 agagggucgacgcgsgua 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database :

Published Applications NA Main:
1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
4: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
5: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*
6: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:*
7: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*
8: /cgn2_6/prodata/1/pubpna/US10F_PUBCOMB.seq:*
9: /cgn2_6/prodata/1/pubpna/US10G_PUBCOMB.seq:*
10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18	100.0	18	3	US-09-824-468-60 Sequence 60, Appl
C 2	18	100.0	18	3	US-09-888-326-485 Sequence 485, Appl
C 3	18	100.0	18	3	US-09-776-479-4 Sequence 4, Appl
C 4	18	100.0	18	3	US-09-776-479-4 Sequence 56, Appl
C 5	18	100.0	18	3	US-09-954-9878-67 Sequence 67, Appl
C 6	18	100.0	18	3	US-09-776-479-4 Sequence 4, Appl
C 7	18	100.0	18	3	US-09-776-479-4 Sequence 56, Appl
C 8	18	100.0	18	3	US-10-112-653-4 Sequence 4, Appl
C 9	18	100.0	18	3	US-10-017-995-4 Sequence 56, Appl
C 10	18	100.0	18	3	US-10-161-229-54 Sequence 54, Appl
C 11	18	100.0	18	3	US-10-187-264A-60 Sequence 60, Appl
C 12	18	100.0	18	3	US-10-265-072-75 Sequence 75, Appl
C 13	18	100.0	18	3	US-10-306-522-60 Sequence 60, Appl
C 14	18	100.0	18	3	US-10-314-578-4 Sequence 4, Appl
C 15	18	100.0	18	3	US-10-314-578-4 Sequence 56, Appl
C 16	18	100.0	18	3	US-10-373-381-47 Sequence 47, Appl
C 17	18	100.0	18	3	US-10-719-493-60 Sequence 60, Appl
C 18	18	100.0	18	3	US-10-627-331-60 Sequence 60, Appl
C 19	18	100.0	18	3	US-10-877-369-47 Sequence 47, Appl
C 20	18	100.0	18	3	US-10-831-778-4 Sequence 4, Appl
C 21	18	100.0	18	3	US-10-831-778-4 Sequence 56, Appl
C 22	18	100.0	18	3	US-10-876-892-47 Sequence 47, Appl
C 23	18	100.0	18	3	US-10-876-892-47 Sequence 47, Appl

C 24	18	100.0	18	8	US-10-876-965-47 Sequence 47, Appl
C 25	18	100.0	18	8	US-10-800-926-1 Sequence 1, Appl
C 26	18	100.0	18	9	US-10-627-413-60 Sequence 60, Appl
C 27	18	100.0	18	9	US-10-921-088-60 Sequence 60, Appl
C 28	18	100.0	18	10	US-11-084-777-67 Sequence 67, Appl
C 29	18	100.0	18	10	US-11-071-836-60 Sequence 60, Appl
C 30	18	100.0	18	10	US-11-110-189-60 Sequence 43, Appl
C 31	18	100.0	17	6	US-10-053-645A-43 Sequence 9, Appl
C 32	17	94.4	17	6	US-10-053-645A-9 Sequence 5, Appl
C 33	17	94.4	17	9	US-10-822-205-5 Sequence 9, Appl
C 34	17	94.4	17	9	US-10-961-458-9 Sequence 9, Appl
C 35	16.4	91.1	20	3	US-09-781-980-4 Sequence 4, Appl
C 36	16	88.9	16	10	US-11-021-729-58 Sequence 58, Appl
C 37	16	88.9	32	3	US-09-965-116A-79 Sequence 79, Appl
C 38	16	88.9	32	3	US-09-965-116A-80 Sequence 80, Appl
C 39	16	88.9	32	8	US-10-694-075-79 Sequence 79, Appl
C 40	16	88.9	32	8	US-10-694-075-80 Sequence 80, Appl
C 41	16	88.9	32	8	US-10-694-383-79 Sequence 79, Appl
C 42	16	88.9	32	8	US-10-694-383-80 Sequence 80, Appl
C 43	16	88.9	32	8	US-10-694-418-79 Sequence 79, Appl
C 44	16	88.9	32	8	US-10-694-418-80 Sequence 80, Appl
C 45	15	83.3	17	6	US-10-053-645A-8 Sequence 8, Appl
C 46	15	83.3	17	9	US-10-961-458-9 Sequence 9, Appl
C 47	15	83.3	337	8	US-10-723-860-668 Sequence 668, Appl
C 48	15	83.3	337	9	US-10-756-149-689 Sequence 689, Appl
C 49	15	83.3	363	7	US-10-918-599-126012 Sequence 126012, A
C 50	15	83.3	381	3	US-09-918-995-34640 Sequence 34640, A
C 51	15	83.3	588	7	US-10-767-701-4082 Sequence 4082, A
C 52	15	83.3	779	8	US-10-478-914-58 Sequence 58, Appl
C 53	15	83.3	1936	3	US-09-954-456-1138 Sequence 1138, A
C 54	15	83.3	1936	8	US-10-843-641A-4165 Sequence 4165, A
C 55	15	83.3	3870	8	US-10-723-860-5301 Sequence 5301, A
C 56	14.8	82.2	18	3	US-09-734-846-69 Sequence 69, Appl
C 57	14.8	82.2	18	6	US-10-302-262-69 Sequence 69, Appl
C 58	14.8	82.2	1512	7	US-10-425-114-26340 Sequence 26340, A
C 59	14.8	82.2	2140405	5	US-10-027-632-76212 Sequence 76212, A
C 60	14.8	82.2	2140405	6	US-10-027-632-76212 Sequence 76212, A
C 61	14.4	80.0	25	8	US-10-719-900-359937 Sequence 359937, A
C 62	14.4	80.0	25	10	US-11-036-317-604153 Sequence 604153, A
C 63	14.4	80.0	378	9	US-10-779-543-11148 Sequence 11148, A
C 64	14.4	80.0	821	8	US-10-425-115-18852 Sequence 18852, A
C 65	14.4	80.0	886	8	US-10-425-115-16778 Sequence 16778, A
C 66	14.4	80.0	957	8	US-10-425-115-16779 Sequence 16779, A
C 67	14.4	80.0	1532	7	US-10-767-701-13328 Sequence 13328, A
C 68	14.4	80.0	2000	3	US-09-938-842A-3764 Sequence 3764, A
C 69	14.4	80.0	2000	3	US-09-938-842A-3764 Sequence 3764, A
C 70	14.4	80.0	2103	7	US-10-767-701-13076 Sequence 13076, A
C 71	14.4	80.0	2193	3	US-09-997-722-55 Sequence 55, Appl
C 72	14.4	80.0	27846	3	US-09-997-722-55 Sequence 55, Appl
C 73	14.4	80.0	36620	7	US-10-380-641-31 Sequence 31, Appl
C 74	14.4	80.0	36620	9	US-10-636-730-31 Sequence 31, Appl
C 75	14.4	80.0	37474	3	US-09-952-066-26 Sequence 26, Appl
C 76	14.4	80.0	37474	3	US-10-380-641-26 Sequence 26, Appl
C 77	14.4	80.0	37474	8	US-10-645-883A-8 Sequence 8, Appl
C 78	14.4	80.0	37474	8	US-10-645-883A-8 Sequence 8, Appl
C 79	14.4	80.0	37474	9	US-10-636-730-26 Sequence 26, Appl
C 80	14.4	80.0	37474	9	US-10-507-098-3 Sequence 3, Appl
C 81	14.4	80.0	38519	3	US-09-952-066-29 Sequence 29, Appl
C 82	14.4	80.0	38519	7	US-10-380-641-29 Sequence 29, Appl
C 83	14.4	80.0	38519	7	US-10-636-730-29 Sequence 29, Appl
C 84	14.4	80.0	104729	8	US-10-723-860-1434 Sequence 1434, A
C 85	14.4	80.0	104729	8	US-10-723-860-1434 Sequence 1434, A
C 86	14.4	80.0	13117	8	US-10-779-543-11148 Sequence 11148, A
C 87	14.4	80.0	13117	8	US-10-779-543-11148 Sequence 11148, A
C 88	14.4	80.0	133179	9	US-10-297-465A-1 Sequence 1, Appl
C 89	14.4	80.0	2731748	7	US-10-053-645A-10 Sequence 10, Appl
C 90	14	77.8	17	6	US-10-961-458-10 Sequence 10, Appl
C 91	14	77.8	17	9	US-10-961-458-10 Sequence 10, Appl
C 92	14	77.8	384	7	US-10-424-599-71632 Sequence 71632, A
C 93	14	77.8	389	7	US-10-424-599-71632 Sequence 71632, A
C 94	14	77.8	1454	4	US-09-925-065A-552179 Sequence 552179, A
C 95	14	77.8	1498	7	US-10-425-114-12591 Sequence 12591, A
C 96	14	77.8	1498	8	US-10-425-114-12591 Sequence 12591, A

389	13.2	73.3	400	9	US-10-498-978-5	Sequence 5, Appl1
390	13.2	73.3	402	3	US-09-214-474A-3	Sequence 7, Appl1
391	13.2	73.3	402	3	US-09-214-474A-7	Sequence 7, Appl1
392	13.2	73.3	426	8	US-10-425-115-118550	Sequence 118550
393	13.2	73.3	432	7	US-10-437-963-38964	Sequence 38964
394	13.2	73.3	451	7	US-10-437-963-3135	Sequence 3135, Ap
395	13.2	73.3	457	7	US-10-437-963-22345	Sequence 22345, A
396	13.2	73.3	468	3	US-09-738-626-597	Sequence 597, App
397	13.2	73.3	474	3	US-09-732-627A-1668	Sequence 1668, Ap
398	13.2	73.3	476	7	US-10-242-535A-33948	Sequence 33948, A
399	13.2	73.3	476	7	US-10-085-783A-33948	Sequence 33948, A
400	13.2	73.3	479	4	US-09-925-065A-220316	Sequence 220316, A
401	13.2	73.3	485	8	US-10-425-115-177668	Sequence 177668, A
402	13.2	73.3	487	5	US-10-027-632-323248	Sequence 323248, A
403	13.2	73.3	487	5	US-10-027-632-323248	Sequence 323248, A
404	13.2	73.3	488	5	US-10-027-632-324208	Sequence 324208, A
405	13.2	73.3	488	6	US-10-027-632-324208	Sequence 324208, A
406	13.2	73.3	490	8	US-10-357-930-10772	Sequence 10772, A
407	13.2	73.3	505	3	US-09-918-995-22116	Sequence 22116, A
408	13.2	73.3	506	3	US-09-974-300-4350	Sequence 4350, Ap
409	13.2	73.3	512	8	US-10-363-345A-30631	Sequence 30631, A
410	13.2	73.3	512	8	US-10-363-345A-30631	Sequence 30631, A
411	13.2	73.3	512	9	US-10-363-483A-30631	Sequence 30631, A
412	13.2	73.3	512	9	US-10-363-483A-30632	Sequence 30632, A
413	13.2	73.3	514	4	US-09-925-065A-334563	Sequence 334563, A
414	13.2	73.3	514	8	US-10-363-345A-5511	Sequence 5511, Ap
415	13.2	73.3	514	8	US-10-363-345A-5512	Sequence 5512, Ap
416	13.2	73.3	514	9	US-10-363-483A-5511	Sequence 5511, Ap
417	13.2	73.3	514	9	US-10-363-483A-5512	Sequence 5512, Ap
418	13.2	73.3	515	5	US-10-027-632-279122	Sequence 279122, A
419	13.2	73.3	515	5	US-10-027-632-279123	Sequence 279123, A
420	13.2	73.3	515	6	US-10-027-632-279122	Sequence 279122, A
421	13.2	73.3	515	6	US-10-027-632-279123	Sequence 279123, A
422	13.2	73.3	521	8	US-10-723-860-1191	Sequence 1191, Ap
423	13.2	73.3	525	8	US-10-363-345A-25831	Sequence 25831, A
424	13.2	73.3	525	8	US-10-363-345A-25832	Sequence 25832, A
425	13.2	73.3	525	9	US-10-363-483A-25831	Sequence 25831, A
426	13.2	73.3	525	9	US-10-363-483A-25832	Sequence 25832, A
427	13.2	73.3	526	4	US-09-925-065A-143833	Sequence 143833, A
428	13.2	73.3	526	4	US-09-925-065A-143834	Sequence 143834, A
429	13.2	73.3	531	6	US-10-029-386-6160	Sequence 6160, Ap
430	13.2	73.3	531	6	US-09-925-065A-742789	Sequence 742789, A
431	13.2	73.3	530	4	US-09-925-065A-505693	Sequence 505693, A
432	13.2	73.3	531	7	US-10-767-701-328	Sequence 328, App
433	13.2	73.3	533	9	US-10-972-079-74607	Sequence 74607, A
434	13.2	73.3	534	9	US-10-972-079-74607	Sequence 74607, A
435	13.2	73.3	534	9	US-10-027-632-207481	Sequence 207481, A
436	13.2	73.3	534	9	US-10-027-632-207481	Sequence 207481, A
437	13.2	73.3	537	8	US-10-363-345A-30361	Sequence 30361, A
438	13.2	73.3	537	8	US-10-363-345A-30362	Sequence 30362, A
439	13.2	73.3	537	9	US-10-363-483A-30361	Sequence 30361, A
440	13.2	73.3	537	9	US-10-363-483A-30362	Sequence 30362, A
441	13.2	73.3	537	9	US-10-363-483A-30362	Sequence 30362, A
442	13.2	73.3	537	9	US-10-363-483A-30362	Sequence 30362, A
443	13.2	73.3	537	9	US-10-363-483A-30362	Sequence 30362, A
444	13.2	73.3	537	9	US-10-363-483A-30362	Sequence 30362, A
445	13.2	73.3	537	9	US-10-363-483A-30362	Sequence 30362, A
446	13.2	73.3	537	9	US-10-363-483A-30362	Sequence 30362, A
447	13.2	73.3	537	9	US-10-363-483A-30362	Sequence 30362, A
448	13.2	73.3	537	9	US-10-363-483A-30362	Sequence 30362, A
449	13.2	73.3	537	9	US-10-363-483A-30362	Sequence 30362, A
450	13.2	73.3	537	9	US-10-363-483A-30362	Sequence 30362, A
451	13.2	73.3	537	9	US-10-363-483A-30362	Sequence 30362, A
452	13.2	73.3	537	9	US-10-363-483A-30362	Sequence 30362, A
453	13.2	73.3	537	9	US-10-363-483A-30362	Sequence 30362, A
454	13.2	73.3	537	9	US-10-363-483A-30362	Sequence 30362, A
455	13.2	73.3	537	9	US-10-363-483A-30362	Sequence 30362, A
456	13.2	73.3	537	9	US-10-363-483A-30362	Sequence 30362, A
457	13.2	73.3	537	9	US-10-363-483A-30362	Sequence 30362, A
458	13.2	73.3	537	9	US-10-363-483A-30362	Sequence 30362, A
459	13.2	73.3	537	9	US-10-363-483A-30362	Sequence 30362, A
460	13.2	73.3	537	9	US-10-363-483A-30362	Sequence 30362, A
461	13.2	73.3	537	9	US-10-363-483A-30362	Sequence 30362, A


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c 973 12.8 71.1 996 9 US-10-200-545-35 Sequence 35, Appl
c 974 12.8 71.1 999 7 US-10-425-114-980 Sequence 980, App
c 975 12.8 71.1 1008 7 US-09-873-367C-313 Sequence 313, App
c 976 12.8 71.1 1008 8 US-10-370-715B-203 Sequence 203, App
c 977 12.8 71.1 1008 9 US-10-843-641A-313 Sequence 313, App
c 978 12.8 71.1 1015 5 US-10-037-270-734 Sequence 734, App
c 979 12.8 71.1 1015 6 US-10-117-722-734 Sequence 734, App
c 980 12.8 71.1 1015 6 US-10-122-851-734 Sequence 734, App
c 981 12.8 71.1 1018 3 US-09-925-298-279 Sequence 279, App
c 982 12.8 71.1 1018 5 US-10-102-806-279 Sequence 279, App
c 983 12.8 71.1 1020 7 US-10-641-643-663 Sequence 663, App
c 984 12.8 71.1 1023 7 US-10-282-122A-13828 Sequence 13828, A
c 985 12.8 71.1 1029 6 US-10-156-761-4339 Sequence 4339, App
c 986 12.8 71.1 1032 6 US-10-156-761-4351 Sequence 4351, App
c 987 12.8 71.1 1037 7 US-10-437-963-32660 Sequence 32660, A
c 988 12.8 71.1 1041 7 US-10-767-701-5877 Sequence 5877, App
c 989 12.8 71.1 1043 4 US-09-925-065A-707999 Sequence 707999, A
c 990 12.8 71.1 1043 4 US-09-925-065A-707999 Sequence 707999, A
c 991 12.8 71.1 1043 9 US-10-887-553A-837 Sequence 837, App
c 992 12.8 71.1 1047 9 US-10-450-763-20815 Sequence 20815, A
c 993 12.8 71.1 1050 6 US-10-156-761-3473 Sequence 3473, App
c 994 12.8 71.1 1052 7 US-10-439-703-65 Sequence 65, Appl
c 995 12.8 71.1 1052 9 US-10-887-553A-473 Sequence 473, App
c 996 12.8 71.1 1078 8 US-10-425-115-170712 Sequence 170712, A
c 997 12.8 71.1 1084 8 US-10-363-345A-34349 Sequence 34349, A
c 998 12.8 71.1 1084 8 US-10-363-345A-34350 Sequence 34350, A
c 999 12.8 71.1 1084 9 US-10-363-483A-34349 Sequence 34349, A
c1000 12.8 71.1 1084 9 US-10-363-483A-34350 Sequence 34350, A

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ALIGNMENTS

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RESULT 1
; US-09-824-468-60/c
; Sequence 60, Application US/09824468
; Patent No. US20020064515A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the
; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
; TITLE OF INVENTION: Cytokines
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/824,468
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/286,098
; PRIOR FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
; US-09-824-468-60

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGUGCGACGCGGUA 1

RESULT 2
; US-09-888-326-485/c
; Sequence 485, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George

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; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AMS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 485
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphorothioate backbone
; US-09-888-326-485

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGUGCGACGCGGUA 1

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RESULT 3
; US-09-776-479-4/c
; Sequence 4, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fournon, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
; US-09-776-479-4

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGUGCGACGCGGUA 1

RESULT 4
; US-09-776-479-56/c
; Sequence 56, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fournon, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the

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TITLE OF INVENTION: Treatment of Asthma and Allergy
FILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 56
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-776-479-56

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGTCGACGCGGTA 1

RESULT 5

US-09-954-987B-67/c
Sequence 67, Application US/09954987B
Publication No. US20030104523A1
GENERAL INFORMATION:
APPLICANT: Stefan Bauer
APPLICANT: Grayson B. Lipford
APPLICANT: Hermann Wagner
TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
FILE REFERENCE: C1041/7016 (AMS)
CURRENT APPLICATION NUMBER: US/09/954,987B
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US 60/233,035
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/263,657
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: US 60/291,726
PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: US 60/300,210
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 230
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 67
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-09-954-987B-67

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGTCGACGCGGTA 1

RESULT 6

US-09-776-479-4/c
Sequence 4, Application US/09776479
Publication No. US20040067902A9
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
APPLICANT: Petersen, Deanna M.
APPLICANT: Fourn, Yves

TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
FILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-776-479-4

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGTCGACGCGGTA 1

RESULT 7

US-09-776-479-56/c
Sequence 56, Application US/09776479
Publication No. US20040067902A9
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
APPLICANT: Petersen, Deanna M.
APPLICANT: Fourn, Yves
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
FILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 56
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-776-479-56

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGTCGACGCGGTA 1

RESULT 8

US-10-112-653-4/c
Sequence 4, Application US/10112653
Publication No. US20030050268A1
GENERAL INFORMATION:
APPLICANT: Kriegl, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
FILE REFERENCE: C01039/70060 (AMS)
CURRENT APPLICATION NUMBER: US/10/112,653
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: US 60/279,642

;; PRIOR FILING DATE: 2001-03-29
;; NUMBER OF SEQ ID NOS: 1040
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 4
;; LENGTH: 18
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-4

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18
Db 18 AGAGGTCGACGCGGTA 1

RESULT 9
US-10-017-995-4/c
; Sequence 4, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bretzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-4

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18
Db 18 AGAGGTCGACGCGGTA 1

RESULT 10
US-10-017-995-56/c
; Sequence 56, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bretzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-56

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18
Db 18 AGAGGTCGACGCGGTA 1

RESULT 11
US-10-161-229-54/c
; Sequence 54, Application US/10161229
; Publication No. US20030100527A1
; GENERAL INFORMATION:
; APPLICANT: Kriegl, Arthur M.
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules for
; FILE REFERENCE: C01039/70061
; CURRENT APPLICATION NUMBER: US/10/161,229
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 09/191,170
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 08/960,774
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-161-229-54

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18
Db 18 AGAGGTCGACGCGGTA 1

RESULT 12
US-10-187-264A-60/c
; Sequence 60, Application US/10187264A
; Publication No. US20030162734A1
; GENERAL INFORMATION:
; APPLICANT: Kriegl, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Methods for Treating and Preventing
; FILE REFERENCE: C01039,70062,US
; CURRENT APPLICATION NUMBER: US/10/187,264A
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/630,319
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 08/960,774
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15

NUMBER OF SEQ ID NOS: 124
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-10-187-264A-60

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGTCGACGCGGTA 18
DB 18 AGAGGTCGACGCGGTA 1

RESULT 13
US-10-265-072-75/c

Sequence 75; Application US/10265072
Publication No. US20030166001A1
GENERAL INFORMATION:
APPLICANT: Lipford, Grayson
TITLE OF INVENTION: TOLL-LIKE RECEPTOR 3 SIGNALING AGONISTS AND ANTAGONISTS
FILE REFERENCE: C01041.70031.US
CURRENT APPLICATION NUMBER: US/10/265,072
CURRENT FILING DATE: 2002-10-05
NUMBER OF SEQ ID NOS: 117
SOFTWARE: PatentIn version 3.1
SEQ ID NO 75
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-10-265-072-75

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGTCGACGCGGTA 18
DB 18 AGAGGTCGACGCGGTA 1

RESULT 14
US-10-306-522-60/c

Sequence 60; Application US/10306522
Publication No. US20030191079A1
GENERAL INFORMATION:
APPLICANT: Kriegl, Arthur M.
APPLICANT: Kliman, Dennis
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: Methods for Treating and Preventing
FILE REFERENCE: C01039.70062.US
CURRENT APPLICATION NUMBER: US/10/306,522
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: US 09/630,319
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 08/960,774
PRIOR FILING DATE: 1997-10-30
PRIOR APPLICATION NUMBER: US 08/738,652
PRIOR FILING DATE: 1996-10-30
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR FILING DATE: 1995-02-07
PRIOR APPLICATION NUMBER: US 08/276,358
PRIOR FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 124
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 60
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-10-306-522-60

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGTCGACGCGGTA 18
DB 18 AGAGGTCGACGCGGTA 1

RESULT 15
US-10-314-578-4/c

Sequence 4; Application US/10314578
Publication No. US20030212026A1
GENERAL INFORMATION:
APPLICANT: Kriegl, Arthur M.
APPLICANT: Schetter, Christian
APPLICANT: Vollmer, Jorg
TITLE OF INVENTION: Immunostimulatory Nucleic Acids
FILE REFERENCE: C1039/7035 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/314,578
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 60/156,113
PRIOR FILING DATE: 1999-09-25
PRIOR APPLICATION NUMBER: US 60/156,135
PRIOR FILING DATE: 1999-09-27
PRIOR APPLICATION NUMBER: US 60/227,436
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 1145
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-10-314-578-4

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGTCGACGCGGTA 18
DB 18 AGAGGTCGACGCGGTA 1

RESULT 16
US-10-314-578-56/c

Sequence 56; Application US/10314578
Publication No. US20030212026A1
GENERAL INFORMATION:
APPLICANT: Kriegl, Arthur M.
APPLICANT: Schetter, Christian
APPLICANT: Vollmer, Jorg
TITLE OF INVENTION: Immunostimulatory Nucleic Acids
FILE REFERENCE: C1039/7035 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/314,578
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 60/156,113
PRIOR FILING DATE: 1999-09-25
PRIOR APPLICATION NUMBER: US 60/156,135
PRIOR FILING DATE: 1999-09-27
PRIOR APPLICATION NUMBER: US 60/227,436
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 1145

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 56
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-10-314-578-56

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUCGACGCGGUA 18
|||||:|||||:|
Db 18 AGAGGGTCGCACGCGGTA 1

RESULT 17
US-10-373-381-47/c
Sequence 47, Application US/10373381
Publication No. US20040030118A1
GENERAL INFORMATION:
APPLICANT: Wagner, Hermann
APPLICANT: Lipford, Grayson
TITLE OF INVENTION: Methods for Regulating Hematopoiesis
TITLE OF INVENTION: Using CpG-Oligonucleotides
FILE REFERENCE: C01041.70035.US
CURRENT APPLICATION NUMBER: US/10/373,381
CURRENT FILING DATE: 2003-02-24
PRIOR APPLICATION NUMBER: US 09/241,653
PRIOR FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: US 60/085,516
PRIOR FILING DATE: 1998-05-14
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 47
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-10-373-381-47

Query Match 100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUCGACGCGGUA 18
|||||:|||||:|
Db 18 AGAGGGTCGCACGCGGTA 1

RESULT 18
US-10-719-493-60/c
Sequence 60, Application US/10719493
Publication No. US20040087538A1
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
TITLE OF INVENTION: Methods of Treating Cancer Using
TITLE OF INVENTION: Immunostimulatory Oligonucleotides
FILE REFERENCE: C1039/7021/HCL
CURRENT APPLICATION NUMBER: US/10/719,493
CURRENT FILING DATE: 2003-11-21
PRIOR APPLICATION NUMBER: US 08/960,774
PRIOR FILING DATE: 1997-10-30
PRIOR APPLICATION NUMBER: US 08/738,652
PRIOR FILING DATE: 1996-10-30
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR FILING DATE: 1995-02-07
PRIOR APPLICATION NUMBER: US 08/276,358
PRIOR FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 123

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-10-719-493-60

Query Match 100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUCGACGCGGUA 18
|||||:|||||:|
Db 18 AGAGGGTCGCACGCGGTA 1

RESULT 19
US-10-627-331-60/c
Sequence 60, Application US/10627331
Publication No. US20040106568A1
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Kliman, Dennis
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: Methods for Treating and Preventing
TITLE OF INVENTION: Infectious Disease
FILE REFERENCE: C01039.70062.US
CURRENT APPLICATION NUMBER: US/10/627,331
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US 09/630,319
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 08/960,774
PRIOR FILING DATE: 1997-10-30
PRIOR APPLICATION NUMBER: US 08/738,652
PRIOR FILING DATE: 1996-10-30
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR FILING DATE: 1995-02-07
PRIOR APPLICATION NUMBER: US 08/276,358
PRIOR FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 124
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-10-627-331-60

Query Match 100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUCGACGCGGUA 18
|||||:|||||:|
Db 18 AGAGGGTCGCACGCGGTA 1

RESULT 20
US-10-877-369-47/c
Sequence 47, Application US/10877369
Publication No. US20040234512A1
GENERAL INFORMATION:
APPLICANT: Wagner, Hermann
APPLICANT: Lipford, Grayson
TITLE OF INVENTION: Methods for Regulating Hematopoiesis
TITLE OF INVENTION: Using CpG-Oligonucleotides
FILE REFERENCE: C1041.70020US01
CURRENT APPLICATION NUMBER: US/10/877,369
CURRENT FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 09/241,653

PRIOR FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: US 60/085,516
PRIOR FILING DATE: 1998-05-14
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 47
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-10-877-369-47

Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGTCGCGACCGGTA 1

RESULT 21
US-10-831-778-4/c
Sequence 4, Application US/10831778
Publication No. US20040235774A1
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
APPLICANT: Petersen, Deanna M.
APPLICANT: Fourn, Yves
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
FILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/831,778
PRIOR FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-10-831-778-4

Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGTCGCGACCGGTA 1

RESULT 22
US-10-831-778-56/c
Sequence 56, Application US/10831778
Publication No. US20040235774A1
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
APPLICANT: Petersen, Deanna M.
APPLICANT: Fourn, Yves
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
FILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/831,778
PRIOR FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 56
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-10-831-778-56

Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGTCGCGACCGGTA 1

RESULT 23
US-10-876-892-47/c
Sequence 47, Application US/10876892
Publication No. US20040235777A1
GENERAL INFORMATION:
APPLICANT: Wagner, Hermann
APPLICANT: Lipford, Grayson
TITLE OF INVENTION: Methods for Regulating Hematopoiesis
FILE REFERENCE: C1041.700020503
CURRENT APPLICATION NUMBER: US/10/876,892
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 09/241,653
PRIOR FILING DATE: 1999-02-02
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 47
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-10-876-892-47

Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGTCGCGACCGGTA 1

RESULT 24
US-10-876-965-47/c
Sequence 47, Application US/10876965
Publication No. US20040235778A1
GENERAL INFORMATION:
APPLICANT: Wagner, Hermann
APPLICANT: Lipford, Grayson
TITLE OF INVENTION: Methods for Regulating Hematopoiesis
FILE REFERENCE: C1041.700020502
CURRENT APPLICATION NUMBER: US/10/876,965
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 09/241,653
PRIOR FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: US 60/085,516
PRIOR FILING DATE: 1998-05-14
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 47
LENGTH: 18
TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-10-876-965-47

Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUGCAGCGGUA 18
DB 18 AGAGGTCGACGCGGTA 1

RESULT 25
US-10-800-926-1
Sequence 1, Application US/10800926
Publication No. US20050032731A1
GENERAL INFORMATION:
APPLICANT: MARSHALL, WILLIAM E.
TITLE OF INVENTION: OLIGORIBONUCLEOTIDES ALERT THE IMMUNE SYSTEM OF ANIMALS
FILE REFERENCE: P01936US06
CURRENT APPLICATION NUMBER: US/10/800,926
CURRENT FILING DATE: 2004-03-15
PRIOR APPLICATION NUMBER: 09/883,550
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 09/193,653
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 08/739,264
PRIOR FILING DATE: 1996-10-29
PRIOR APPLICATION NUMBER: 08/517,016
PRIOR FILING DATE: 1995-08-18
PRIOR APPLICATION NUMBER: 08/376,175
PRIOR FILING DATE: 1995-01-20
PRIOR APPLICATION NUMBER: 08/059,745
PRIOR FILING DATE: 1993-05-11
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 1
LENGTH: 18
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-800-926-1

Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUGCAGCGGUA 18
DB 1 AGAGGGUGCAGCGGUA 18

RESULT 26
US-10-627-413-60/C
Sequence 60, Application US/10627413
Publication No. US20050101554A1
GENERAL INFORMATION:
APPLICANT: Kriesel, Arthur M.
APPLICANT: Kleinman, Dennis
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: Methods for Treating and Preventing
TITLE OF INVENTION: Infectious Disease
FILE REFERENCE: C01039,70062.US
CURRENT APPLICATION NUMBER: US/10/627,413
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US 09/630,319
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 08/960,774

PRIOR FILING DATE: 1997-10-30
PRIOR APPLICATION NUMBER: US 08/738,652
PRIOR FILING DATE: 1996-10-30
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR FILING DATE: 1995-02-07
PRIOR APPLICATION NUMBER: US 08/276,358
PRIOR FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 124
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-10-627-413-60

Query Match 100.0%; Score 18; DB 9; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUGCAGCGGUA 18
DB 18 AGAGGTCGACGCGGTA 1

RESULT 27
US-10-921-086-60/C
Sequence 60, Application US/10921086
Publication No. US20050101557A1
GENERAL INFORMATION:
APPLICANT: Kriesel, Arthur M.
APPLICANT: Kline, Joel N.
TITLE OF INVENTION: Methods of Treating Allergic and
TITLE OF INVENTION: Asthmatic Disorders Using Immunostimulatory Oligonucleotides
FILE REFERENCE: C1039/7020/HCL
CURRENT APPLICATION NUMBER: US/10/921,086
CURRENT FILING DATE: 2004-08-17
PRIOR APPLICATION NUMBER: US/09/337,584
PRIOR FILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: US 08/960,774
PRIOR FILING DATE: 1997-10-30
PRIOR APPLICATION NUMBER: US 08/738,652
PRIOR FILING DATE: 1996-10-30
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR FILING DATE: 1995-02-07
PRIOR APPLICATION NUMBER: US 08/276,358
PRIOR FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-10-921-086-60

Query Match 100.0%; Score 18; DB 9; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUGCAGCGGUA 18
DB 18 AGAGGTCGACGCGGTA 1

RESULT 28
US-11-084-777-67/C
Sequence 67, Application US/11084777
Publication No. US20050181422A1
GENERAL INFORMATION:
APPLICANT: Stefan Bauer

APPLICANT: Grayson B. Lipford
APPLICANT: Hermann Wagner
TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
FILE REFERENCE: C1041.70016US02
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US 09/954,987
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US 60/300,210
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/291,726
PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: US 60/263,657
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: US 60/233,035
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 230
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 67
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-11-084-777-67

Query Match 100.0%; Score 18; DB 10; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGTCGACGCGGTA 1

RESULT 29
US-11-071-836-60/c
Sequence 60, Application US/11071836
Publication No. US20050182017A1
GENERAL INFORMATION:
APPLICANT: Kriegl, Arthur M.
TITLE OF INVENTION: Methods of Redirecting an Immune
FILE REFERENCE: C1039/7022/HCL
CURRENT FILING DATE: 2005-03-03
PRIOR APPLICATION NUMBER: US 08/960,774
PRIOR FILING DATE: 1997-10-30
PRIOR APPLICATION NUMBER: US 08/738,652
PRIOR FILING DATE: 1996-10-30
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR FILING DATE: 1995-02-07
PRIOR APPLICATION NUMBER: US 08/276,358
PRIOR FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-11-071-836-60

Query Match 100.0%; Score 18; DB 10; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGTCGACGCGGTA 1

RESULT 30
US-11-110-189-60/c
Sequence 60, Application US/11110189
Publication No. US20050197314A1
GENERAL INFORMATION:
APPLICANT: Kriegl, Arthur M.
TITLE OF INVENTION: Methods and Products for Stimulating the
TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
FILE REFERENCE: C1039/7026/HCL
CURRENT FILING DATE: 2005-04-19
PRIOR APPLICATION NUMBER: US/09/286,098
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: US 60/080,729
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-11-110-189-60

Query Match 100.0%; Score 18; DB 10; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGTCGACGCGGTA 1

RESULT 31
US-10-053-645A-43
Sequence 43, Application US/10053645A
Publication No. US20030176376A1
GENERAL INFORMATION:
APPLICANT: Robert E. Klem
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A
TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CRB DECOY OLIGOMERS, BCL-2
FILE REFERENCE: 10412-022-999
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US/10/053,645A
PRIOR FILING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 43
LENGTH: 57
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of artificial sequence: Synthetic Antisense
US-10-053-645A-43

Query Match 100.0%; Score 18; DB 6; Length 57;
Best Local Similarity 88.9%; Pred. No. 11;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18
DB 37 AGAGGTCGACGCGGTA 54

RESULT 32
US-10-053-645A-9/c

```
/ Sequence 9, Application US/10053645A
/ Publication No. US20030176376A1
/ GENERAL INFORMATION:
/ APPLICANT: Robert B. Klem
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A
/ TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CBR DECOY OLIGOMERS, BCL-2
/ TITLE OF INVENTION: ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF
/ FILE REFERENCE: 10412-022-999
/ CURRENT APPLICATION NUMBER: US/10/053,645A
/ PRIOR FILING DATE: 2002-01-22
/ PRIOR APPLICATION NUMBER: 60/263,244
/ PRIOR FILING DATE: 2001-01-22
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Description of artificial sequence: Synthetic Antisense
/ OTHER INFORMATION: Oligonucleotide
US-10-053-645A-9
```

```
Query Match          94.4%; Score 17; DB 6; Length 17;
Best Local Similarity 88.2%; Pred. No. 45;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 2 GAGGUGCGACGCGGUA 18
DB 17 GAGGTCGCACGCGGTA 1
```

```
RESULT 33
US-10-822-205-5/c
/ Sequence 5, Application US/10822205
/ Publication No. US20040235773A1
/ GENERAL INFORMATION:
/ APPLICANT: GREENWALD, RICHARD B.
/ APPLICANT: ZHAO, HONG
/ TITLE OF INVENTION: POLYMERIC OLIGONUCLEOTIDE PRODRUGS
/ FILE REFERENCE: 213.1152CIP
/ CURRENT APPLICATION NUMBER: US/10/822,205
/ CURRENT FILING DATE: 2004-04-09
/ PRIOR APPLICATION NUMBER: 60/462,070
/ PRIOR FILING DATE: 2003-04-13
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 5
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: oligonucleotide
US-10-822-205-5
```

```
Query Match          94.4%; Score 17; DB 8; Length 17;
Best Local Similarity 88.2%; Pred. No. 45;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 2 GAGGUGCGACGCGGUA 18
DB 17 GAGGTCGCACGCGGTA 1
```

```
RESULT 34
US-10-961-458-9/c
/ Sequence 9, Application US/10961458
/ Publication No. US20050170377A1
/ GENERAL INFORMATION:
/ APPLICANT: Reed, John C.
/ TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION
/ FILE REFERENCE: 04040/1200990-US7
```

```
/ CURRENT APPLICATION NUMBER: US/10/961,458
/ CURRENT FILING DATE: 2004-10-07
/ PRIOR APPLICATION NUMBER: US/10/961,458
/ PRIOR FILING DATE: 2004-10-07
/ PRIOR APPLICATION NUMBER: US 09/375,514
/ PRIOR FILING DATE: 1999-08-17
/ PRIOR APPLICATION NUMBER: US 09/080,285
/ PRIOR FILING DATE: 1998-05-18
/ PRIOR APPLICATION NUMBER: US 08/465,485
/ PRIOR FILING DATE: 1995-06-05
/ PRIOR APPLICATION NUMBER: US 08/124,256
/ PRIOR FILING DATE: 1993-09-20
/ PRIOR APPLICATION NUMBER: US 07/840,716
/ PRIOR FILING DATE: 1992-02-21
/ PRIOR APPLICATION NUMBER: US 07/288,692
/ PRIOR FILING DATE: 1988-12-22
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 9
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-961-458-9
```

```
Query Match          94.4%; Score 17; DB 9; Length 17;
Best Local Similarity 88.2%; Pred. No. 45;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 2 GAGGUGCGACGCGGUA 18
DB 17 GAGGTCGCACGCGGTA 1
```

```
RESULT 35
US-09-781-980-4/c
/ Sequence 4, Application US/09781980
/ Publication No. US20010029035A1
/ GENERAL INFORMATION:
/ APPLICANT: EISENHUT, MICHAEL
/ APPLICANT: MIER, WALTER
/ APPLICANT: ERITJA, RAMON
/ APPLICANT: HABERKORN, UWE
/ TITLE OF INVENTION: OLIGONUCLEOTIDE CONJUGATES
/ FILE REFERENCE: 2502498.991110
/ CURRENT APPLICATION NUMBER: US/09/781,980
/ CURRENT FILING DATE: 2001-02-14
/ PRIOR APPLICATION NUMBER: DE 100 06 572
/ PRIOR FILING DATE: 2000-02-14
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: oligonucleotide
US-09-781-980-4
```

```
Query Match          91.1%; Score 16.4; DB 3; Length 20;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGTCGCACACGCGTA 1
```

```
RESULT 36
US-11-021-729-58/c
/ Sequence 58, Application US/11021729
/ Publication No. US20050203042A1
/ GENERAL INFORMATION:
```



```
APPLICANT: FRIEDEN, MIRIAM
APPLICANT: HANSEN, JENS BO
APPLICANT: OROM, HENRIK
APPLICANT: WESTERGARD, MAJKEN
APPLICANT: THRUDE, CHARLOTTE ALBAEK
TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF BCL-2
FILE REFERENCE: 50533-60537
CURRENT APPLICATION NUMBER: US/11/021,729
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/521,594
PRIOR FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: 60/586,340
PRIOR FILING DATE: 2004-07-07
PRIOR APPLICATION NUMBER: 60/558,392
PRIOR FILING DATE: 2004-03-31
PRIOR APPLICATION NUMBER: 60/532,844
PRIOR FILING DATE: 2003-12-23
PRIOR APPLICATION NUMBER: DK PA 2004 01629
PRIOR FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: DK PA 2004 01069
PRIOR FILING DATE: 2004-07-07
PRIOR APPLICATION NUMBER: DK PA 2004 00517
PRIOR FILING DATE: 2004-03-31
PRIOR APPLICATION NUMBER: DK PA 2003 01929
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.3
SEQ ID NO 58
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
FEATURE:
OTHER INFORMATION: oligonucleotide
NAME/KEY: misc_feature
LOCATION: (1)
OTHER INFORMATION: modified LNA nucleotide
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2)
OTHER INFORMATION: 5-methyl cytosine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15)
OTHER INFORMATION: modified LNA nucleotide
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)-(16)
OTHER INFORMATION: Phosphorothioate linkage
US-11-021-729-58

Query Match      88.9%; Score 16; DB 10; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2  GAGGTCGACGCGGCU 17
DB      16  GAGGTCGACGCGGT 1

RESULT 37
US-09-965-116A-79/c
Sequence 79, Application US/09965116A
Patent No. US20020137714A1
GENERAL INFORMATION:
APPLICANT: Kandimala, Ekambar R.
APPLICANT: Zhao, Qiyuan
APPLICANT: Yu, Dong
```

```
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: Modulation of Immunostimulatory Activity of Immunostimulatory
TITLE OF INVENTION: Modified oligodeoxynucleotide phosphorothioate Analogs by
TITLE OF INVENTION: Positional Chemical Changes
FILE REFERENCE: HYZ-479CP (47508,577)
CURRENT APPLICATION NUMBER: US/09/965,116A
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 09/712,898
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US 60/235,452
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 60/235,453
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 79
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified linkage of oligodeoxynucleotide phosphorothioate
NAME/KEY: modified_base
LOCATION: 16
OTHER INFORMATION: 3'-3' linkage
US-09-965-116A-80

Query Match      88.9%; Score 16; DB 3; Length 32;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3  AGGTCGACGCGGCUA 18
DB      16  AGGTCGACGCGGTA 1

RESULT 38
US-09-965-116A-80/c
Sequence 80, Application US/09965116A
Patent No. US20020137714A1
GENERAL INFORMATION:
APPLICANT: Kandimala, Ekambar R.
APPLICANT: Zhao, Qiyuan
APPLICANT: Yu, Dong
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: Modulation of Immunostimulatory Activity of Immunostimulatory
TITLE OF INVENTION: Modified oligodeoxynucleotide phosphorothioate Analogs by
FILE REFERENCE: HYZ-479CP (47508,577)
CURRENT APPLICATION NUMBER: US/09/965,116A
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 09/712,898
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US 60/235,452
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 60/235,453
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 80
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified linkage of oligodeoxynucleotide phosphorothioate
NAME/KEY: modified_base
LOCATION: 16
OTHER INFORMATION: 3'-3' linkage
US-09-965-116A-80

Query Match      88.9%; Score 16; DB 3; Length 32;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 AGGGUCGACGCGGUA 18
||||:|||||:|
Db 32 AGGGTCGACGCGGTA 17

RESULT 39
US-10-694-075-79/c
; Sequence 79, Application US/10694075
; Publication No. US20040266709A1
; GENERAL INFORMATION:
; APPLICANT: Kandimalle, Ekambar R.
; APPLICANT: Zhao, QiuYan
; APPLICANT: Yu, Dong
; APPLICANT: Agrawal, Sudhir
; TITLE OF INVENTION: Modulation of Immunostimulatory Activity of
; TITLE OF INVENTION: Immunostimulatory
; TITLE OF INVENTION: Modified oligodeoxynucleotide phosphorothioate Analogs by
; FILE REFERENCE: HYZ-479CP (47508.577)
; CURRENT APPLICATION NUMBER: US/10/694,075
; PRIOR FILING DATE: 2003-10-27
; PRIOR APPLICATION NUMBER: US/09/965,116
; PRIOR FILING DATE: 2002-03-08
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/235,452
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 60/235,453
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified linkage of oligodeoxynucleotide
; OTHER INFORMATION: phosphorothioate
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 16
; OTHER INFORMATION: 5'-5' linkage
US-10-694-075-79
Query Match 88.9%; Score 16; DB 8; Length 32;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 AGGGUCGACGCGGUA 18
||||:|||||:|
Db 16 AGGGTCGACGCGGTA 1

; PRIOR APPLICATION NUMBER: US 09/712,898
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/235,452
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 60/235,453
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified linkage of oligodeoxynucleotide
; OTHER INFORMATION: phosphorothioate
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 16
; OTHER INFORMATION: 3'-3' linkage
US-10-694-075-80

Query Match 88.9%; Score 16; DB 8; Length 32;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 AGGGUCGACGCGGUA 18
||||:|||||:|
Db 32 AGGGTCGACGCGGTA 17

RESULT 41
US-10-694-383-79/c
; Sequence 79, Application US/10694383
; Publication No. US20040266710A1
; GENERAL INFORMATION:
; APPLICANT: Kandimalle, Ekambar R.
; APPLICANT: Zhao, QiuYan
; APPLICANT: Yu, Dong
; APPLICANT: Agrawal, Sudhir
; TITLE OF INVENTION: Modulation of Immunostimulatory Activity of
; TITLE OF INVENTION: Immunostimulatory
; TITLE OF INVENTION: Modified oligodeoxynucleotide phosphorothioate Analogs by
; FILE REFERENCE: HYZ-479CP (47508.577)
; CURRENT APPLICATION NUMBER: US/10/694,383
; PRIOR FILING DATE: 2003-10-27
; PRIOR APPLICATION NUMBER: US/09/965,116
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US 09/712,898
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/235,452
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 60/235,453
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified linkage of oligodeoxynucleotide
; OTHER INFORMATION: phosphorothioate
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 16
; OTHER INFORMATION: 5'-5' linkage
US-10-694-383-79

Query Match 88.9%; Score 16; DB 8; Length 32;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGTCGACGCGGUA 18
||||:|||||:|
DB 16 AGGTCGACGCGGTA 1

RESULT 42

US-10-694-383-80/c
Sequence 80, Application US/10694383
Publication No. US20040266710A1
GENERAL INFORMATION:
APPLICANT: Kandimala, Ekambar R.
APPLICANT: Zhao, Qiyuan
APPLICANT: Yu, Dong
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: Modulation of Immunostimulatory Activity of
TITLE OF INVENTION: Immunostimulatory
TITLE OF INVENTION: Modified oligodeoxynucleotide phosphorothioate Analogs by
FILE REFERENCE: HYZ-479CP (47508.577)
CURRENT APPLICATION NUMBER: US/10/694,383
CURRENT FILING DATE: 2003-10-27
PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/965,116
PRIOR FILING DATE: CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 09/712,898
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US 60/235,452
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 60/235,453
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 80
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified linkage of oligodeoxynucleotide
OTHER INFORMATION: phosphorothioate
NAME/KEY: modified_base
LOCATION: 16
OTHER INFORMATION: 3'-3' linkage
US-10-694-383-80

Query Match 88.9%; Score 16; DB 8; Length 32;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGTCGACGCGGUA 18
||||:|||||:|
DB 32 AGGTCGACGCGGTA 17

RESULT 43

US-10-694-418-79/c
Sequence 79, Application US/10694418
Publication No. US20050026858A1
GENERAL INFORMATION:
APPLICANT: Kandimala, Ekambar R.
APPLICANT: Zhao, Qiyuan
APPLICANT: Yu, Dong
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: Modulation of Immunostimulatory Activity of Immunostimulatory
TITLE OF INVENTION: Modified oligodeoxynucleotide phosphorothioate Analogs by
FILE REFERENCE: HYZ-479CP (47508.577)
CURRENT APPLICATION NUMBER: US/10/694,418
CURRENT FILING DATE: 2003-10-27
PRIOR APPLICATION NUMBER: US/09/965,116
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 09/712,898
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US 60/235,452

PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 60/235,453
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 79
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified linkage of oligodeoxynucleotide phosphorothioate
FEATURE:
NAME/KEY: modified_base
LOCATION: 16
OTHER INFORMATION: 5'-5' linkage
US-10-694-418-79

Query Match 88.9%; Score 16; DB 8; Length 32;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGTCGACGCGGUA 18
||||:|||||:|
DB 16 AGGTCGACGCGGTA 1

RESULT 44

US-10-694-418-80/c
Sequence 80, Application US/10694418
Publication No. US20050026858A1
GENERAL INFORMATION:
APPLICANT: Kandimala, Ekambar R.
APPLICANT: Zhao, Qiyuan
APPLICANT: Yu, Dong
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: Modulation of Immunostimulatory Activity of Immunostimulatory
TITLE OF INVENTION: Modified oligodeoxynucleotide phosphorothioate Analogs by
FILE REFERENCE: HYZ-479CP (47508.577)
CURRENT APPLICATION NUMBER: US/10/694,418
CURRENT FILING DATE: 2003-10-27
PRIOR APPLICATION NUMBER: US/09/965,116
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 09/712,898
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US 60/235,452
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 60/235,453
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 80
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified linkage of oligodeoxynucleotide phosphorothioate
FEATURE:
NAME/KEY: modified_base
LOCATION: 16
OTHER INFORMATION: 3'-3' linkage
US-10-694-418-80

Query Match 88.9%; Score 16; DB 8; Length 32;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGTCGACGCGGUA 18
||||:|||||:|
DB 32 AGGTCGACGCGGTA 17

RESULT 45

US-10-053-645A-8/c
; Sequence 8, Application US/10053645A
; Publication No. US2003016376A1
; GENERAL INFORMATION:
; APPLICANT: Robert E. Klem
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A
; TITLE OF INVENTION: CHIL-PROLIFERATIVE DISORDER USING CBE DECOY OLIGOMERS, BCL-2
; TITLE OF INVENTION: ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF
; FILE REFERENCE: 10412-022-999
; CURRENT APPLICATION NUMBER: US/10/053,645A
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/263,244
; PRIOR FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: Synthetic Antisense
; OTHER INFORMATION: Oligonucleotide
US-10-053-645A-8

Query Match 83.3%; Score 15; DB 6; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.2e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGGCGACGCG 15
Db 15 AGAGGGGCGACGCG 1

RESULT 46
US-10-961-458-8/c
; Sequence 8, Application US/10961458
; Publication No. US20050170377A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION
; FILE REFERENCE: 04040/1200990-US7
; CURRENT APPLICATION NUMBER: US/10/961,458
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: US/10/961,458
; PRIOR FILING DATE: 2004-10-07
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: US 09/375,514
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: US 09/080,285
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: US 08/465,485
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/124,256
; PRIOR FILING DATE: 1993-09-20
; PRIOR APPLICATION NUMBER: US 07/840,716
; PRIOR FILING DATE: 1992-02-21
; PRIOR APPLICATION NUMBER: US 07/288,692
; PRIOR FILING DATE: 1988-12-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-961-458-8

Query Match 83.3%; Score 15; DB 9; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.2e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGGCGACGCG 15
Db 15 AGAGGGGCGACGCG 1

RESULT 47
US-10-723-860-668
; Sequence 668, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natassha
; APPLICANT: Gineburg, Wendy M.
; APPLICANT: Zlocnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 668
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-668

Query Match 83.3%; Score 15; DB 8; Length 337;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGGCGACGCGG 16
Db 128 GAGGGGCGACGCGG 142

RESULT 48
US-10-756-149-689
; Sequence 689, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natassha
; APPLICANT: Zlocnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 689
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-756-149-689

Query Match 83.3%; Score 15; DB 9; Length 337;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGGCGACGCGG 16
Db 128 GAGGGGCGACGCGG 142

RESULT 49
US-10-424-599-126012/c
; Sequence 126012, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B
 CURRENT APPLICATION NUMBER: US/10/424,599
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 285684
 SEQ ID NO 126012
 LENGTH: 363
 TYPE: DNA
 ORGANISM: Glycine max
 FEATURES:
 OTHER INFORMATION: Clone ID: PAT_MRT3847_84798C.1
 US-10-424-599-126012

Query Match 83.3%; Score 15; DB 7; Length 363;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGTCGCGCGG 15
 |||||:|||||
 DB 19 AGAGGTCGCGCGG 5

RESULT 50
 US-09-918-995-34640
 Sequence 34640, Application US/09918995
 Publication No. US20030073623A1
 GENERAL INFORMATION:
 APPLICANT: Hyseq, Inc.
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
 FILE REFERENCE: 20411-756
 CURRENT APPLICATION NUMBER: US/09/918,995
 CURRENT FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: US/09/235,076
 PRIOR FILING DATE: 1999-01-20
 NUMBER OF SEQ ID NOS: 38054
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 34640
 LENGTH: 381
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-918-995-34640

Query Match 83.3%; Score 15; DB 3; Length 381;
 Best Local Similarity 93.3%; Pred. No. 3.2e+02;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGTCGCGCGG 16
 |||||:|||||
 DB 20 GAGGTCGCGCGG 34

Search completed: March 19, 2006, 07:52:28
 Job time: 2721.85 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:35:23 ; Search time 1694.77 Seconds
(without alignments)
496.922 Million cell updates/sec

Title: US-10-800-926-1

Perfect score: 18

Sequence: 1 agaggggucgacgcgga 18

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database :

EST: *
1: gb_esc1: *
2: gb_esc2: *
3: gb_esc3: *
4: gb_esc4: *
5: gb_esc5: *
6: gb_esc6: *
7: gb_esc7: *
8: gb_esc8: *
9: gb_esc9: *
10: gb_esc10: *
11: gb_esc11: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	91.1	448	1	AA796833 VP15G04.r
2	16.4	91.1	759	2	AA796833 VP15G04.r
3	16.4	91.1	791	10	AG0903738 GSTC0477
4	16.4	91.1	854	10	CG0565737 PUGG38TD
5	16.4	91.1	891	10	CG117658 PUFYD777B
6	16.4	91.1	730	5	CG117700 PUFYD777D
7	16.4	88.9	730	5	BX765851 BX765851
8	15.4	85.6	296	1	BB081347 BB081347
9	15.4	85.6	479	5	BO810184 1030015H0
10	15.4	85.6	521	3	BM344647 r57603.y
11	15.4	85.6	546	7	CN122209 TGBSTy12
12	15.4	85.6	600	3	BM355249 r722f03.y
13	15.4	85.6	614	9	AG0946516 Sheared D
14	15.4	85.6	630	9	AG0953132 Shared D
15	15.4	85.6	667	10	AG0833294 Pan trogl
16	15.4	85.6	713	3	BJ650743 BJ650743
17	15.4	85.6	752	3	BJ662705 BJ662705
18	15.4	85.6	760	3	BP684217 BP684217
19	15.4	85.6	770	8	DR729209 AGENCOURT
20	15.4	85.6	771	3	BP692517 BP692517
21	15.4	85.6	812	10	CZ195323 AIAA-aad3
22	15.4	85.6	906	5	BU908733 AGENCOURT

23	15.4	85.6	926	8	CV762975
24	15.4	85.6	1101	10	CNS001U1
25	15.4	85.6	1204	10	AG034417 Pan trogl
26	15.4	85.6	1310	10	AG038547
27	15	83.3	99	2	BS958176
28	15	83.3	108	2	BS942250 ax22h10.x
29	15	83.3	132	2	BP978759 602149290
30	15	83.3	149	2	BP214752 601846671
31	15	83.3	153	2	BS613515
32	15	83.3	197	2	BS941945
33	15	83.3	300	1	AU100090
34	15	83.3	314	5	BX115113
35	15	83.3	337	1	AA393273
36	15	83.3	349	3	BM851628
37	15	83.3	376	10	CM842063
38	15	83.3	396	6	CB929313
39	15	83.3	412	4	BE045111
40	15	83.3	413	4	BC018628
41	15	83.3	414	2	BC337115
42	15	83.3	426	8	R09557
43	15	83.3	429	6	CA453513
44	15	83.3	463	6	CD705931
45	15	83.3	487	6	CD698611
46	15	83.3	492	5	BU660456
47	15	83.3	493	7	CR736151
48	15	83.3	530	10	CM452151
49	15	83.3	546	6	CB138822
50	15	83.3	547	2	BS552352
51	15	83.3	550	6	CD693735
52	15	83.3	555	2	BS552470
53	15	83.3	561	2	BC333304
54	15	83.3	567	7	CY569581
55	15	83.3	581	6	CF303740
56	15	83.3	582	3	BP292420
57	15	83.3	582	3	BP26066
58	15	83.3	582	3	BP355098
59	15	83.3	583	3	BP211803
60	15	83.3	583	3	BP274647
61	15	83.3	583	3	BP355140
62	15	83.3	583	3	BP356018
63	15	83.3	596	2	B1222655
64	15	83.3	603	1	AV716468
65	15	83.3	619	7	CM481852
66	15	83.3	631	3	BM172294
67	15	83.3	632	3	DN997647
68	15	83.3	638	10	CE744759
69	15	83.3	656	3	B1333488
70	15	83.3	657	11	LBAP092G09
71	15	83.3	680	10	CM353224
72	15	83.3	682	6	CD885633
73	15	83.3	688	3	B1548301
74	15	83.3	712	10	CM353223
75	15	83.3	720	3	B1761653
76	15	83.3	722	1	AV716032
77	15	83.3	734	2	BC718649
78	15	83.3	737	3	BE760478
79	15	83.3	737	8	CB760150
80	15	83.3	751	2	BC706282
81	15	83.3	760	5	BU941920
82	15	83.3	769	2	BC718555
83	15	83.3	769	5	BU956708
84	15	83.3	774	3	B1764038
85	15	83.3	778	3	B1831665
86	15	83.3	796	6	CD110282
87	15	83.3	814	2	BC706281
88	15	83.3	820	2	BC722826
89	15	83.3	826	10	ATH517146
90	15	83.3	834	6	CB960175
91	15	83.3	859	5	BU953601
92	15	83.3	861	5	BK456870
93	15	83.3	872	8	CX755243
94	15	83.3	890	5	BK400383
95	15	83.3	890	6	CA489684


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972 13.8 76.7 552 9 AZ335078 1M0064B15
973 13.8 76.7 553 10 CG115574
974 13.8 76.7 552 10 BM002537
975 13.8 76.7 554 6 BQ816831
976 13.8 76.7 554 6 CF753658
977 13.8 76.7 554 11 CG299562
978 13.8 76.7 554 11 P178L
979 13.8 76.7 555 6 CB832315
980 13.8 76.7 555 7 CN780155
981 13.8 76.7 555 7 CG3030687
982 13.8 76.7 555 10 AY421650
983 13.8 76.7 555 10 AY421651
984 13.8 76.7 558 11 DE121380
985 13.8 76.7 559 3 B0886423
986 13.8 76.7 560 3 BM176786
987 13.8 76.7 560 6 CD527456
988 13.8 76.7 560 6 CO390758
989 13.8 76.7 561 3 BM189038
990 13.8 76.7 561 3 BM694591
991 13.8 76.7 561 7 CO330893
992 13.8 76.7 562 3 BM828073
993 13.8 76.7 563 3 BM354128
994 13.8 76.7 565 3 B0184512
995 13.8 76.7 565 3 BM002095
996 13.8 76.7 565 6 CB833469
997 13.8 76.7 565 9 AZ816236
998 13.8 76.7 565 10 CL178760
999 13.8 76.7 567 7 COS11329
1000 13.8 76.7 568 7 CV461090

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ALIGNMENTS

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RESULT 1
AA796833 448 bp mRNA linear EST 09-FEB-1998
LOCUS VPI504.r1 Soares_mammary_gland_NBMWG Mus musculus cDNA clone
DEFINITION IMAGE:1068726 5', mRNA sequence.
ACCESSION AA796833
VERSION AA796833.1 GI:2859788
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 448)
Marte,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisler,S., Kucaba,T., Lacey,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Stepien,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

```

```

TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Maira W/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through INM; contact the
IMAGE Consortium (info@image.jnl.gov) for further information.
MG1:591086
Seq primer: -28m13 rev2 ET from Amerisham
High quality sequence scop: 388.
Location/Qualifiers
1..448
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

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/clone="IMAGE:1068726"
/sex="male"
/tissue_type="mammary gland"
/dev stage="4 weeks"
/lab host="DH10B"
/clone_idb="Soares_mammary_gland_NBMWG"
/notes="Organ: mammary gland; Vector: pT73D-Pac
(pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo (dT) primer [5',
TGTTCACATCGAGGAGCGGCGGATGTTTTTTTTTTTTTTTTTTT
T 3'], double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."

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ORIGIN

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Query Match 91.1%; Score 16.4; DB 1; Length 448;
Best Local Similarity 88.9%; Pred. No. 5.9e+02;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1 AGAGGCGCGACGCGGUA 18
DB 9 AGAGGCGCGACGCGGTA 26

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RESULT 2
AQ903738/c 759 bp DNA linear GSS 09-JAN-2001
LOCUS GSS04779 Trypanosoma cruzi random genomic library Trypanosoma
DEFINITION cruzi genomic clone G24D14, genomic survey sequence.
ACCESSION AQ903738
VERSION AQ903738.2 GI:9378045
KEYWORDS GSS.
SOURCE Trypanosoma cruzi
ORGANISM Trypanosoma cruzi
REFERENCE Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases 1 to 759)
Aguero,F., Verdun,R., Fraach,A.C.C. and Sanchez,D.O.
A random sequencing approach for the analysis of the trypanosoma
cruzi genome: general structure, large gene and repetitive DNA
families, and gene discovery
Genome Res. 10 (12), 1996-2005 (2000)
1116094
JOURNAL PUBMED
COMMENT On Jul 21, 2000 this sequence version replaced gi:6484020.
Contact: Sanchez D.O.
Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
San Martin)
Av. Gral Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martin, Buenos
Aires, Argentina
Tel: (54-11) 4580/7255/7
Fax: (54-11) 4752-9639
Email: dsanchez@ib.unsam.edu.ar
Seq primer: T7
Class: Shotgun.

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FEATURES
source
1..759
/organism="Trypanosoma cruzi"
/mol_type="genomic DNA"
/strain="CL-Brener"
/db_xref="taxon:5693"
/clone="G24D14"

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/cell_type="epimastigote"
/clone_idb="Trypanosoma cruzi random genomic library"
/notes="Vector: pBS(-) (Stratagene); T. cruzi DNA was
randomly sheared using a nebulizer and the 1 to 2 kb range
was gel purified and cloned into the dephosphorylated
HincII site of the vector."

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ORIGIN

Query Match 91.1%; Score 16.4; DB 9; Length 759;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACGCGGUA 18
|||||:|||||:|
665 AGAGGCTCGACGCGTTA 648

RESULT 3
CG056737 791 bp DNA linear GSS 19-AUG-2003
CG056737/c PUFYD777B_ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa059603,
DEFINITION genomic survey sequence.
ACCESSION CG056737 GI:33928917
VERSION CG056737.1
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 791)
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1..791
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_1lb="ZMMBTa059603"
/note="Vector: PCR4-TOPO, Site_1: EcoRI; 0.6-1.0 kb high
cot selected genomic DNA library"

ORIGIN
Query Match 91.1%; Score 16.4; DB 10; Length 791;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACGCGGUA 18
|||||:|||||:|
730 AGAGGCTCGACGCGTTA 713

RESULT 4
CG117698 854 bp DNA linear GSS 20-AUG-2003
CG117698/c PUFYD777B_ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0759N10,
DEFINITION genomic survey sequence.
ACCESSION CG117698 GI:34001135
VERSION CG117698.1
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 854)
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and

REFERENCE
AUTHORS

TITLE Benetzen, J.
JOURNAL Maize Genomics Consortium
COMMENT Unpublished (2003)
Other_GSSs: PUFYD777D
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1..854
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTa0759N10"
/clone_1lb="ZM_0.6_1.0_KB"
/note="Vector: PCR4-TOPO, Site_1: EcoRI; 0.6-1.0 kb high
cot selected genomic DNA library"

ORIGIN
Query Match 91.1%; Score 16.4; DB 10; Length 854;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACGCGGUA 18
|||||:|||||:|
365 AGAGGCTCGACGCGTTA 382

RESULT 5
CG117700 891 bp DNA linear GSS 20-AUG-2003
CG117700/c PUFYD777D_ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0759N10,
DEFINITION genomic survey sequence.
ACCESSION CG117700 GI:34001137
VERSION CG117700.1
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 891)
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUFYD777B
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1..891
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTa0759N10"
/clone_1lb="ZM_0.6_1.0_KB"
/note="Vector: PCR4-TOPO, Site_1: EcoRI; 0.6-1.0 kb high
cot selected genomic DNA library"

ORIGIN

Query Match 91.1%; Score 16.4; DB 10; Length 891;
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGGUCCACGCGGUA 18
 |||||:|||||:|||||:
 Db 725 AGAGGGTCCACGCGTA 708

RESULT 6
 BX765851 730 bp mRNA linear EST 10-DEC-2003
 LOCUS BX765851 Normalized Anopheles Fat Body (NAFB) Library Anopheles
 DEFINITION gambiae cDNA clone AGCCU12TR, mRNA sequence.
 ACCESSION BX765851
 VERSION BX765851
 KEYWORDS GI:39673060
 SOURCE EST.
 ORGANISM Anopheles gambiae (African malaria mosquito)
 Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoides;
 Culicidae; Anophelinae; Anopheles.
 1 (bases 1 to 730)
 Lobo, N.L., Gardner, M., Romans, P. and Collins, F.H.
 Anopheles gambiae EST, Center for Tropical Disease Research and
 Training
 Unpublished (2003)
 Contact: Frank H. Collins
 Center for Tropical Disease Research and Training
 University of Notre Dame
 Notre Dame, IN 46556, USA
 Tel: 574-631-9245
 Fax: 574-631-3996
 Email: frank.h.collins.75@nd.edu.

FEATURES
 source Location/Qualifiers
 1..730
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /db_xref="taxon:7165"
 /clone="AGCCU12TR"
 /lab_host="R. coli DH10B"
 /clone_1lb="Normalized Anopheles Fat Body (NAFB) Library"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: EcoRI (5' end); Site_2: NotI (3' end); a
 directionally cloned and normalized, oligo-T primed cDNA
 library constructed from equal numbers of 24 and 40 hr
 post Plasmodium imui infection, 4xrr and 135 strain adult
 female mosquito abdomens (omitting ovaries and midguts):
 Bonaldo, Lennon & Soares (1996): Normalization and
 Subtraction: Two Approaches to Facilitate Gene Discovery,
 Genome Research 6, 791-806. ESTs sequenced from the M13
 reverse priming site reading from the 5' ends of the cDNAs
 are indicated by 'R' in the clone name."

ORIGIN

Query Match 88.9%; Score 16; DB 5; Length 730;
 Best Local Similarity 87.5%; Pred. No. 9.5e+02;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGUCCACGCGGU 17
 |||||:|||||:|||||:
 Db 8 GAGGGTCCACGCGGT 23

RESULT 7
 CX774850 841 bp mRNA linear EST 25-JAN-2005
 LOCUS CX774850
 DEFINITION UI-EH-HG2-aap-c-17-0-UI.s1 UI-EH-HG2 Emiliaania huxleyi cDNA clone
 ACCESSION CX774850
 VERSION CX774850
 KEYWORDS GI:58185203
 SOURCE EST.
 Emiliaania huxleyi

ORGANISM Emiliaania huxleyi
 Eukaryota; Haptophyceae; Isochrysidales; Emiliaania.
 1 (bases 1 to 841)
 Bonaldo, M.F., Lennon, G. and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)

JOURNAL PUBMED
 8889548
 Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu
 Tissue Procurement: Provasoli-Gulliard National Center for Culture
 of Marine Phytoplankton (CCMP)
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/distribution.html>
 The following repetitive elements were found in this cDNA
 sequence: 1-30, >AT-rich#Low_complexity (matched complement)
 277-322, >GC-rich#Low_complexity
 Seq primer: M13 FORWARD
 POLYA=yes.

FEATURES
 source Location/Qualifiers
 1..841
 /organism="Emiliaania huxleyi"
 /mol_type="mRNA"
 /strain="CCMP 371"
 /db_xref="taxon:2903"
 /clone="UI-EH-HG2-aap-c-17-0-UI"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_1lb="UI-EH-HG2"
 /note="Vector: pT73-Pac (Pharmacia) with a modified
 polylinker; Site_1: EcoRI; Site_2: NotI; UI-EH-HG2 is a
 normalized library derived from UI-EH-HG1. The library was
 constructed and normalized according to Bonaldo, Lennon
 and Soares, Genome Research, 6:791-806, 1996. First strand
 cDNA synthesis was primed with an oligo-dT primer
 containing a Not I site. Double stranded cDNA was ligated
 to an EcoRI adaptor, digested with Not I, and cloned
 directionally into pT73-Pac vector. The oligonucleotide
 used to prime the synthesis of first-strand cDNA contains
 a library tag sequence that is located between the Not I
 site and the (dT)18 tail. The sequence tag for this
 library is GAGGCTAGT. Tissue was obtained from the
 Provasoli-Gulliard National Center for Culture of Marine
 Phytoplankton (CCMP).
 TAG TISSUE=Emiliaania huxleyi coccolithophorid
 TAG LIB=UI-EH-HG2
 TAG_SEQ=GAGGCTAGT"

ORIGIN

Query Match 88.9%; Score 16; DB 8; Length 841;
 Best Local Similarity 93.8%; Pred. No. 9.5e+02;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUCCACGCGG 16
 |||||:|||||:|||||:
 Db 726 AGAGGGTCCACGCGG 741

RESULT 8
 BB081347 296 bp mRNA linear EST 27-JUN-2000
 LOCUS BB081347
 DEFINITION BB081347 RIKEN full-length enriched, adult male diencephalon Mus
 musculus cDNA clone g330168K08 3' similar to L07924 Mus musculus
 guanine nucleotide dissociation stimulator for a ras-related GTPase
 mRNA, mRNA sequence.
 ACCESSION BB081347

KEYWORDS	BB081347.1 GI:8646407
SOURCE	Esf.
ORGANISM	Mus musculus (house mouse)
AUTHORS	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurionae; Muridae; Muridae; Mus. 1 (bases 1 to 296) Komno H., Aizawa K., Akahira S., Akiyama J., Arakawa T., Carninci P., Endo T., Fukuda S., Fukushima Y., Hara A., Hayatsu N., Hirozane T., Hoti F., Ishii Y., Ishikawa J., Ishikawa T., Itoh M., Izawa M., Kadota K., Kagawa I., Kai C., Kawai J., Kituchi N., Kiyosawa H., Koima Y., Kondo S., Koya S., Kusihara C., Kusakabe M., Matsuyama T., Miki R., Mizuno Y., Nakamura M., Oda H., Okazaki Y., Ono T., Owa C., Saito H., Sakai C., Sato K., Shibata K., Shibata Y., Shigemoto Y., Shinagawa A., Shiraki T., Sogabe Y., Suganara Y., Suzuki H., Suzuki H., Tagawa A., Takahashi F., Tomimaga N., Toyota T., Tsunoda Y., Watanishi A., Watanabe S., Yamamura T., Yamataka I., Yano R., Yasunishi A., Yokota T., Yoshida K., Yoshiki A., Yoshino M., Muramatsu M. and Hayashizaki Y.
TITLE	RIKEN Mouse ESTs (komno.H., et al.)
JOURNAL	Unpublished (2000)
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gscc.riken.jp, URL:http://genome.gsc.riken.jp/ Carninci P., Nishiyama Y., Westover A., Itoh M., Nagoka S., Sasaki N., Okazaki Y., Muramatsu M. and Hayashizaki Y. Thermostabilization and thermocycling of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itch M., Kitsuami T., Akiyama J., Shibata K., Izawa M., Kawai J., Tomaru Y., Carninci P., Shibata Y., Ozawa Y., Muramatsu M., Okazaki Y. and Hayashizaki Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci P. and Hayashizaki Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
FEATURES	Location/Qualifiers
SOURCE	1..296 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="taxon:10090" /cclone="g93j0168X08" /bex="male" /tissue_type="diencephalon" /dev_stage="adult" /lab_host="DH10B" /cclone_idb="RIKEN full-length enriched, adult male diencephalon" /note="Site 1: SalI, Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGGAGAGAGATCCAAAGCTCTTTTTCCTTTTTTTTNN 3'] cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGGAGAGATTCGTGAATTATAATTAATCCCCCCCCCCC

```

ORIGIN
Query Match      85.6%; Score 15.4; DB 1; Length 296;
Best Local Similarity 82.4%; Pred. No. 2e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY
1 AGAGGGTCCGACCGCGGT 17
|||||:|||||:
21 AGAGGGTCCGACCGCGGT 5

RESULT 9
BO810184/c      479 bp      mRNA      linear      EST 01-AUG-2002
LOCUS           1030015H07.Y1 C. reinhardtii CC-1690, Deflagellation (normalized),
DEFINITION      Lambda zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
VERSION          BO810184
ACCESSION       BO810184
KEYWORDS        BO810184.1 GI:22052335
SOURCE          EST.
ORGANISM        Chlamydomonas reinhardtii
                Chlamydomonas reinhardtii
                Eukaryote; Viridiplantae; Chlorophyta; Chlorophyceae;
                Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.
REFERENCE       1 (bases 1 to 479)
AUTHORS         Groseman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C.,
                Lefebvre,P., McDermott,J.P., Shrager,J., Slightow,C. and Stern,D.
TITLE           Analyses of the Chlamydomonas reinhardtii Genome: A Model,
                Unicellular System for Analyzing Gene Function and Regulation in
                Vascular Plants. Project: 1030
                Unpublished (2002)
COMMENT         Contract: Charles Hauser
                DCMB Box 91000
                Duke University
                Durham, NC 27708-1000
                Tel: 919 613 8159
                Fax: 919 613 8177
                Email: chauser@duke.edu.
                Location/Qualifiers
FEATURES
Source
1..479
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lhb="C. reinhardtii CC-1690, Deflagellation
(normalized), Lambda Zap II"
/notes="Vector: pBluescript II SK-, Site 1: EcoRI, Site 2:
XhoI; Deflagellation library, constructed by John Davies
and Jeffrey McDermott, combines cDNAs from CC-1690 cells
which had been re-synthesizing flagella for 15, 30 and 60
min after being deflagellated by pH shock. PolyA mRNA was
purified from each sample, pooled and cDNA synthesized.
The cDNA was directionally cloned into lambda zap II
(Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
zap clones by superinfection with Exsist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al., (1996) Genome Research 6: 791-806."
ORIGIN
Query Match      85.6%; Score 15.4; DB 5; Length 479;
Best Local Similarity 88.2%; Pred. No. 2e+03;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY
1 AGAGGGTCCGACCGCGGT 17
|||||:|||||:
459 AGAGGGTCCGACCGCGGT 443

RESULT 10

```

BM344647/c 521 bp mRNA linear EST 23-JUN-2002
 LOCUS r157603.y1 Globodera rostochiensis J2 pCDNAII Smant v1 Globodera
 DEFINITION rostochiensis cDNA 5' similar to SW:HG1_MOUSE 009173 HOMOGENTISATE
 1,2-DIOXYGENASE ; mRNA sequence.

ACCESSION BM344647 GI:18081562
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 1 (bases 1 to 521)
 McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
 Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
 Bowers, Y., Gibbons, M., Rittner, E., Bennett, J., Franklin, C.,
 Tsagarashvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
 Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
 Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
 McCann, R., Waterston, R. and Wilson, R.
 The Washington Univ. Nematode EST Project, 1999
 Unpublished (1999)
 Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu

FEATURES
 source
 1..521
 /organism="Globodera rostochiensis"
 /mol_type="mRNA"
 /db_xref="taxon:31243"
 /dev_stage="J2"
 /lab_host="DH10B"
 /clone_lib="Globodera rostochiensis J2 pCDNAII Smant v1"
 /note="Vector: pCDNAII (Invitrogen); Site 1: BclXI;
 Site 2: EcoRI; The library was donated for sequencing by
 Geert Smant from Wageningen University, Laboratory of
 Nematology, The Netherlands."

ORIGIN
 Query Match 85.6%; Score 15.4; DB 3; Length 521;
 Best Local Similarity 88.2%; Pred. No. 2e+03;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGUCGCGCGCGGUA 18
 |||||
 Db 268 GAGGAGCGCGCGGTA 252

RESULT 11
 LOCUS CN122209 546 bp mRNA linear EST 01-APR-2004
 DEFINITION TgESTzy121e08.y1 TgVEG118 Tachyzoite cDNA Library-2 Toxoplasma
 gondii cDNA clone TgESTzy121e08.y1 5', mRNA sequence.

ACCESSION CN122209
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 1 (bases 1 to 546)
 Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioke, J.A., White, M.,
 Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M.,

Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M.,
 Rittner, E., Bennett, J., Franklin, C., Tsagarashvili, R., Ronko, I.,
 Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.
 Toxoplasma EST Project
 Unpublished (2001)
 Contact: Clifton, S.
 Toxoplasma EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: toxo@wustl.wustl.edu
 Contact David Sibley (toxos@bcm.tmc.edu) for further
 information relating to organism, libraries, or clone availability.
 Seq primer: -40UP from G1bco
 High quality sequence stop: 546.

FEATURES
 source
 1..546
 /organism="Toxoplasma gondii"
 /mol_type="mRNA"
 /strain="VEG"
 /db_xref="taxon:5811"
 /clone="TgESTzy121e08.y1"
 /dev_stage="Tachyzoite"
 /lab_host="Gc10"
 /clone_lib="TgVEG118 Tachyzoite cDNA Library-2"
 /note="Vector: pBluescript SK; Site 1: EcoRI, Site 2:
 XhoI; The library was constructed by Kellang Tang, Robert
 Cole and L. David Sibley at Washington University. cDNAs
 were synthesized from poly(A)+ RNasey oligo d(T) priming,
 size-selected and directionally cloned into the Uni-ZAP XR
 lambda vector (Stratagene). The primary library was mass
 excised as phagemids and rescued from the SOLR cells. The
 plasmid library was recovered from the SOLR cells and
 transformed in mass into Gc10 cells for sequencing.
 WARNING: the library may contain a small percentage
 contaminants from human fibroblast cells."

ORIGIN
 Query Match 85.6%; Score 15.4; DB 7; Length 546;
 Best Local Similarity 82.4%; Pred. No. 2e+03;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGUCGCGCGCGGUA 18
 |||||
 Db 349 GAGGTCGCGCGGTA 365

RESULT 12
 LOCUS BM355249 600 bp mRNA linear EST 23-JUN-2002
 DEFINITION r122f03.y1 Globodera rostochiensis J2 pCDNAII Smant v1 Globodera
 rostochiensis cDNA 5' similar to SW:HG1_MOUSE 009173 HOMOGENTISATE
 1,2-DIOXYGENASE ; mRNA sequence.

ACCESSION BM355249
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 1 (bases 1 to 600)
 McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
 Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
 Bowers, Y., Gibbons, M., Rittner, E., Bennett, J., Franklin, C.,
 Tsagarashvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
 Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
 Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
 McCann, R., Waterston, R. and Wilson, R.
 The Washington Univ. Nematode EST Project, 1999
 Unpublished (1999)
 Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estwats@wustl.edu
The library was contributed by Dr. Geert Smant of the Laboratory of
Nematology at Wageningen University, Wageningen,
Netherlands (geert.smant@wur.nl). DNA sequencing by:
Washington University Genome Sequencing Center
Seq primer: -40RP from G1bco
High quality sequence stop: 481.
Location/Qualifiers
1. 600
/organism="Globodera rostochiensis"
/mol_type="mRNA"
/db_xref="taxon:31243"
/dev_stage="J2"
/lab_host="DH10B"
/note="Vector: pCDNAII (Invitrogen); Site_1: Becki;
Site_2: EcoRI; The library was donated for sequencing by
Geert Smant from Wageningen University, Laboratory of
Nematology, The Netherlands."

ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 600;
Best Local Similarity 88.2%; Pred. No. 2e+03;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGGUA 18
|||||
DB 293 GAGGGACGACGCGGTA 277

RESULT 13
LOCUS A0946516 614 bp DNA linear GSS 27-JAN-2000
DEFINITION Sheared DNA-49A17.TF Sheared DNA Trypanosoma brucei genomic clone
ACCESSION A0946516
VERSION A0946516.1 GI:6769781
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Bukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 614)
AUTHORS El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Sub, E., Malek, J., Fujii, C.,
Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S.,
Donelson, J., Frazer, C. and Adams, M.
TITLE Determination of clone end sequences from Trypanosoma brucei GUTat
10.1 sheared DNA library
COMMENT Other GSSs: Sheared DNA-49A17.TR
JOURNAL Contact: Najib M. El-Sayed
DEPARTMENT Department of Eukaryotic Genomics
INSTITUTE The Institute for Genomic Research
ADDRESS 9712 Medical Center Dr., Rockville, MD 20850, USA
TEL 301 838 0200
FAX 301 838 0208
EMAIL nelsayed@tigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/cdb/mdb/tbdb/.
Seq primer: M13-Forward
Class: shotgun.
Location/Qualifiers
1. 614
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TRBU927/4 GUTat 10.1"
/db_xref="taxon:5691"

FEATURES
source

ORIGIN

Query Match 85.6%; Score 15.4; DB 9; Length 614;
Best Local Similarity 82.4%; Pred. No. 2e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGGUA 18
|||||
DB 76 GAGGGTCGACGCGGTA 92

RESULT 14
LOCUS A0953132 630 bp DNA linear GSS 27-JAN-2000
DEFINITION Sheared DNA-43M6.TF Sheared DNA Trypanosoma brucei genomic clone
ACCESSION A0953132
VERSION A0953132.1 GI:6776397
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Bukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 630)
AUTHORS El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Sub, E., Malek, J., Fujii, C.,
Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S.,
Donelson, J., Frazer, C. and Adams, M.
TITLE Determination of clone end sequences from Trypanosoma brucei GUTat
10.1 sheared DNA library
COMMENT Other GSSs: Sheared DNA-43M6.TR
JOURNAL Contact: Najib M. El-Sayed
DEPARTMENT Department of Eukaryotic Genomics
INSTITUTE The Institute for Genomic Research
ADDRESS 9712 Medical Center Dr., Rockville, MD 20850, USA
TEL 301 838 0200
FAX 301 838 0208
EMAIL nelsayed@tigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/cdb/mdb/tbdb/.
Seq primer: M13-Forward
Class: shotgun.
Location/Qualifiers
1. 630
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TRBU927/4 GUTat 10.1"
/db_xref="taxon:5691"

FEATURES
source

/clone="Sheared DNA-49A17"
/note="Vector: pUC18; Site 1: SmaI; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRBU927/4 GUTat 10.1) was mechanically
sheared to give a tight size distribution (approx 2 kb).
The v + i method used for the library construction is
described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun
sequencing projects. In Genome Sequencing: A Practical
Approach, eds. M. Vaudin and B. Barrell, Oxford University
Press, 1999)."

sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

ORIGIN

Query Match 85.6%; Score 15.4; DB 9; Length 630;
Best Local Similarity 82.4%; Pred. No. 2e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GAGGUGCGACGCGUA 18
Db 397 GAGGTCGACGCGCTA 413

RESULT 15
AG083294 667 bp DNA linear GSS 03-NOV-2001
LOCUS Pan troglodytes DNA, clone: PTB-080L03.R, genomic survey sequence.
DEFINITION AG083294
VERSION AG083294.1 GI:16635096
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Pan.

REFERENCE
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of library PTB
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 667)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suenryo-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimbes@sc.riken.go.jp, URL: http://hsp.gsc.riken.go.jp/), Tel: 81-45-503-9111, Fax: 81-45-503-9170
COMMENT Clones are derived from the chimpanzee BAC library PTB. This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS

SEQUENCING: M13Rev
LIBRARY Vector : PKS145
R Site 1 : SacI
R Site 2 : SacI
Location/Qualifiers
1. 667
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-080L03.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN

Query Match 85.6%; Score 15.4; DB 10; Length 667;
Best Local Similarity 82.4%; Pred. No. 2e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGAGGUGCGACGCGU 17
Db 499 AGAGGTCGACGCGGT 515

RESULT 16
Bj650743 713 bp mRNA linear EST 07-OCT-2004
LOCUS Bp650743/c
DEFINITION Bp650743 Eptaretus burgeri adult Eptaretus burgeri cDNA clone

hg121h06 5', mRNA sequence.
Bj650743
VERSION Bj650743.1 GI:53865604
KEYWORDS EST.
SOURCE Eptaretus burgeri (Inshore hagfish)
ORGANISM Eptaretus burgeri
Bukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes; Myxiniidae; Eptarellinae; Eptaretus.

REFERENCE
AUTHORS Suzuki, T., Shin-I, T., Kohara, Y. and Kasahara, M.
TITLE Transcriptional analysis of hagfish leukocytes: a framework for understanding the immune system of jawless fishes
JOURNAL Dev. Comp. Immunol. 28 (10), 993-1003 (2004)
PUBMED 15236930
COMMENT Contact: Tadao Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tsbini@genes.nig.ac.jp.
Location/Qualifiers

FEATURES
source 1..713
/organism="Eptaretus burgeri"
/mol_type="mRNA"
/db_xref="taxon:7764"
/clone="hg121h06"
/cell_type="leukocyte-like cell"
/dev_stage="adult"
/clone_lib="Eptaretus burgeri adult"
/note="wild caught animal"

ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 713;
Best Local Similarity 88.2%; Pred. No. 2e+03;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGAGGUGCGACGCGU 17
Db 523 AGAGGACGACGCGGT 507

RESULT 17
Bj662705 752 bp mRNA linear EST 07-OCT-2004
LOCUS Bj662705 Eptaretus burgeri adult Eptaretus burgeri cDNA clone
DEFINITION hg121h06 3', mRNA sequence.
VERSION Bj662705
KEYWORDS EST.
SOURCE Eptaretus burgeri (Inshore hagfish)
ORGANISM Eptaretus burgeri
Bukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes; Myxiniidae; Eptarellinae; Eptaretus.

REFERENCE
AUTHORS Suzuki, T., Shin-I, T., Kohara, Y. and Kasahara, M.
TITLE Transcriptional analysis of hagfish leukocytes: a framework for understanding the immune system of jawless fishes
JOURNAL Dev. Comp. Immunol. 28 (10), 993-1003 (2004)
PUBMED 15236930
COMMENT Contact: Tadao Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tsbini@genes.nig.ac.jp.
Location/Qualifiers

FEATURES
source 1..752
/organism="Eptaretus burgeri"
/mol_type="mRNA"
/db_xref="taxon:7764"
/clone="hg121h06"

ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 752;
Best Local Similarity 88.2%; Pred. No. 2e+03;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGAGGUGCCACGCGGU 17
|||||
567 AGAGGAGCCACGCGGT 563

RESULT 18
BP684217/c 760 bp mRNA linear EST 27-JUL-2004
LOCUS BP684217 Osada Taira anterior neuroectoderm (ANE) PCS105 cDNA
DEFINITION library Xenopus laevis cDNA clone XL445e24ex 5', mRNA sequence.
ACCESSION BP684217 GI:46032172
VERSION BP684217
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis

REFERENCE
AUTHORS Osada, S., Kitayama, A., Ueno, N. and Taira, M.
TITLE Expression analysis of genes which are expressed in the anterior neuroectoderm of Xenopus embryos
JOURNAL Unpublished (2004)
COMMENT Contact: Masamori Taira
Department of Biological Sciences
Graduate School of Science, University of Tokyo; CREST, Japan
Science and Technology Corporation, Japan
7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
Tel: 81-03-5841-4434
Fax: 81-03-5841-4434
Email: m.taira@biol.s.u.-tokyo.ac.jp,
URL: http://www.shigen.nig.ac.jp/nbrp/xenopus/est/
Location/Qualifiers
1..760
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL445e24ex"
/tissue_type="anterior neuroectoderm"
/dev_stage="late gastrula (stage 12.5)"
/clone_1lb="Osada Taira anterior neuroectoderm (ANE) PCS105 cDNA library"

ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 760;
Best Local Similarity 88.2%; Pred. No. 2e+03;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GAGGUGCCACGCGGUA 18
|||||
454 GAGGUGCCACGCGGUA 438

RESULT 19
DR729209/c 770 bp mRNA linear EST 15-JUL-2005
LOCUS DR729209 AGENCOURT 55139068 NICHD XGC Emb9 Xenopus laevis cDNA clone
DEFINITION IMAGE:797866 5', mRNA sequence.
ACCESSION DR729209
VERSION DR729209.1 GI:70903321
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis

REFERENCES
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: csapbs-remail.nih.gov
Tissue Procurement: Dr. Igor David
cDNA Library Preparation: Express Genomics
DNA Sequencing by: The I.M.A.G.E. Consortium (LNLN)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LLM17106 row: 1 column: 16
High quality sequence stop: 538.
Location/Qualifiers
1..770
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:797862c"
/tissue_type="Embryonic stage 17/19"
/lab_host="DH10B TONa"
/clone_1lb="NICHD XGC Emb9"
/note="Organ: embryo; Vector: pExpress-1; Site 1: ScoreV; Site 2: NotI; cDNA was primed using oligo-dT primer; 5'-GACATGTTCTGATCGGACGCGCCCTT)25-3' and cloned into the ScoreV/NotI sites of pExpress-1. Size selection 1.4kb resulted in an average insert size of 2.1kb. This is a non-normalized primary library (normalized library is NICHD XGC Emb10) and was constructed by Express Genomics (Frederick, MD). Note: this is a Xenopus Gene Collection (http://xgc.nci.nih.gov/) library."

ORIGIN

Query Match 85.6%; Score 15.4; DB 8; Length 770;
Best Local Similarity 88.2%; Pred. No. 2e+03;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GAGGUGCCACGCGGUA 18
|||||
451 GAGGUGCCACGCGGUA 435

RESULT 20
BP692517/c 771 bp mRNA linear EST 27-JUL-2004
LOCUS BP692517 Osada Taira anterior neuroectoderm (ANE) PCS105 cDNA
DEFINITION library Xenopus laevis cDNA clone XL468m17ex 5', mRNA sequence.
ACCESSION BP692517
VERSION BP692517.1 GI:46040472
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis

REFERENCES
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopus;
JOURNAL Xenopus laevis
COMMENT Contact: Masamori Taira
Department of Biological Sciences
Graduate School of Science, University of Tokyo; CREST, Japan
Science and Technology Corporation, Japan
7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan

Tel: 81-03-5841-4434
 Fax: 81-03-5841-4434
 Email: m_taira@biol.s.u-tokyo.ac.jp,
 URL: http://www.shigen.nig.ac.jp/nbrp/xenopus/est/.

FEATURES

source

1..771
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="X1468ml7ex"
 /tissue_type="anterior neuroectoderm"
 /dev_stage="late gastrula (stage 12.5)"
 /clone_1ib="Osada Taira anterior neuroectoderm (ANE)
 PSI05 cDNA library"

ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 771;
 Best Local Similarity 88.2%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGUCCAGCGCGUA 18
 |||||
 Db 314 GAGGGCGCAGCGCGTA 298

RESULT 21

C2195323

LOCUS A1AA-aad31k01.g1 Ancylostoma caninum whole genome shotgun library
 DEFINITION (A1AGSS 001) Ancylostoma caninum genomic, genomic survey sequence.
 C2195323
 C2195323.1 GI:59179408

ACCESSION C2195323 812 bp DNA linear GSS 10-FEB-2005
 VERSION C2195323.1
 KEYWORDS GSS.

SOURCE Ancylostoma caninum (dog hookworm)
 ORGANISM Buxaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
 Ancylostomatidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.

REFERENCE 1 (bases 1 to 812)
 Mltreva,M., McCarter,J.P., Page,D., Rittler,E., Tsagarashvili,R.,
 Ronko,I., Martin,J., Wylie,T., Dante,M., Meyer,R., Messina,D.,
 Waterson,R.H., Clifton,S.W. and Wilson,R.

Ancylostoma caninum (dog hookworm)
 Genome Survey sequences from the parasitic nematode Ancylostoma
 caninum
 Unpublished (2004)

JOURNAL Contact: Mltreva M
 COMMENT Washington University in St. Louis
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: nematode@watson.wustl.edu
 Genomic DNA provided by John Hawdon (ntmjh@wumc.edu) DNA
 sequenced by Washington University Genome Sequencing Center
 Class: shotgun.

FEATURES

source

Location/Qualifiers
 1..812
 /organism="Ancylostoma caninum"
 /mol_type="genomic DNA"
 /strain="Baltimore"
 /db_xref="taxon:29170"
 /dev_stage="Adult"
 /lab_host="GS10"
 /clone_1ib="Ancylostoma caninum whole genome shotgun
 library (A1AGSS 001)"
 /note="Vector: pOTW13; Site 1: BstXI; Site 2: BstXI;
 Ancylostoma caninum genomic DNA was randomly sheared,
 end-repaired and size fractionated to enrich for 2-4 kb
 fragments. Genomic DNA was provided by John Hawdon
 (ntmjh@wumc.edu) at George Washington University.
 Sequencing by Washington University Genome Sequencing
 Center, St. Louis, MO."

ORIGIN

Query Match 85.6%; Score 15.4; DB 10; Length 812;
 Best Local Similarity 88.2%; Pred. No. 2e+03;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCCAGCGCGU 17
 |||||
 Db 274 AGAGGUGCCAGCGCGT 290

RESULT 22

BU908733/C

LOCUS BU908733 906 bp mRNA linear EST 17-OCT-2002
 DEFINITION AGENCOURT 10487935 NICHD_XGC_Emb1 Xenopus laevis cDNA clone
 IMAGE:6634258 5', mRNA sequence.
 BU908733
 BU908733.1 GI:24090647

ACCESSION BU908733
 VERSION BU908733
 KEYWORDS EST
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Xenopus laevis
 Buxaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoes; Pipidae;
 Xenopodinae; Xenopus; Xenopus.

REFERENCE 1 (bases 1 to 906)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapb@remail.nih.gov

Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILM at:
 http://image.llnl.gov
 Plate: LLM14206 row: 1 column: 10
 High quality sequence stop: 615.

FEATURES

source

Location/Qualifiers
 1..906
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="IMAGE:6634258"
 /tissue_type="embryo (stage 10)"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NICHD_XGC_Emb1"
 /note="Vector: pCMV-SF0R6; Site 1: NotI; Site 2: SalI;
 cloned unidirectionally. Primer: Oligo dt. Average insert
 size 1.55 kb. Constructed by Life Technologies. Note: This
 is a Xenopus Gene Collection (XGC) library."

ORIGIN

Query Match 85.6%; Score 15.4; DB 5; Length 906;
 Best Local Similarity 88.2%; Pred. No. 2e+03;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGUCCAGCGCGUA 18
 |||||
 Db 392 GAGGGCGCAGCGCGTA 376

RESULT 23

CV762975/C

LOCUS CV762975 926 bp mRNA linear EST 09-NOV-2004
 DEFINITION FGAS057364 Triticum aestivum FGAS: Library 2 Gate 3 Triticum
 aestivum cDNA, mRNA sequence.
 CV762975
 CV762975.1 GI:55604086

ACCESSION CV762975
 VERSION CV762975
 KEYWORDS EST
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 1 (bases 1 to 926)
 Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
 Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
 Link, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilson, D.,
 Peniket, C., Roach, J.L., and Sarhan, F.
 Functional Genomes of Abiotic Stress in Wheat and Canola Crops
 Unpublished (2003)
 TITLE
 JOURNAL
 COMMENT

Contact: Wm L Crosby
 Bioinformatics
 University of Saskatchewan, Department of Computer Science
 1C101 Engineering Building, 57 Campus Drive, Saskatoon,
 Saskatchewan, S7N 5A9, Canada
 Tel: 306 966 1769
 Fax: 306 966 2033
 Email: fgas_estcs@usask.ca
 This sequence is the direct result of the base calling software
 Phred (default parameters). It is the raw base calls. To aid in the
 identification of the high quality insert the software Lucy
 (default parameters) has been run on this sequence. Lucy identified
 the region [79,333].
 Plate: WEP032 row: C column: 03.

FEATURES

source

1. 926
 Location/Qualifiers
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /db_xref="taxon:4565"
 /clone_lib="Triticum aestivum FGAS: library 2 Gate 3"
 /note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Aerial
 parts (crown and leaf) of wheat cultivar Norstar from
 control and long exposure times to low temperature. 4 mRNA
 populations were combined before constructing the library;
 7 days non-acclimated plants and 1, 23, and 53 days
 cold-acclimated at 4C. Non-acclimated and cold-acclimated
 plants were grown in vermiculite. This is the only library
 that was done according to the Invitrogen manual, and
 therefore, a percentage of clones will not have the 3
 prime end because of NciI digestion within the cDNA."

ORIGIN

Query Match 85.6%; Score 15.4; DB 8; Length 926;
 Best Local Similarity 82.4%; Pred. No. 2e+03;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGGGCGACGCGGU 17
 |||||:|||||:
 Db 447 AGAGGGGCGCGCGGT 431

RESULT 24
 CNS00101 1101 bp DNA linear GSS 03-JUN-1999
 LOCUS
 DEFINITION
 Drosophila melanogaster genome survey sequence TET3 end of BAC #
 BACR05D14 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 AL061582
 GI:4939944
 GSS.
 Drosophila melanogaster (fruit fly)
 SOURCE
 ORGANISM
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1101)
 Genoscope.
 Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazuo Osoegawa and
 Aaron Mammotter in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
 P1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
 Location/Qualifiers
 1. 1101
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /clone="BACR05D14"
 /clone_lib="RPCI-98"
 /note="end : TET3"

FEATURES

source

Query Match 85.6%; Score 15.4; DB 10; Length 1101;
 Best Local Similarity 88.2%; Pred. No. 2e+03;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

ORIGIN

QY 2 GAGGGGCGACCGCGUA 18
 |||||:|||||:
 Db 604 GAGGGGCGACCGCGTA 620

RESULT 25
 AG034417 1204 bp DNA linear GSS 01-NOV-2001
 LOCUS
 DEFINITION
 Pan troglodytes DNA, clone: PTB-009M03.F, genomic survey sequence.
 AG034417
 AG034417.1 GI:16561290
 GSS.
 Pan troglodytes (chimpanzee)
 SOURCE
 ORGANISM
 Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Pan.
 1
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Totoki, Y., Watanabe, H., and Sakaki, Y.
 BAC end sequences of library PTB
 Unpublished
 2 (bases 1 to 1204)
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Totoki, Y., Watanabe, H., and Sakaki, Y.
 Direct Submission
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail: chipbes@sc.riken.go.jp, URL: <http://hgp.gsc.riken.go.jp/>,
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)
 Clones are derived from the chimpanzee BAC library PTB This BAC end
 was generated during the R&D process and may have higher chance of
 clone tracking errors.
 PRIMERS
 Sequencing: -21M13
 LIBRARY
 Vector : pKS145
 R.Site 1 : SacI
 R.Site 2 : SacI
 Location/Qualifiers
 1. 1204
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="PTB-009M03.F"
 /sex="male"

COMMENT

FEATURES

source

```

ORIGIN
    /cell_type="lymphoblast"
    /clone_lib="PTB Chimpanzee Male BAC Library"

Query Match      85.6%; Score 15.4; DB 10; Length 1204;
Best Local Similarity 82.4%; Pred. No. 2e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 GAGGUGCGACGCGGUA 18
        |||:|||||:|
        496 GAGGUGCGACGCGGTA 512

RESULT 26
AG038547      1310 bp      DNA      linear      GSS 01-NOV-2001
LOCUS      Pan troglodytes DNA, clone: PTB-015G04.F, genomic survey sequence.
ACCESSION      AG038547
VERSION      AG038547.1 GI:16567272
KEYWORDS      GSS.
SOURCE      Pan troglodytes (chimpanzee)
ORGANISM      Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Pan.

REFERENCE
AUTHORS      Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
            Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE      BAC end sequences of Library PTB
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 1310)
AUTHORS      Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
            Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE      Direct Submissions
JOURNAL      Submitted (02-NOV-2001) Ageo Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail: chimpanzee@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
            Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT      Clones are derived from the chimpanzee BAC library PTB. This BAC end
            was generated during the Rad process and may have higher chance of
            clone tracking errors.
            PRIMERS
            Sequencing: -21M13
            LIBRARY
            Vector : pKS145
            R Site 1 : SacI
            R Site 2 : SacI
            Location/Qualifiers
            1. 1310
            /organism="Pan troglodytes"
            /mol_type="genomic DNA"
            /db_xref="taxon:9598"
            /clone="PTB-015G04.F"
            /sex="male"
            /cell_type="lymphoblast"
            /clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN

Query Match      85.6%; Score 15.4; DB 10; Length 1310;
Best Local Similarity 82.4%; Pred. No. 1.9e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 GAGGUGCGACGCGGUA 18
        |||:|||||:|
        1136 GAGGUGCGACGCGGTA 1152

RESULT 27
BE958176      99 bp      mRNA      linear      EST 04-OCT-2000
LOCUS      BE958176
DEFINITION      601644634F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929792 5',
            mRNA sequence.

```

```

ACCESSION      BE958176
VERSION      BE958176.1 GI:10568881
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
            1 (bases 1 to 99)
            NIH-MGC http://mgs.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-rt@mail.nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: CLONETECH Laboratories, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            plate: L16M763 row: c column: 09
            High quality sequence stop: 99.
            Location/Qualifiers
            1. 99
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:3929792"
            /tissue_type="primitive neuroectoderm"
            /lab_host="DH10B (T1 phage-resistant)"
            /clone_lib="NIH MGC 56"
            /note="Organ: brain; Vector: pNMR-H1B (Clontech); Site_1:
            SfiI (ggcgccatcgcc); Site_2: SfiI (ggccatcgcc);
            Double-stranded cDNA was prepared from cell line RNA. 5'
            and 3' adaptors were used in cloning as follows: 5'
            adaptor sequence: 5'-CACGGCATATGACC-3' and 3' adaptor
            sequence: 5'-ATTCTAGAGCGCGGCGGCGACATG-dT(30)BN-3'
            (where B = A, C, G, or T). Average
            insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
            contained inserts by PCR. This library was enriched for
            full-length clones and was constructed by Clontech
            Laboratories (Palo Alto, CA)."

ORIGIN

Query Match      83.3%; Score 15; DB 2; Length 99;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 GAGGUGCGACGCGG 16
        |||:|||||:|
        8 GAGGUGCGACGCGG 22

RESULT 28
BG942250      108 bp      mRNA      linear      EST 15-JAN-2003
LOCUS      BG942250
DEFINITION      ax22h10.x1 Hembase; Erythroid Progenitor Cells (LCB:ax library)
            Homo sapiens cDNA clone ax22h10 random, mRNA sequence.
            BG942250
            BG942250.1 GI:14341622
            EST.
            Homo sapiens (human)
            SOURCE      Homo sapiens
            ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
            1 (bases 1 to 108)
            Gubin, A.N., Mjoroge, J.M., Bouffard, G.G. and Miller, J.L.
            Gene expression in proliferating human erythroid cells
            Genomics 59 (2), 168-177 (1999)
            10409428
            Contact: Jeffery L. Miller

```


Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
20892, USA
Tel: 301 402 2373
Fax: 301 435 5148
Email: jmf7emh.gov
DNA Sequencing and analyses by National Institutes of Health
Intramural Sequencing Center (NISC).
Plate: 22 row: h column: 10
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
1. 108
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ax22h10"
/sex="unknown"
/tissue_type="blood"
/cell_type="Erythroid Cells"
/cell_line="Primary Culture of Peripheral Blood
Mononuclear Cells"
/dev_stage="Progenitor; EPO responsive CD71++++"
/lab_host="SOLR"
/clone_1ib="Hembase; Erythroid Progenitor Cells (LCB:ax
library)"
/note="Organ: blood; Vector: Lambda ZAP II; Site_1: EcoRI;
Site_2: EcoRI; 65,000 proliferating erythroid cells from
the buffy coat of a blood donation were obtained by flow
cytometric separation after a 5-day culture period in the
presence of erythropoietin. Total RNA was purified from
the sorted cell population using TRIzol reagent. RNA (0.3
ug) was converted into double stranded cDNA using
Clontech's Capfinder cDNA Library Construction Kit
(Clontech) according to the manufacturer's protocol and
cloned into EcoRI digested Lambda Zap II vector
(Stratagene). The phage library was amplified ex vivo
to in vivo excision in SOLR cells. Individual colonies
were grown, and the cDNA inserts were sequenced in high
throughput (NIH Intramural sequencing center
http://www.nisc.nih.gov/)."

ORIGIN
Query Match 83.3%; Score 15; DB 2; Length 108;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 GAGGGGCGCAGCGCG 16
Db 28 GAGGGGCGCAGCGCG 42
RESULT 29 132 bp mRNA linear EST 22-JAN-2001
BF978759 60219290F2 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4308047 5',
LOCUS mRNA sequence.
DEFINITION
ACCESSION BF978759
VERSION BF978759.1 GI:12345974
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 132)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straubeberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DCFD/DPF
cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1179 row: c column: 24
High quality sequence stop: 132.
Location/Qualifiers
1. 132
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4308047"
/tissue_type="melanotic melanoma, high MDR"
/lab_host="DH10B (TI phage-resistant)"
/clone_1ib="NIH MGC 62"
/note="Organ: skin; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcgagc); Site_2: SfiI (ggccatcgagc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATTATGACC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGGCGCGCATG-dt(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

ORIGIN
Query Match 83.3%; Score 15; DB 2; Length 132;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 GAGGGGCGCAGCGCG 16
Db 18 GAGGGGCGCAGCGCG 32
RESULT 30 149 bp mRNA linear EST 06-NOV-2000
BF214752 601846671F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4077880 5',
LOCUS mRNA sequence.
DEFINITION
ACCESSION BF214752
VERSION BF214752.1 GI:11108338
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 149)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straubeberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM933 row: m column: 17
High quality sequence stop: 149.
Location/Qualifiers
1. 149
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4077880"
/tissue_type="from acute myelogenous leukemia"

```

/1ab host="DH10B (TI phage-resistant)"
/clone lib="NIH_MGC_55"
/notes="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgctcgccg); Site 2: SfiI
(ggcattatggcc); Double-stranded cDNA was prepared from
cell line RNA. 5' and 3' adaptors were used in cloning as
follows: 5' adaptor sequence: 5'-CACGGCATTATGCC-3' and
3' adaptor sequence:
5'-ATTCTAGAGCGCGAGCGCGCACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."
```

Query Match 83.3%; Score 15; DB 2; Length 149;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGG 16
|||||
38 GAGGGTCCGACGCGG 52

Db 38 GAGGGTCCGACGCGG 52

RESULT 31
BG613515 153 bp mRNA linear EST 18-APR-2001
LOCUS 602641444F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4772411 5',
DEFINITION mRNA sequence.
ACCESSION BG613515
VERSION BG613515.1 GI:13664886
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;
Homidae; Homo.
1 (bases 1 to 153)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgsaps-f@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1642 row: h column: 12
High quality sequence stop: 153.
Location/Qualifiers
1. 153
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4772411"
/tissue_type="embryonal carcinoma"
/1ab host="DH10B (TI phage-resistant)"
/clone lib="NIH_MGC_61"
/notes="Organ: testis; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcgctcgccg); Site 2: SfiI (ggcattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCATTATGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGAGCGCGCACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC

FEATURES
source

```

Library."
```

Query Match 83.3%; Score 15; DB 2; Length 153;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGG 16
|||||
38 GAGGGTCCGACGCGG 52

Db 38 GAGGGTCCGACGCGG 52

RESULT 32
BG941945 197 bp mRNA linear EST 15-JAN-2003
LOCUS ax19c04.x1 Hembase; Erythroid Progenitor Cells (LCB:ax library)
DEFINITION Homo sapiens cDNA clone ax19c04 random, mRNA sequence.
ACCESSION BG941945
VERSION BG941945.1 GI:14341317
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;
Homidae; Homo.
1 (bases 1 to 197)
Gubin, A.N., Njoroge, J.M., Bouffard, G.G. and Miller, J.L.
Gene expression in proliferating human erythroid cells
Genomics 59 (2), 168-177 (1999)
10409428
Contact: Jeffery L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
20892, USA
Tel: 301 402 2373
Fax: 301 435 5148
Email: jmf@nih.gov
DNA Sequencing and analyses by National Institutes of Health
Intramural Sequencing Center (NISC).
Plate: 19 row: C column: 04
Seq primer: -21M3 forward primer (ABI).
Location/Qualifiers
1. 197
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ax19c04"
/sex="unknown"
/tissue_type="blood"
/cell_type="Erythroid Cells"
/cell_line="Primary Culture of Peripheral Blood
Mononuclear Cells"
/dev stage="Progenitor; EPO responsive CD71++++"
/1ab host="SOLR"
/clone lib="Hembase; Erythroid Progenitor Cells (LCB:ax
library)"
/notes="Organ: blood; Vector: Lambda ZAP II; Site 1: EcoRI;
Site 2: EcoRI. 65,000 proliferating erythroid cells from
the buffy coat of a blood donation were obtained by flow
cytometric separation after a 5-day culture period in the
presence of erythropoietin. Total RNA was purified from
the sorted cell population using RNeasy reagent. RNA (0.3
ug) was converted into double stranded cDNA using
Clontech's Capfinder cDNA library Construction Kit
(Clontech) according to the manufacturer's protocol and
cloned into EcoRI digested lambda Zap II vector
(Stratagene). The phage library was amplified once prior
to in vivo excision in SOLR cells. Individual colonies
were grown, and the cDNA inserts were sequenced in high
throughput (NISC intramural sequencing center
http://www.nisc.nih.gov/)."

FEATURES
source

ORIGIN

Query Match 83.3%; Score 15; DB 2; Length 197;
 Best Local Similarity 93.3%; Pred. No. 3.3e+03;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCCG 16
 |||||:|||||
 31 GAGGTCGCACGCCG 45

RESULT 33
 AUI00090 300 bp mRNA linear EST 23-JAN-2004
 LOCUS AUI00090 SUGANO Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION LNC06538 similar to Human mitochondrial transcription factor 1
 mRNA, mRNA sequence.

ACCESSION AUI00090
 VERSION AUI00090.1 GI:13551219
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Suzuki, Y., Tsunoda, T., Sese, J., Taira, H., Mizushima-Sugano, J.,
 Kato, H., Oka, T., Isogai, T., Tanaka, T., Nakamura, Y., Suyama, A.,
 Sakaki, Y., Morishita, S., Okubo, K. and Sugano, S.
 Identification and characterization of the potential promoter
 regions of 1031 kinds of human genes
 Genome Res. 11 (5), 677-684 (2001)
 11337467

TITLE
 JOURNAL
 PUBMED
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES
 source
 1..300
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="LNC06538"
 /clone_1ib="Sugano Homo sapiens cDNA library"

ORIGIN
 Query Match 83.3%; Score 15; DB 1; Length 300;
 Best Local Similarity 93.3%; Pred. No. 3.3e+03;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCCG 16
 |||||:|||||
 40 GAGGTCGCACGCCG 54

RESULT 34
 BX115113 314 bp mRNA linear EST 07-FEB-2003
 LOCUS BX115113 Soares testis NHT Homo sapiens cDNA clone IMAGE98F081786
 DEFINITION ; IMAGE:728071, mRNA sequence.
 BX115113
 BX115113.1 GI:27879949
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 JOURNAL
 COMMENT 1 (bases 1 to 314)

AUTHORS
 Ebert, L., Hell, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
 Radloff, U., Schneider, D. and Korn, B.
 Human Unigeneset - RZPD3
 Unpublished (2003)
 JOURNAL
 COMMENT Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD; IMAG998F081786.
 RZPDLIB; I.M.A.G.B. cDNA clone collection;
 Human Unigeneset - RZPD3 (RZPDLIB No.972)
 http://www.rzpd.de/CloneCards/cgi-
 bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 101
 Fax: +49 30 32639 111
 www.rzpd.de
 This clone is available royalty-free from RZPD;
 contact RZPD (clone@rzpd.de) for further information. Seq primer:
 M13r, Primer sequence: TTTCACACGGAACACTATGAC.

FEATURES
 source
 1..314
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAG998F081786 ; IMAGE:728071"
 /sex="male"
 /lab_host="DH10B"
 /clone_1ib="Soares testis NHT"
 /note="Vector: pRT3D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was prepared from mRNA obtained from Clontech
 Laboratories, Inc., and primed with a Not I - oligo (dT)
 primer [5']
 TGTATCATCTGAAATGAGAGCGCCGCCCAATTTTATTTT 3']
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pRT3D vector. Library
 went through one round of normalization to Cot5, and was
 constructed by Bento Soares and W. Fatima Bonaudo."

ORIGIN
 Query Match 83.3%; Score 15; DB 5; Length 314;
 Best Local Similarity 93.3%; Pred. No. 3.3e+03;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCCG 16
 |||||:|||||
 128 GAGGTCGCACGCCG 142

RESULT 35
 AA393273 337 bp mRNA linear EST 12-AUG-1997
 LOCUS AA393273
 DEFINITION zt74d04.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:728071
 5' similar to gb:M62810 MITOCHONDRIAL TRANSCRIPTION FACTOR 1
 PRECURSOR (HUMAN);, mRNA sequence.
 AA393273
 AA393273.1 GI:2046241
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
 Moore, B., Schenkenberg, K., Steptoe, M., Tan, P., Theisling, B.,
 White, T., Wyllie, T., Waterston, R. and Wilson, R.
 WashU-Merck EST Project 1997
 Unpublished (1997)
 JOURNAL
 COMMENT Contact: Wilson RK

Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 This clone is available royalty-free through LML; contact the
 IMAGS Consortium (info@image.lml.gov) for further information.
 Insert Length: 1084 Std Error: 0.00
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 163.

FEATURES

source
 1..337
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:5924983"
 /db_xref="taxon:9606"
 /clone="IMAGE:728071"
 /sex="male"
 /lab_host="DH10B"
 /clone_lib="Soares, testis, NHT"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was prepared from mRNA obtained from Clontech
 Laboratories, Inc., and primed with a Not I - oligo(dT)
 primer [5'
 TGTTCACCAATCTGAGCTGAGCGCGCCCAATTTTTTTTTTTT 3'].
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization to Cos5, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 83.3%; Score 15; DB 1; Length 337;
 Best Local Similarity 93.3%; Pred. No. 3.2e+03;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGTCCGACGCGG 16
 |||||:|||||
 Db 128 GAGGGTCCGACGCGG 142

RESULT 36
 BM851628 349 bp mRNA linear EST 06-MAR-2002
 LOCUS K-EST0132545 S13KMS5 Homo sapiens cDNA S13KMS5-44-D04 5',
 DEFINITION mRNA sequence.
 ACCESSION BM851628.1 GI:19208027
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo
 1 (bases 1 to 349)
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
 Oh, K.J., Chaong, J.E., Sohn, H.Y., Kim, D.M., Park, H.S., Kim, S. and
 Kim, Y.S.
 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Beon-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongseung@mail.kribb.re.kr
 Plate: 44 row: D column: 04
 High quality sequence stop: 349.
 FEATURES
 source
 1..349
 /organism="Homo sapiens"

/mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S13KMS5-44-D04"
 /tissue_type="myeloma"
 /cell_line="KMS-5"
 /lab_host="Top10F"
 /clone_lib="S13KMS5"
 /note="Vector: pCNS; Site 1: EcoRI, Site 2: NotI; The poly
 (A) + RNA was dephosphorylated with bacterial alkaline
 phosphatase (BAP) and then dephosphorylated with tobacco acid
 pyrophosphatase (TAP). The dephosphorylated intact mRNA was
 ligated with DNA-RNA linker including EcoRI site by
 treatment of T4 RNA ligase and the first strand cDNA was
 synthesized from oligo dT-selected mRNA by priming with
 dt-tailed vector. The dt-tailed vector was adjusted to
 have about 60nt. The cDNA vector was circularized with E.
 coli DNA ligase after digestion of EcoRI which site is
 also included in vector. An RNA strand converted to a DNA
 strand by Okayama-Berg method. The obtained cDNA vectors
 were used for transformation of competent cells E. coli
 Top10F by electroporation method. The cDNA libraries
 constructed by this method are full-length enriched cDNA
 library."

ORIGIN

Query Match 83.3%; Score 15; DB 3; Length 349;
 Best Local Similarity 93.3%; Pred. No. 3.2e+03;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGTCCGACGCGG 16
 |||||:|||||
 Db 40 GAGGGTCCGACGCGG 54

RESULT 37
 CW842063/c 376 bp DNA linear GSS 26-NOV-2004
 LOCUS ET11920.Ds3.04.14.2003.jw95.376 Arabidopsis thaliana Landsberg Ds
 DEFINITION insertion lines Arabidopsis thaliana genomic clone ET11920, genomic
 survey sequence.
 ACCESSION CW842063.1 GI:56097853
 VERSION GSS.
 KEYWORDS Arabidopsis thaliana (thale cress)
 SOURCE Arabidopsis thaliana
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 376)
 May, B.P., Stomkowski, J., Arroyo, J.-M., Vaughn, M.W., Shen, R.,
 McComble, W.R. and Martienssen, R.A.
 Arabidopsis genomic sequences flanking Ds enhancer and gene traps
 in transgenic lines
 JOURNAL Unpublished (2004)
 COMMENT Contact: Martienssen RA
 Cold Spring Harbor Laboratory
 1 Bungtown Rd., Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8322
 Fax: 516 367 8369
 Email: martienss@cshl.org
 This sequence flanks a Ds transposon carrying an enhancer trap in
 line ET11920. The transposon is located upstream of At1g72290.
 Nucleotides 1..32 are derived from Zea mays transposon Ds.
 Class: transposon-tagged.
 FEATURES
 source
 1..376
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Landsberg erecta"
 /db_xref="taxon:3702"
 /clone="ET11920"
 /clone_lib="Arabidopsis thaliana Landsberg Ds insertion
 lines"

/note="lines of Arabidopsis thaliana were generated which each contain a Ds transposon carrying a glucuronidase reporter gene. Genomic DNA flanking the transposon insertion in each line was amplified by PCR and directly sequenced. More information is available at <http://genetrap.cshl.edu>."

ORIGIN

Query Match 83.3%; Score 15; DB 10; Length 376;
Best Local Similarity 86.7%; Pred. No. 3.2e+03;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGCGCAGCGCG 17
||||:|||||
96 AGGTCGACGCCGT 82

RESULT 38
CB929313/c 396 bp mRNA linear EST 28-APR-2003
LOCUS AB41_41.H09.g1.A012 Abscissic acid-treated seedlings Sorghum bicolor
DEFINITION CDNA clone AB41_41.H09.A012 5', mRNA sequence.
ACCESSION CB929313
VERSION CB929313.1 GI:30165584
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 396)
Cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S.,
Klein, R.K., Liang, C., Sun, F., Sullivan, R., Shah, M., Buchanan, C.D.,
Bastman, A. and Pratt, L.H.
An EST database from Sorghum: AB41-treated seedlings
Unpublished (2003)
Other ESTs: AB41_41.H09.b1.A012
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmp@pratt.uga.edu

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

source

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: Sug5 (CTTCTGCTTAAGAGCTGCG).
Location/Qualifiers
1..396
/organism="Sorghum bicolor"
/mol_type="mRNA"
/db_xref="taxon:4558"
/clone="AB41_41.H09.A012"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Abcissic acid-treated seedlings"
/note="Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The library was prepared from polyA+ RNA from seedlings grown in hydroponic culture. After 12 days, medium was supplemented with 1 mM abscissic acid (ABA), while leaves were misted with a solution of 1 mM ABA. Roots and leaves were harvested after 3, 6, 12, and 24 hr and material from all time points was combined prior to RNA isolation. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5'-prime DraIII site is CACTGTG, 3'-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

ORIGIN

Query Match 83.3%; Score 15; DB 6; Length 396;
Best Local Similarity 93.3%; Pred. No. 3.2e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGCGCAGCGCG 16
||||:|||||
28 GAGGTCGACGCCG 14

RESULT 39
BE045111 412 bp mRNA linear EST 08-JUN-2000
LOCUS hm28f08.x1 NCI CGAP Thy7 Homo sapiens CDNA clone IMAGE:3023463.3,
DEFINITION similar to gb:M62810 MITOCHONDRIAL TRANSCRIPTION FACTOR 1 PRECURSOR (HUMAN); mRNA sequence.
ACCESSION BE045111
VERSION BE045111.1 GI:8362164
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 412)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strussberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue procurement: Klaus Kaserer M.D., Bruno Niederle M.D., Mike
Emmert-Buck M.D., Ph.D., Vlado Knezevic M.D.
CDNA Library Preparation: Krizman Laboratory
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
High quality sequence atp: 319.
Location/Qualifiers
1..412
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3023463"
/tissue_type="collicular adenoma (benign lesion)"
/lab_host="DH10B"
/clone_lib="NCI CGAP Thy7"
/note="Organ: thyroid; Vector: pAMP10; mRNA made from thyroid adenoma (benign), cDNA made by oligo-dT priming. Non-directionally cloned into UDG sites. Size-selected on agarose gel, average insert size 500 bp. Primary library. CDNA Library Preparation: David B. Krizman, Ph.D.
REFERENCE: Krizman et al. (1996) Cancer Research 56:5380-5383."

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

source

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: Sug5 (CTTCTGCTTAAGAGCTGCG).
Location/Qualifiers
1..396
/organism="Sorghum bicolor"
/mol_type="mRNA"
/db_xref="taxon:4558"
/clone="AB41_41.H09.A012"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Abcissic acid-treated seedlings"
/note="Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The library was prepared from polyA+ RNA from seedlings grown in hydroponic culture. After 12 days, medium was supplemented with 1 mM abscissic acid (ABA), while leaves were misted with a solution of 1 mM ABA. Roots and leaves were harvested after 3, 6, 12, and 24 hr and material from all time points was combined prior to RNA isolation. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5'-prime DraIII site is CACTGTG, 3'-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

ORIGIN

Query Match 83.3%; Score 15; DB 2; Length 412;
Best Local Similarity 93.3%; Pred. No. 3.2e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGCGCAGCGCG 16
||||:|||||
20 GAGGTCGACGCCG 34

RESULT 40
BC018628 413 bp mRNA linear HTC 06-DEC-2001
LOCUS BC018628

DEFINITION Homo sapiens, similar to transcription factor A, mitochondrial, clone IMAGE:4552415, mRNA.

ACCESSION BC018628

VERSION BC018628.1 GI:17391377

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

AUTHORS 1 (bases 1 to 413)

TITLE Strausberg, R.

JOURNAL Direct Submission

Submitted (03-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: cgabbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada

infobcsc.bc.ca

Steven Jones, Jennifer Amano, Ian Bosdet, Yaron Butterfield, Susana Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzywiński, Reta Kutche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeary, Steven Ness, Pawan Pandoh, Anna-Liisa Prabh, Parvaneh Saeedi, Jacqueline Schein, Duane Smalish, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>

Series: IRL Plate: 40 Row: d Column: 1

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4507400

This clone has the following problem: frame shifted.

FEATURES

source

1..413

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4552415"

/tissue_type="uterus, leiomyosarcoma"

/clone_id="NIH_MGC_46"

/lab_host="DH10B-R"

/note="Vector: pOTB7"

ORIGIN

Query Match 83.3%; Score 15; DB 4; Length 413;

Best Local Similarity 93.3%; Pred. No. 3.2e+03;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCGG 16

|||||

16 GAGGTCGACGCGG 30

RESULT 41

BC337115 414 bp mRNA linear EST 27-FEB-2001

LOCUS 60234393F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4552415 5',

DEFINITION mRNA sequence.

ACCESSION BC337115

VERSION BC337115.1 GI:13143553

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 414)

REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

<http://image.lnl.gov>

Plate: LNCM1248 row: 1 column: 24

High quality sequence start: 4

High quality sequence stop: 413.

FEATURES

source

1..414

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4552415"

/tissue_type="leiomyosarcoma cell line"

/lab_host="DH10B (phage-resistant)"

/clone_id="NIH_MGC_46"

/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; XhoI sites using the following 5' adaptor: GGCCGAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

ORIGIN

Query Match 83.3%; Score 15; DB 2; Length 414;

Best Local Similarity 93.3%; Pred. No. 3.2e+03;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCGG 16

|||||

17 GAGGTCGACGCGG 31

RESULT 42

R09557 426 bp mRNA linear EST 05-APR-1995

LOCUS yf27904.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone

DEFINITION IMAGE:128118 3', mRNA sequence.

ACCESSION R09557

VERSION R09557.1 GI:761480

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 426)

Hillier, L., Clark, N., Dubugue, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaastis, B., Waterston, R., Williamson, A., Woldmann, P. and Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

CONTACT: Wilson RK

Washington University School of Medicine

444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.musc1.edu

Insert Size: 817
High quality sequence stops: 404 Source: IMAGE Consortium, LNLN. This clone is available royalty-free through LNLN; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 817 Std Error: 0.00
Seq primer: -21m13
High quality sequence stop: 404.

FEATURES

source

Location/Qualifiers
1. .426
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:480279"
/db_xref="taxon:9606"
/clone="IMAGE:128118"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen 1NPLS"
/note="Organ: Liver and Spleen; Vector: pRTT3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGATTAAATTAAGACTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pRTT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 83.3%; Score 15; DB 8; Length 426;
Best Local Similarity 86.7%; Pred. No. 3.2e+03;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGGTCCGACGCCGGU 17
|||||
318 AGGGTCCGACGCCGT 332

Db

RESULT 43
CA453513 429 bp mRNA linear EST 12-NOV-2002
LOCUS AGENCOURT 10578892 NIH_MGC_127 Homo sapiens CDNA clone
DEFINITION IMAGE:6717438 5', mRNA sequence.
CA453513
CA453513.1 GI:24902339

EST.
Homo sapiens (human)
Homo sapiens
Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 429)

NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC) unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@gsf-r@mail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: LNCM3034 row: c column: 06
High quality sequence stop: 409.

COMMENT

JOURNAL

JOURNAL

FEATURES

source

Location/Qualifiers
1. .429
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6717438"

/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_127"
/note="Vector: pDNR-LIB; Site_1: SfiI (ggccatcagcc); Site_2: SfiI (ggccgctcggc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
5'-AAGCAGTGTATCAAGAGTACGTCATTACGCGCG-3' and 5'-ATTCTAGAGCCGAGCGCGCCACATG-dT(30)NK-3'. Full-length enriched library was constructed using the clonech creator SMART kit and size-selected to contain the 1-2 kb size fraction (other fractions present in NIH_MGC_126 and NIH_MGC_128). Library created in the laboratory of T. Uedl, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC library."

ORIGIN

Query Match 83.3%; Score 15; DB 6; Length 429;
Best Local Similarity 93.3%; Pred. No. 3.2e+03;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGTCCGACGCCGG 16
|||||
15 GAGGGTCCGACGCCGG 29

Db

RESULT 44
CD705931 463 bp mRNA linear EST 25-JUN-2003
LOCUS EST22458 human nasopharynx Homo sapiens CDNA, mRNA sequence.
DEFINITION CD705931
ACCESSION CD705931
VERSION CD705931.1 GI:32236561

EST.
Homo sapiens (human)
Homo sapiens
Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 463)
Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx

Unpublished (2003)
Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East,
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsu.edu.cn

COMMENT

JOURNAL

JOURNAL

FEATURES

source

Location/Qualifiers
1. .463
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx CDNA library from southern Chinese"

ORIGIN

Query Match 83.3%; Score 15; DB 6; Length 463;
Best Local Similarity 93.3%; Pred. No. 3.2e+03;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGTCCGACGCCGG 16
|||||
49 GAGGGTCCGACGCCGG 63

Db

RESULT 45
LOCUS CD698611 487 bp mRNA linear EST 25-JUN-2003
DEFINITION B015134 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD698611
VERSION CD698611.1 GI:32227094
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 487)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsuns.edu.cn
Location/Qualifiers
1. 487
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/notes="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN
Query Match 83.3%; Score 15; DB 6; Length 487;
Best Local Similarity 93.3%; Pred. No. 3.2e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCGG 16
|||||:|||||
Db 61 GAGGTCGACGCGG 75

RESULT 46
LOCUS BU660456 492 bp mRNA linear EST 30-SEP-2002
DEFINITION c160C06.21 Hembase; Erythroid Precursor Cells (LCB:c1 library) Homo sapiens cDNA clone c160C06 5', mRNA sequence.
ACCESSION BU660456
VERSION BU660456.1 GI:23372638
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 492)
AUTHORS Gubin,A.N., Lee,Y.T., Bouffard,G.G. and Miller,J.L.
TITLE Gene Expression in Human Erythroid Precursor Cells
JOURNAL Unpublished (2002)
COMMENT Contact: Jeffery L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda, MD 20892, USA
Tel: 301 402 2373
Fax: 301 435 5148
Email: jlm7femh.gov
The c1 library was constructed by Alexander Gubin, Ph.D. in the Laboratory of Chemical Biology, NIDDK, NIH. DNA Sequencing and/or

analyses by National Institutes of Health Intramural Sequencing Center (NISC). More information available at:
<http://hembase.niddk.nih.gov>
Plate: 60 row: c column: 06
Seq primer: 5' lambda-TripLex2 Sequencing Primer.
Location/Qualifiers
1. 492
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="c160C06"
/sex="unknown"
/tissue_type="blood"
/cell_line="Erythroid Precursor Cells"
/cell_line="Primary Culture of Peripheral Blood Mononuclear Cells"
/dev_stage="Precursor erythroblasts, GPA++"
/lab_host="DH5alpha"
/clone_lib="Hembase; Erythroid Precursor Cells (LCB:c1 library)"
/notes="Organ: blood; Vector: pTriplex2; Site 1: SfiI; Site 2: SfiI; A complementary DNA (cDNA) library from human erythroid precursor cells was constructed using SMART PCR (polymerase chain reaction) cDNA library Construction Kit (Clontech, Palo Alto, CA) according to the manufacturer's directions, but with slight modifications. Briefly, reverse transcription was performed in the presence of 1 umol/L peptide nucleic acid (PNA) oligos (N-terminal)-biotin-GTC-CAC-CCG-AAG-CTT-G-(C-terminal) and (N-terminal)-biotin-C(T/C)T-GAA-GTT-CTC-AGG-A-(C-terminal). Synthesized cDNA was digested with SfiI and size-selected on a 1% agarose gel (>800bp). Large-scale sequencing of the library was performed by the NIH Intramural Sequencing Center (NISC).
<http://www.nisc.nih.gov/>."

ORIGIN
Query Match 83.3%; Score 15; DB 5; Length 492;
Best Local Similarity 93.3%; Pred. No. 3.2e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCGG 16
|||||:|||||
Db 28 GAGGTCGACGCGG 42

RESULT 47
LOCUS CR736151 493 bp mRNA linear EST 10-DEC-2004
DEFINITION CR736151 Soares testis NHT Homo sapiens cDNA clone IMAGE998B164415
ACCESSION CR736151
VERSION CR736151.1 GI:51586228
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 493)
AUTHORS Ebert,L., Heil,O., Hennig,S., Korn,B., Neubert,P., Patsch,B., Peters,M., Radelof,U. and Schneider,D.
TITLE I.M.A.G.E. cDNA Clone Collection
JOURNAL Unpublished (2004)
COMMENT Contact: Inge Axlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD: IMAGE998B164415.
RZPDLIB: I.M.A.G.E. cDNA Clone Collection;
Contact: Inge Axlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de

This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r. Primer sequence: TTTCACACAGGAAACAGCTATGAC.

FEATURES

source

1. 493

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAG998B1C4415 ; IMAGB:1737519"

/sex="male"

/lab_host="DH10B"

/clone_lib="Soares_tesla_NHT"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5']

Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo.

ORIGIN

Query Match 83.3%; Score 15; DB 7; Length 493;

Best Local Similarity 93.3%; Pred. No. 3.2e+03; Indels 0; Gaps 0;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGGCGCAGCGCG 16

DB 299 GAGGGTCCGACCGCG 313

RESULT 48 530 bp DNA linear GSS 02-NOV-2004
CWA52151/c SORGHUM bicolor genomic clone f53001f192120, genomic survey
LOCUS SORGHUM bicolor genomic clone f53001f192120, genomic survey
DEFINITION

Accession: CWA52151 GI:55200112
Version: GSS.
Keywords: SORGHUM bicolor (sorghum)

Source: SORGHUM bicolor (sorghum)
Organism: SORGHUM bicolor (sorghum)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 530)

Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,
Jones, J., Plick, E., Rohlfing, T., Fries, J., Bradford, K.,
McMenamy, J., Smith, M., Holman, H., Roe, B.A., Wiley, G., Korf, I. F.,
Rabinowicz, P.D., Lakey, N., McComb, W.R., Jeddeloh, J.A. and
Martensen, R.A.
Sorghum genome sequencing by methylation filtration

PLoS Biol. 3 (1), e13 (2005)
15660154
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: f53001f192 row: 1 column: 20
Seq primer: f Forward
Class: methylation filtered
High quality sequence stop: 530.

FEATURES

source

1. 530

ORIGIN

Query Match 83.3%; Score 15; DB 10; Length 530;

Best Local Similarity 93.3%; Pred. No. 3.2e+03; Indels 0; Gaps 0;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGGCGCAGCGCG 16

DB 24 GAGGGTCCGACCGCG 10

RESULT 49 546 bp mRNA linear EST 29-JAN-2003
CB138822 K-EST0191737 LSHLK1 Homo sapiens cDNA clone LSHLK1-36-B10 5', mRNA
LOCUS SORGHUM bicolor genomic clone f53001f192120, genomic survey
DEFINITION

Accession: CB138822 GI:28110953
Version: EST.
Keywords: Homo sapiens (human)

Source: Homo sapiens (human)
Organism: Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 546)

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 36 row: B column: 10
High quality sequence stop: 546.

FEATURES

source

1. 546

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="LSHLK1-36-B10"

/sex="M"

/cell_line="HLK-1"

/lab_host="T010P"

/clone_lib="LSHLK1"

/note="Organ: Liver; Vector: pCNS-D2; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including
BcoRI site by treatment of T4 RNA ligase and the first
strand cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
BcoRI which site is also included in vector. An RNA strand

converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells *E. coli* Top10[®] by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

Db 533 GAGGTCGACGCGG 518
Search completed: March 18, 2006, 20:01:40
Job time : 1762.77 secs

ORIGIN

Query Match 83.3%; Score 15; DB 6; Length 547;
Best Local Similarity 93.3%; Pred. No. 3.2e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGTCGACGCGG 16
Db 17 GAGGTCGACGCGG 31

RESULT 50

BE552352/c 547 bp mRNA linear EST 10-AUG-2000
LOCUS hy06605.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:3196544 3'
DEFINITION similar to gb:M62810 MITOCHONDRIAL TRANSCRIPTION FACTOR 1 PRECURSOR
(HUMAN); mRNA sequence.

ACCESSION BE552352
VERSION BE552352.1 GI:9794044
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 547)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML, send email to:
info@image.liml.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 481.
Location/Qualifiers

FEATURES

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3196544"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_1ib="NCI CGAP GC6"
/note="Vector: pTZ19D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI-CGAP GC4 was prepared, and
88 circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonids
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 83.3%; Score 15; DB 2; Length 547;
Best Local Similarity 93.3%; Pred. No. 3.2e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGTCGACGCGG 16

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:35:23 ; Search time 68,8846 Seconds
(without alignments)
464,488 Million cell updates/sec

Title: US-10-800-926-1

Perfect score: 18
Sequence: 1 agagagugcagcgcgua 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 88878028 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	18	100.0	18	3	US-08-960-774-60	Sequence 60, Appl
C 4	18	100.0	18	3	US-09-191-170-54	Sequence 54, Appl
C 5	18	100.0	18	3	US-09-337-619-60	Sequence 60, Appl
C 6	18	100.0	18	3	US-09-954-987B-67	Sequence 67, Appl
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C 8	17	94.4	17	3	US-09-080-285-9	Sequence 9, Appl
C 9	17	94.4	17	3	US-09-724-426-9	Sequence 9, Appl
C 10	17	94.4	17	3	US-09-724-426-9	Sequence 9, Appl
C 11	15	83.3	17	2	US-08-465-485A-8	Sequence 8, Appl
C 12	15	83.3	17	3	US-09-080-285-8	Sequence 8, Appl
C 13	15	83.3	17	3	US-09-724-426-8	Sequence 8, Appl
C 14	15	83.3	17	3	US-09-724-426-8	Sequence 8, Appl
C 15	15	83.3	17	3	US-09-108-673A-25	Sequence 25, Appl
C 16	15	83.3	955	3	US-09-949-016-2432	Sequence 2432, Ap
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C 18	15	83.3	2036	3	US-09-949-016-4795	Sequence 4795, Ap
C 19	15	83.3	12993	3	US-09-949-016-14174	Sequence 14174, A
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C 25	14.4	80.0	37474	3	US-09-952-060-26	Sequence 26, Appl
C 26	14.4	80.0	38519	3	US-09-952-060-29	Sequence 29, Appl
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C 29	14.4	80.0	4403765	3	US-09-103-840A-2	Sequence 2, Appl
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C 83	13.4	74.4	1407	3	US-09-902-540-4633	Sequence 4633, Ap
C 84	13.4	74.4	1500	3	US-09-174-768-3	Sequence 3, Appl
C 85	13.4	74.4	1530	3	US-09-489-039A-2429	Sequence 2429, Ap
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C 87	13.4	74.4	1563	3	US-09-252-991A-15934	Sequence 15934, A
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C 96	13.4	74.4	3007	3	US-08-480-474-33	Sequence 33, Appl
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C 976 12.2 67.8 3567 3 US-10-011-146-1 Sequence 1, Appl1
C 977 12.2 67.8 3588 3 US-09-302-540-4681 Sequence 4681, Ap
C 978 12.2 67.8 3591 2 US-08-162-809-13 Sequence 13, Appl
C 979 12.2 67.8 3650 3 US-09-949-016-5637 Sequence 5637, Ap
C 980 12.2 67.8 3725 3 US-10-160-719A-13 Sequence 13, Appl
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C 982 12.2 67.8 3725 3 US-10-160-719A-41 Sequence 41, Appl
C 983 12.2 67.8 3725 3 US-10-209-059-45 Sequence 45, Appl
C 984 12.2 67.8 3768 3 US-09-332-522E-7 Sequence 7, Appl
C 985 12.2 67.8 3768 3 US-08-506-296B-20 Sequence 20, Appl
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C 992 12.2 67.8 4702 2 US-08-530-198-8 Sequence 8, Appl1
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C 994 12.2 67.8 4702 2 US-08-728-470-8 Sequence 8, Appl1
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C 996 12.2 67.8 4761 3 US-09-302-540-739 Sequence 739, App
C 997 12.2 67.8 4794 2 US-08-617-697-7 Sequence 7, Appl1
C 998 12.2 67.8 4803 2 US-08-617-697-8 Sequence 8, Appl1
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ALIGNMENTS

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RESULT 1
US-09-030-701-28/c
; Sequence 28, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; TITLE OF INVENTION: UNMETHYLATED CPG DINUCLEOTIDE IN THE TREATMENT OF
; TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030, 701B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039, 405
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-28
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Best Local Similarity 88.9%; Pred. No. 5.7;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Db 18 AGAGGGTCCGACCGCGTA 1
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RESULT 2
US-09-286-098-60/c
; Sequence 60, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Weiner, George
```

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; TITLE OF INVENTION: Methods and Products for Stimulating the
; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
; TITLE OF INVENTION: Cyclokin
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/286, 098
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080, 729
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
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; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-286-098-60
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Best Local Similarity 88.9%; Pred. No. 5.7;
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Db 18 AGAGGGTCCGACCGCGTA 1
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; Sequence 60, Application US/08960774
; Patent No. 6239116
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; GENERAL INFORMATION:
; APPLICANT: Krieg et al.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960, 774
; FILING DATE: 30-October-1997
; CLASSIFICATION: 514
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652
; FILING DATE: October 30, 1996
; CLASSIFICATION: 514
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; ATTORNEY/AGENT INFORMATION:
; NAME: Hallie, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08918/012001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
```

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; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 60:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-960-774-60
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Best Local Similarity 88.9%; Pred. No. 5.7;
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Db 18 AGAGGUGCGACCGCGTA 1

RESULT 4
US-09-191-170-54/c
Sequence 54, Application US/09191170

Patent No. 6429199

GENERAL INFORMATION:

APPLICANT: Kriegl, Arthur M.

APPLICANT: Hartmann, Gunther

TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules

TITLE OF INVENTION: For Activating Dendritic Cells

FILE REFERENCE: C1039/7017

CURRENT APPLICATION NUMBER: US/09/191,170

EARLIER FILING DATE: 1998-11-13

EARLIER APPLICATION NUMBER: US 08/960,774

EARLIER FILING DATE: 1997-10-30

EARLIER APPLICATION NUMBER: US 08/738,652

EARLIER FILING DATE: 1996-10-30

EARLIER APPLICATION NUMBER: US 08/386,063

EARLIER FILING DATE: 1995-02-07

EARLIER APPLICATION NUMBER: US 08/276,358

EARLIER FILING DATE: 1994-07-15

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 54

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: synthetic oligonucleotide

US-09-191-170-54

Query Match

Best Local Similarity 100.0%; Score 18; DB 3; Length 18;

Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACCGCGUA 18

Db 18 AGAGGUGCGACCGCGTA 1

RESULT 5
US-09-337-619-60/c
Sequence 60, Application US/09337619

Patent No. 6653292

GENERAL INFORMATION:

APPLICANT: Kriegl, Arthur M.

TITLE OF INVENTION: Methods of Treating Cancer Using

FILE REFERENCE: C1039/7021/HCL

CURRENT APPLICATION NUMBER: US/09/337,619

EARLIER FILING DATE: 1999-06-21

EARLIER APPLICATION NUMBER: US 08/960,774

EARLIER FILING DATE: 1997-10-30

EARLIER APPLICATION NUMBER: US 08/738,652

EARLIER FILING DATE: 1996-10-30

EARLIER APPLICATION NUMBER: US 08/386,063

EARLIER FILING DATE: 1995-02-07

EARLIER APPLICATION NUMBER: US 08/276,358

NUMBER OF SEQ ID NOS: 123

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 60

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Oligonucleotide

US-09-337-619-60

Query Match

Best Local Similarity 100.0%; Score 18; DB 3; Length 18;

Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACCGCGUA 18

Db 18 AGAGGUGCGACCGCGTA 1

RESULT 6
US-09-954-987B-67/c
Sequence 67, Application US/09954987B

Patent No. 6943240

GENERAL INFORMATION:

APPLICANT: Stefan Bauer

APPLICANT: Grayson B. Lipford

APPLICANT: Hermann Wagner

TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF

FILE REFERENCE: C1041/7016 (AMS)

CURRENT APPLICATION NUMBER: US/09/954,987B

EARLIER FILING DATE: 2001-09-17

EARLIER APPLICATION NUMBER: US 60/233,035

EARLIER FILING DATE: 2000-09-15

EARLIER APPLICATION NUMBER: US 60/263,657

EARLIER FILING DATE: 2001-01-23

EARLIER APPLICATION NUMBER: US 60/291,726

EARLIER FILING DATE: 2001-05-17

EARLIER APPLICATION NUMBER: US 60/300,210

EARLIER FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 230

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 67

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic oligonucleotide

US-09-954-987B-67

Query Match

Best Local Similarity 100.0%; Score 18; DB 3; Length 18;

Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 18 AGAGGUGCGACCGCGTA 1

RESULT 7
US-08-465-485A-9/c
Sequence 9, Application US/08465485A

Patent No. 5831066

GENERAL INFORMATION:

APPLICANT: Reed, John

TITLE OF INVENTION: Regulation of bcl-2 Gene Expression

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSER: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

STREET: 1755 S. Jefferson Davis Hwy., Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-9

Query Match 94.4%; Score 17; DB 2; Length 17;
Best Local Similarity 88.2%; Pred. No. 19;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGGUA 18
||||:|||||:|
DB 17 GAGGGTCGACGCGGTA 1

RESULT 8

US-09-080-285-9/c
Sequence 9, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
STEERT, 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-9

Query Match 94.4%; Score 17; DB 3; Length 17;
Best Local Similarity 88.2%; Pred. No. 19;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGGUA 18
||||:|||||:|
DB 17 GAGGGTCGACGCGGTA 1

RESULT 9

US-09-724-426-9/c
Sequence 9, Application US/09724426
Patent No. 6414134
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of BCL-2 Gene Expression
FILE REFERENCE: 10412-024
CURRENT APPLICATION NUMBER: US/09/724,426
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-426-9

Query Match 94.4%; Score 17; DB 3; Length 17;
Best Local Similarity 88.2%; Pred. No. 19;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGGUA 18
||||:|||||:|
DB 17 GAGGGTCGACGCGGTA 1

RESULT 10

US-09-724-425-9/c
Sequence 9, Application US/09724425
Patent No. 6841541
GENERAL INFORMATION:
APPLICANT: Reed, John C.
TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION
FILE REFERENCE: 04040/1200990-US7
CURRENT APPLICATION NUMBER: US/09/724,425
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/375,514
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: US 09/080,285
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: US 08/465,485
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/124,256
PRIOR FILING DATE: 1993-09-20

PRIOR APPLICATION NUMBER: US 07/840,716
PRIOR FILING DATE: 1992-02-21
PRIOR APPLICATION NUMBER: US 07/288,692
PRIOR FILING DATE: 1988-12-22
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-425-9

Query Match 94.4%; Score 17; DB 3; Length 17;
Best Local Similarity 88.2%; Pred. No. 19;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGAGGUGCGACGCGGA 18
17 AGAGGTCGACGCGGA 1

RESULT 11
US-08-465-485A-8/c
Sequence 8, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-8

Query Match 83.3%; Score 15; DB 2; Length 17;

Best Local Similarity 93.3%; Pred. No. 1.9e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCG 15
15 AGAGGTCGACGCG 1

RESULT 12
US-09-080-285-8/c
Sequence 8, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-8

Query Match 83.3%; Score 15; DB 3; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.9e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCG 15
15 AGAGGTCGACGCG 1

RESULT 13
US-09-724-426-8/c

```

; Sequence 8, Application US/09724426
; Patent No. 6414134
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of BCL-2 Gene Expression
; FILE REFERENCE: 10412-024
; CURRENT APPLICATION NUMBER: US/09/724,426
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 8
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-724-426-8

Query Match      83.3%; Score 15; DB 3; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.9e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGAGGUGCGACGCG 15
Db      15 AGAGGTCGACGCG 1

RESULT 14
US-09-724-425-8/c
; Sequence 8, Application US/09724425
; Patent No. 6841541
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION
; FILE REFERENCE: 04040/1200990-US7
; CURRENT APPLICATION NUMBER: US/09/724,425
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/375,514
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: US 09/080,285
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: US 08/465,485
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/124,256
; PRIOR FILING DATE: 1993-09-20
; PRIOR APPLICATION NUMBER: US 07/840,716
; PRIOR FILING DATE: 1992-02-21
; PRIOR APPLICATION NUMBER: US 07/288,692
; PRIOR FILING DATE: 1988-12-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-724-425-8

Query Match      83.3%; Score 15; DB 3; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.9e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGAGGUGCGACGCG 15
Db      15 AGAGGTCGACGCG 1

RESULT 15
US-09-108-673A-25/c
; Sequence 25, Application US/09108673A
; Patent No. 6887906
; GENERAL INFORMATION:
; APPLICANT: Ching-Leou Teng and Greg Hardee
; TITLE OF INVENTION: Compositions and Methods for the Delivery of
; TITLE OF INVENTION: Oligonucleotides Via the Alimentary Canal
; NUMBER OF SEQUENCES: 132
```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 6887906r1s LLP
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/108,673A
; FILING DATE: July 1, 1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/886,829
; FILING DATE: 01-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: 1SIS-3105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568 3439
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; FEATURE:
; OTHER INFORMATION: Antisense to bcl-2 mRNA
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO 95/08350 (SEQ ID NO: 8)
; FILING DATE: 20-SEP-1994
; PUBLICATION DATE: 30-MAR-1995
; US-09-108-673A-25

Query Match      83.3%; Score 15; DB 3; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.9e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGAGGUGCGACGCG 15
Db      15 AGAGGTCGACGCG 1

RESULT 16
US-09-949-016-2432
; Sequence 2432, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2432
; LENGTH: 955
; TYPE: DNA
; ORGANISM: Human
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US-09-949-016-2432

Query Match

Best Local Similarity 83.3%; Score 15; DB 3; Length 955;
Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGG 16

DB 134 GAGGTCGCACGCGG 148

RESULT 17

US-09-949-016-2433

Sequence 2433, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2433

LENGTH: 955

TYPE: DNA

ORGANISM: Human

US-09-949-016-2433

Query Match

Best Local Similarity 83.3%; Score 15; DB 3; Length 955;
Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGG 16

DB 134 GAGGTCGCACGCGG 148

RESULT 18

US-09-949-016-4795

Sequence 4795, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4795

LENGTH: 2036

TYPE: DNA

ORGANISM: Human

US-09-949-016-4795

Query Match

Best Local Similarity 83.3%; Score 15; DB 3; Length 2036;
Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGG 16

DB 134 GAGGTCGCACGCGG 148

RESULT 19

US-09-949-016-14174

Sequence 14174, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 14174

LENGTH: 12993

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(12993)

OTHER INFORMATION: n = A,T,C or G

US-09-949-016-14174

Query Match

Best Local Similarity 83.3%; Score 15; DB 3; Length 12993;
Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGG 16

DB 2134 GAGGTCGCACGCGG 2148

RESULT 20

US-09-949-016-14175

Sequence 14175, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 14175

LENGTH: 12993

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(12993)

OTHER INFORMATION: n = A,T,C or G

US-09-949-016-14175

Query Match 83.3%; Score 15; DB 3; Length 12993;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCGG 16
DB 2134 GAGGUGCGACGCGG 2148

RESULT 21
US-09-949-016-16537
Sequence 16537, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 16537
LENGTH: 14587
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(14587)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16537

Query Match 83.3%; Score 15; DB 3; Length 14587;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCGG 16
DB 2134 GAGGUGCGACGCGG 2148

RESULT 22
US-07-841-651-1/C
Sequence 1, Application US/07841651
Patent No. 5410031
GENERAL INFORMATION:
APPLICANT: Pajor, Ana M
TITLE OF INVENTION: Cloning and Functional Expression of a
TITLE OF INVENTION: Mammalian Na+/Nucleoside Cotransporter: A Member of the
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Sheldon E. Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
COUNTRY: USA
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/841,651
FILING DATE: 19920224

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mandel, Saralynn
REGISTRATION NUMBER: 31,853
REFERENCE/DOCKET NUMBER: 8772
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 795-6321
TELEFAX: (818) 796-4000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2238 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Oryctolagus cuniculus
FEATURE:
NAME/KEY: CDS
LOCATION: 7..2022
US-07-841-651-1

Query Match 80.0%; Score 14.4; DB 2; Length 2238;
Best Local Similarity 87.5%; Pred. No. 3.6e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGG 16
DB 1548 AGAGGUGCGACGCGG 1533

RESULT 23
US-08-311-731A-138/C
Sequence 138, Application US/08311731A
Patent No. 6583266
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSER: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 35961 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular

MOLECULAR TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mycobacterium leprae
US-08-311-731A-138

Query Match 80.0%; Score 14.4; DB 3; Length 35961;
Best Local Similarity 87.5%; Pred. No. 3.5e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGG 16
DB 1594 AGAGGCTCCGACGCGG 1579

RESULT 24
US-09-952-060-31/c
Sequence 31, Application US/09952060
Patent No. 6733993
GENERAL INFORMATION:
APPLICANT: Emili, Emilio A.
APPLICANT: Youil, Rima
APPLICANT: Bett, Andrew J.
APPLICANT: Chen, Ling
APPLICANT: Kaslow, David C.
APPLICANT: Shiver, John W.
APPLICANT: Toner, Timothy J.
APPLICANT: Casimiro, Danilo R.
TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS
TITLE OF INVENTION: VACCINES EXPRESSING CODON OPTIMIZED HIV1-GAG, POL, NEF AND
TITLE OF INVENTION: MODIFICATIONS
FILE REFERENCE: 20747Y
CURRENT APPLICATION NUMBER: US/09/952,060
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: PCT/US01/28861
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/317,814
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/279,056
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 60/233,180
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 31
LENGTH: 36620
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Codon optimized DNA encoding pMRKADSHIV-1 nef,
US-09-952-060-31

Query Match 80.0%; Score 14.4; DB 3; Length 36620;
Best Local Similarity 87.5%; Pred. No. 3.5e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGG 16
DB 25690 AGAGGCTCCGACGCGG 25675

RESULT 25
US-09-952-060-26/c
Sequence 26, Application US/09952060
Patent No. 6733993
GENERAL INFORMATION:
APPLICANT: Emili, Emilio A.
APPLICANT: Youil, Rima
APPLICANT: Bett, Andrew J.
APPLICANT: Chen, Ling
APPLICANT: Kaslow, David C.

APPLICANT: Shiver, John W.
APPLICANT: Toner, Timothy J.
APPLICANT: Casimiro, Danilo R.
TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS
TITLE OF INVENTION: VACCINES EXPRESSING CODON OPTIMIZED HIV1-GAG, POL, NEF AND
TITLE OF INVENTION: MODIFICATIONS
FILE REFERENCE: 20747Y
CURRENT APPLICATION NUMBER: US/09/952,060
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: PCT/US01/28861
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/317,814
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/279,056
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 60/233,180
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 37474
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DNA encoding pMRKAD5 HIV-1 gag, noncoding
US-09-952-060-26

Query Match 80.0%; Score 14.4; DB 3; Length 37474;
Best Local Similarity 87.5%; Pred. No. 3.5e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGG 16
DB 26555 AGAGGCTCCGACGCGG 26540

RESULT 26
US-09-952-060-29/c
Sequence 29, Application US/09952060
Patent No. 6733993
GENERAL INFORMATION:
APPLICANT: Emili, Emilio A.
APPLICANT: Youil, Rima
APPLICANT: Bett, Andrew J.
APPLICANT: Chen, Ling
APPLICANT: Kaslow, David C.
APPLICANT: Shiver, John W.
APPLICANT: Toner, Timothy J.
APPLICANT: Casimiro, Danilo R.
TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS
TITLE OF INVENTION: VACCINES EXPRESSING CODON OPTIMIZED HIV1-GAG, POL, NEF AND
TITLE OF INVENTION: MODIFICATIONS
FILE REFERENCE: 20747Y
CURRENT APPLICATION NUMBER: US/09/952,060
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: PCT/US01/28861
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/317,814
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/279,056
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 60/233,180
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 38519
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Codon optimized DNA encoding pMRKADSHIV-1 pol,
US-09-952-060-29

Query Match 80.0%; Score 14.4; DB 3; Length 38519;
Best Local Similarity 87.5%; Pred. No. 3.5e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUCGACCGCG 16
DB 27589 AGAGGUCGACCGCG 27574

RESULT 27
US-09-949-016-12147/c
Sequence 12147, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12147
LENGTH: 767677
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(767677)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12147

Query Match 80.0%; Score 14.4; DB 3; Length 767677;
Best Local Similarity 93.8%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUCGACCGCG 16
DB 516926 AGAGGUCGACCGCG 516911

RESULT 28
US-09-949-016-17361/c
Sequence 17361, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17361
LENGTH: 767677
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature

LOCATION: (1)....(767677)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17361

Query Match 80.0%; Score 14.4; DB 3; Length 767677;
Best Local Similarity 93.8%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUCGACCGCG 16
DB 516926 AGAGGUCGACCGCG 516911

RESULT 29
US-09-103-840A-2
Sequence 2, Application US/09103840A

Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 80.0%; Score 14.4; DB 3; Length 4403765;
Best Local Similarity 81.2%; Pred. No. 2.2e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGUCGACCGCGU 17
DB 789126 GAGGUCGACCGCGU 789141

RESULT 30
US-09-103-840A-2/c
Sequence 2, Application US/09103840A

Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 80.0%; Score 14.4; DB 3; Length 4403765;
Best Local Similarity 87.5%; Pred. No. 2.2e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGGGGCGCAGCGCGTA 18
DB 991739 AGGGGCGCAGCGCGTA 991724

RESULT 31
US-09-103-840A-1
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT FILING DATE: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 80.0%; Score 14.4; DB 3; Length 4411529;
Best Local Similarity 81.2%; Pred. No. 2.2e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGGCGCAGCGCGT 17
DB 787164 GAGGGGCGCAGCGCGT 787179

RESULT 32
US-09-103-840A-1/c
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT FILING DATE: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 80.0%; Score 14.4; DB 3; Length 4411529;
Best Local Similarity 87.5%; Pred. No. 2.2e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGGGGCGCAGCGCGTA 18
DB 991738 AGGGGCGCAGCGCGTA 991723

RESULT 33
US-08-465-485A-10/c
Sequence 10, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Portney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-10

Query Match 77.8%; Score 14; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 6.2e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGGCGCAGCGCGTA 18
DB 17 GGGGCGCAGCGCGTA 4

RESULT 34
US-09-080-285-10/c
Sequence 10, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400

CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-10

Query Match 77.8%; Score 14; DB 3; Length 17;
Best Local Similarity 85.7%; Pred. No. 6.2e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGUCGACGCGGUA 18
||:|||||||:
DB 17 GGTCCGACGCGGTA 4

RESULT 35
US-09-724-426-10/c
Sequence 10, Application US/09724426
Patent No. 6415134
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of BCL-2 Gene Expression
FILE REFERENCE: 10412-024
CURRENT APPLICATION NUMBER: US/09/724,426
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.0
SEQ ID NO 10
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-426-10

Query Match 77.8%; Score 14; DB 3; Length 17;
Best Local Similarity 85.7%; Pred. No. 6.2e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGUCGACGCGGUA 18
||:|||||||:
DB 17 GGTCCGACGCGGTA 4

RESULT 36
US-09-724-425-10/c
Sequence 10, Application US/09724425
Patent No. 6841541
GENERAL INFORMATION:
APPLICANT: Reed, John C.
TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION
FILE REFERENCE: 04040/1200990-US7
CURRENT APPLICATION NUMBER: US/09/724,425
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/375,514
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: US 09/080,285
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: US 08/465,485
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/124,256
PRIOR FILING DATE: 1993-09-20
PRIOR APPLICATION NUMBER: US 07/840,716
PRIOR FILING DATE: 1992-02-21
PRIOR APPLICATION NUMBER: US 07/288,692
PRIOR FILING DATE: 1988-12-22
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-425-10

Query Match 77.8%; Score 14; DB 3; Length 17;
Best Local Similarity 85.7%; Pred. No. 6.2e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGUCGACGCGGUA 18
||:|||||||:
DB 17 GGTCCGACGCGGTA 4

RESULT 37
US-09-108-673A-26/c
Sequence 26, Application US/09108673A
Patent No. 6887906
GENERAL INFORMATION:
APPLICANT: Ching-Leon Teng and Greg Hardee
TITLE OF INVENTION: Compositions and Methods for the Delivery of
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSES: Woodcock Washburn Kurtz Mackiewicz & No. 6887906x1s LLP
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/108,673A
FILING DATE: July 1, 1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,829
FILING DATE: 01-JUL-1997
ATTORNEY/AGENT INFORMATION:

NAME: Paul K. Legard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-3105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
FEATURE:
OTHER INFORMATION: Antisense to bcl-2 mRNA
PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO 95/08350 (SEQ ID NO: 9)
FILING DATE: 20-SEP-1994
PUBLICATION DATE: 30-MAR-1995
US-09-108-673A-26

Query Match 77.8%; Score 14; DB 3; Length 17;
Best Local Similarity 85.7%; Pred. No. 6.2e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGUGCGACCGCGTA 18
DB 17 GGTCGACGCGGTA 4

RESULT 38
US-09-108-673A-27/C
Sequence 27, Application US/09108673A
Patent No. 6887906
GENERAL INFORMATION:
APPLICANT: Ching-Leou Teng and Greg Hardee
TITLE OF INVENTION: Compositions and Methods for the Delivery of
TITLE OF INVENTION: Oligonucleotides Via the Alimentary Canal
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 6887906ris LLP
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/108,673A
FILING DATE: JULY 1, 1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,829
FILING DATE: 01-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-3105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
FEATURE:

OTHER INFORMATION: Antisense to bcl-2 mRNA
PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO 95/08350 (SEQ ID NO: 10)
FILING DATE: 20-SEP-1994
PUBLICATION DATE: 30-MAR-1995
US-09-108-673A-27

Query Match 77.8%; Score 14; DB 3; Length 17;
Best Local Similarity 85.7%; Pred. No. 6.2e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGUGCGACCGCGTA 18
DB 17 GGTCGACGCGGTA 4

RESULT 39
US-09-270-767-5572/C
Sequence 5572, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5572
LENGTH: 397
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-5572

Query Match 77.8%; Score 14; DB 3; Length 397;
Best Local Similarity 92.9%; Pred. No. 5.9e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACCGG 15
DB 34 GAGGUGCGACCGG 21

RESULT 40
US-09-270-767-20854/C
Sequence 20854, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20854
LENGTH: 397
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-20854

Query Match 77.8%; Score 14; DB 3; Length 397;
Best Local Similarity 92.9%; Pred. No. 5.9e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACCGG 15
DB 34 GAGGUGCGACCGG 21

RESULT 41
US-09-676-519-19
Sequence 19, Application US/09676519

Patent No. 6737508
GENERAL INFORMATION:
APPLICANT: PELETTIER, JERRY
APPLICANT: GROES, PHILIPPE
APPLICANT: DUBOW, MICHAEL
TITLE OF INVENTION: DNA SEQUENCES FROM STAPHYLOCOCCUS AUREUS BACTERIOPHAGES
FILE REFERENCE: 073406-0404
CURRENT APPLICATION NUMBER: US/09/676,519
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/407,804
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: 60/110,992
PRIOR FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 43576
TYPE: DNA
ORGANISM: Staphylococcus bacteriophage
US-09-676-519-19

Query Match 76.7%; Score 13.8; DB 3; Length 43576;
Best Local Similarity 92.9%; Pred. No. 5.5e+02;

Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCG 14

DB 31337 AGAGGUGCGACGCG 31350

RESULT 42
US-10-019-455A-15/C
Sequence 15, Application US/10019455A
Patent No. 6797483
GENERAL INFORMATION:
APPLICANT: ITOH, YASUAKI
APPLICANT: NISHI, KAZUORI
APPLICANT: OGI, KAZUHIRO
APPLICANT: OKUBO, SHOICHI
APPLICANT: MOGI, SHINICHI
APPLICANT: NOGUCHI, YUKO
TITLE OF INVENTION: NOVEL PEPTIDE AND DNA THEREOF
FILE REFERENCE: 56804-46342
CURRENT APPLICATION NUMBER: US/10/019,455A
CURRENT FILING DATE: 2002-04-22
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-019-455A-15

Query Match 76.7%; Score 13.8; DB 3; Length 24;
Best Local Similarity 82.4%; Pred. No. 7.8e+02;

Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCGGUA 18

DB 18 GATGGGCGACGCGGTA 2

RESULT 43
US-09-270-767-7758
Sequence 7758, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7758
LENGTH: 335
TYPE: DNA
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: n means any nucleotide
US-09-270-767-7758

Query Match 76.7%; Score 13.8; DB 3; Length 335;
Best Local Similarity 76.5%; Pred. No. 7.5e+02;

Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCGGUA 18

DB 91 GAGGATCGCACGCGGTA 107

RESULT 44
US-09-270-767-23040
Sequence 23040, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23040
LENGTH: 335
TYPE: DNA
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: n means any nucleotide
US-09-270-767-23040

Query Match 76.7%; Score 13.8; DB 3; Length 335;
Best Local Similarity 76.5%; Pred. No. 7.5e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCGGUA 18

DB 91 GAGGATCGCACGCGGTA 107

RESULT 45
US-09-513-999C-2747/C
Sequence 2747, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 2747
LENGTH: 364
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:

NAME/KEY: CDS
LOCATION: 27..362
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18
OTHER INFORMATION: w=a or t
US-09-513-999C-2747

Query Match 76.7%; Score 13.8; DB 3; Length 364;
Best Local Similarity 76.5%; Pred. No. 7.4e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGGUA 18
DB 73 GAGGGTCCGCTCGGTA 57

RESULT 46
US-09-270-767-25712/C

Sequence 25712, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:

APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25712
LENGTH: 523
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-25712

Query Match 76.7%; Score 13.8; DB 3; Length 523;
Best Local Similarity 76.5%; Pred. No. 7.5e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGU 17
DB 151 AGGGGTCCGACGCGGT 135

RESULT 47
US-09-270-767-10334/C

Sequence 10334, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10334
LENGTH: 600
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-10334

Query Match 76.7%; Score 13.8; DB 3; Length 600;
Best Local Similarity 76.5%; Pred. No. 7.4e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGU 17
DB 228 AGTGGTCCGACGCGGT 212

RESULT 48
US-09-949-016-150767/C

Sequence 150767, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 150767
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-150767

Query Match 76.7%; Score 13.8; DB 3; Length 601;
Best Local Similarity 76.5%; Pred. No. 7.4e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGU 17
DB 163 AGGGGTCCGACGCGGT 147

RESULT 49
US-09-252-991A-8441

Sequence 8441, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 8441
LENGTH: 1107
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8441

Query Match 76.7%; Score 13.8; DB 3; Length 1107;
Best Local Similarity 82.4%; Pred. No. 7.4e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGU 17
DB 1031 AGAGGGCGCGCGGT 1047

RESULT 50
US-09-902-540-9637/C

Sequence 9637, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B
 CURRENT APPLICATION NUMBER: US/09/902,540
 CURRENT FILING DATE: 2001-07-10
 PRIOR APPLICATION NUMBER: 60/217,883
 PRIOR FILING DATE: 2000-07-10
 NUMBER OF SEQ ID NOS: 16825
 SEQ ID NO 9637
 LENGTH: 1236
 TYPE: DNA
 ORGANISM: Myxococcus xanthus
 US-09-902-540-9637

Query Match 76.7%; Score 13.8; DB 3; Length 1236;
 Best Local Similarity 82.4%; Pred. No. 7.4e+02;
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 GAGGGGCGCACGGCGGTA 18
 Db 494 GTGGGGCGCACGGCGGTA 478

Search completed: March 18, 2006, 18:39:20
 Job time : 99.8846 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using SW model

Run on: March 18, 2006, 18:34:54 ; Search time 401.923 Seconds
(without alignments)
331.640 Million cell updates/sec

Title:	US-10-800-926-3
Perfect score:	20
Sequence:	1 agguacagccaggaucga 20

Gapov 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database : N_GeneSeq_21:*

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2: genebegn1990s: *
3: genebegn2000bs: *
4: genebegn2001as: *
5: genebegn2001bs: *
6: genebegn2002as: *
7: genebegn2002bs: *
8: genebegn2003as: *
9: genebegn2003bs: *
10: genebegn2003cs: *
11: genebegn2003ds: *
12: genebegn2004as: *
13: genebegn2004bs: *
14: genebegn2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	100.0	20	4	AAE9262	AAE9262 Immunosti
2	20	100.0	20	6	ABE77907	ABE77907 Arglogene
3	20	100.0	20	6	ABR38704	ABR38704 Immunosti
4	20	100.0	20	9	ACD9663	ACD9663 Immunosti
5	20	100.0	20	9	ADB36764	ADB36764 Immunosti
6	20	100.0	20	13	ADU89707	ADU89707 Allergic
7	20	100.0	20	14	ADW79936	ADW79936 Bacterial
8	18	90.0	5253	10	ABT40830	ABT40830 Toxicity
9	18	90.0	5253	13	ADV33876	ADV33876 Rat cardi
10	16.8	84.0	720	3	AAZ50957	AAZ50957 Pseudomon
11	16.8	84.0	735	11	ABD09355	ABD09355 Pseudomon
12	16.8	84.0	145068	13	ABD33090	ABD33090 Murine ca
13	16.4	82.0	246	3	AAE10633	AAE10633 Fusarium
14	16.4	82.0	246	13	ADU54674	ADU54674 Fusarium
15	16.4	82.0	246	14	ADZ92677	ADZ92677 Fusarium
16	16.4	82.0	1308	13	ADX13768	ADX13768 Plant full
17	16.4	82.0	31632	9	ADA03035	ADA03035 Mouse Ror
18	16.4	82.0	31632	9	ADA66319	ADA66319 Mouse Ror
19	16.4	82.0	31632	10	ADB72773	ADB72773 Mouse Ror

20	16.4	82.0	96599	9	ADA02933	Mouse	Bra
21	16.4	82.0	96599	10	ADB72671	Mouse	Bra
22	16.4	82.0	96599	10	ADC95413	Mouse	Bra
23	16.4	82.0	96599	12	ADM74558	Mouse	Bra
24	16	80.0	2550	4	ABL20341	Mouse	Bra
25	16	80.0	2668	4	ABL059903	Drosophila	
26	16	80.0	4972	4	ABL20340	Drosophila	
27	16	80.0	4989	4	ABL059902	Drosophila	
28	16	80.0	90615	12	ADG97556	Mouse	Bra
29	16	80.0	96599	12	ADC85298	Mouse	Bra
30	16	80.0	96600	9	ADA02819	Human	Bra
31	16	80.0	96600	10	ADA02819	Mouse	Bra
32	16	80.0	96600	12	ADM742557	Mouse	Bra
33	16	80.0	144411	12	ADM74414	Mouse	Bra
34	16	80.0	144446	12	ADP74215	Equine	h
35	16	80.0	145444	12	ADP74213	Equine	h
36	16	80.0	145596	12	ADP74212	Equine	h
37	16	80.0	241711	14	ADZ13116	Mouse	Bra
38	15.8	79.0	537	11	ABD15945	Pseudomoc	
39	15.8	79.0	537	11	ABD15921	Pseudomoc	
40	15.8	79.0	542	5	ABV15922	Human	pro
41	15.8	79.0	592	5	ABV45722	Human	pro
42	15.8	79.0	693	5	AA89740	DNA	encod
43	15.8	79.0	978	4	ABL04139	Drosophila	
44	15.8	79.0	1023	11	ABD14617	Pseudomoc	
45	15.8	79.0	1044	13	ABD16472	Pseudomoc	
46	15.8	79.0	1057	3	AAZ61623	CDNA	enco
47	15.8	79.0	1057	3	AAZ61623	CDNA	enco
48	15.8	79.0	1057	3	AAZ61623	CDNA	enco
49	15.8	79.0	1057	3	AAZ61623	CDNA	enco
50	15.8	79.0	1057	3	AAZ61623	CDNA	enco
51	15.8	79.0	1057	3	AAZ61623	CDNA	enco
52	15.8	79.0	1057	3	AAZ61623	CDNA	enco
53	15.8	79.0	1057	3	AAZ61623	CDNA	enco
54	15.8	79.0	1057	3	AAZ61623	CDNA	enco
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56	15.8	79.0	1057	3	AAZ61623	CDNA	enco
57	15.8	79.0	1057	3	AAZ61623	CDNA	enco
58	15.8	79.0	1057	3	AAZ61623	CDNA	enco
59	15.8	79.0	1057	3	AAZ61623	CDNA	enco
60	15.8	79.0	1057	3	AAZ61623	CDNA	enco
61	15.8	79.0	1057	3	AAZ61623	CDNA	enco
62	15.8	79.0	1057	3	AAZ61623	CDNA	enco
63	15.8	79.0	1057	3	AAZ61623	CDNA	enco
64	15.8	79.0	1057	3	AAZ61623	CDNA	enco
65	15.8	79.0	1057	3	AAZ61623	CDNA	enco
66	15.8	79.0	1057	3	AAZ61623	CDNA	enco
67	15.4	77.0	448	3	AAZ93530	Expansin	
68	15.4	77.0	448	3	AAZ93530	Expansin	
69	15.4	77.0	448	3	AAZ93530	Expansin	
70	15.4	77.0	448	3	AAZ93530	Expansin	
71	15.4	77.0	448	3	AAZ93530	Expansin	
72	15.4	77.0	448	3	AAZ93530	Expansin	
73	15.4	77.0	448	3	AAZ93530	Expansin	
74	15.4	77.0	448	3	AAZ93530	Expansin	
75	15.4	77.0	448	3	AAZ93530	Expansin	
76	15.4	77.0	448	3	AAZ93530	Expansin	
77	15.4	77.0	448	3	AAZ93530	Expansin	
78	15.4	77.0	448	3	AAZ93530	Expansin	
79	15.4	77.0	448	3	AAZ93530	Expansin	
80	15.4	77.0	448	3	AAZ93530	Expansin	
81	15.4	77.0	448	3	AAZ93530	Expansin	
82	15.4	77.0	448	3	AAZ93530	Expansin	
83	15.4	77.0	448	3	AAZ93530	Expansin	
84	15.4	77.0	448	3	AAZ93530	Expansin	
85	15.4	77.0	448	3	AAZ93530	Expansin	
86	15.4	77.0	448	3	AAZ93530	Expansin	
87	15.4	77.0	448	3	AAZ93530	Expansin	
88	15.4	77.0	448	3	AAZ93530	Expansin	
89	15.4	77.0	448	3	AAZ93530	Expansin	
90	15.4	77.0	448	3	AAZ93530	Expansin	
91	15.4	77.0	448	3	AAZ93530	Expansin	
92	15.4	77.0	448	3	AAZ93530	Expansin	

385	14.8	74.0	2056	6	ABV94273	Breast ca	458	14.8	74.0	3143	12	ADP23503	Adf33503 Human CDN
386	14.8	74.0	2056	10	ADP81427	Leukemia	459	14.8	74.0	3143	12	ADP33486	Adf33486 Human CDN
387	14.8	74.0	2068	5	AA544943	CDNA enco	460	14.8	74.0	3143	12	ADP26953	Adf26953 Human CDN
388	14.8	74.0	2079	5	AA544942	CDNA enco	461	14.8	74.0	3143	12	ADP27589	Adf27589 Human CDN
389	14.8	74.0	2085	13	AD549931	Bacterial	462	14.8	74.0	3143	12	ADP41183	Adf41183 Human CDN
390	14.8	74.0	2095	8	ABX63665	Human CDN	463	14.8	74.0	3143	12	ADP32862	Adf32862 Human CDN
391	14.8	74.0	2098	5	AA544944	CDNA enco	464	14.8	74.0	3143	12	ADP25228	Adf25228 Human CDN
392	14.8	74.0	2217	11	ACL30450	Rice abio	465	14.8	74.0	3143	12	ADP26329	Adf26329 Human CDN
393	14.8	74.0	2238	10	ACC69003	Human neu	466	14.8	74.0	3143	12	ADP34118	Adf34118 Human CDN
394	14.8	74.0	2328	11	ACL30010	Rice abio	467	14.8	74.0	3143	12	ADP46355	Adf46355 Human CDN
395	14.8	74.0	2356	6	ABZ11172	Human pol	468	14.8	74.0	3143	12	ADG50341	Adg50341 Human CDN
396	14.8	74.0	2356	12	ADM43690	Novel hum	469	14.8	74.0	3143	12	ADG49717	Adg49717 Human CDN
397	14.8	74.0	2409	6	ABX31797	DNA enco	470	14.8	74.0	3143	12	ADG51589	Adg51589 Human CDN
398	14.8	74.0	2503	2	AAO55347	Sequence	471	14.8	74.0	3143	12	ADG48469	Adg48469 Human CDN
399	14.8	74.0	2509	12	ADQ67506	Novel hum	472	14.8	74.0	3143	12	ADG49093	Adg49093 Human CDN
C 399	14.8	74.0	2587	12	ADQ67506	Novel hum	473	14.8	74.0	3143	12	ADG50965	Adg50965 Human CDN
C 399	14.8	74.0	2587	12	ADQ67506	Novel hum	474	14.8	74.0	3143	12	ADG58909	Adg58909 Human CDN
C 400	14.8	74.0	2587	12	ADQ67506	Novel hum	475	14.8	74.0	3143	12	ADG52365	Adg52365 Human CDN
401	14.8	74.0	2672	4	AD110378	Human cel	476	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
402	14.8	74.0	2672	10	AD110378	Human cel	477	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
403	14.8	74.0	2672	12	ADT43813	Bacterial	478	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
404	14.8	74.0	2706	13	ADT43813	Bacterial	479	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
405	14.8	74.0	2801	6	ABQ61196	Human PRO	480	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
406	14.8	74.0	2832	12	ADP78171	Human ext	481	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
407	14.8	74.0	2850	12	ADQ83547	Human tum	482	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
408	14.8	74.0	2850	13	ADQ84722	Human tum	483	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
409	14.8	74.0	2850	13	ADQ84722	Human tum	484	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
C 410	14.8	74.0	2981	10	ADB62165	Human CDN	485	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
C 411	14.8	74.0	3042	4	AAK53428	Human pol	486	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
C 412	14.8	74.0	3042	4	AAK53428	Human pol	487	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
C 413	14.8	74.0	3104	4	AD110376	Human mem	488	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
414	14.8	74.0	3104	10	AD110376	Human mem	489	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
415	14.8	74.0	3104	12	AD110376	Human mem	490	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
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417	14.8	74.0	3143	3	AACT8494	Human PRO	492	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
418	14.8	74.0	3143	3	AACT8494	Human PRO	493	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
419	14.8	74.0	3143	8	ACAC3601	Novel hum	494	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
420	14.8	74.0	3143	8	ACAC3601	Novel hum	495	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
421	14.8	74.0	3143	8	ACAC3601	Novel hum	496	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
422	14.8	74.0	3143	8	ACAC3601	Novel hum	497	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
423	14.8	74.0	3143	8	ACAC3601	Novel hum	498	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
424	14.8	74.0	3143	9	AD29747	Novel hum	499	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
425	14.8	74.0	3143	9	AD29747	Novel hum	500	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
426	14.8	74.0	3143	9	AD29747	Novel hum	501	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
427	14.8	74.0	3143	9	AD29747	Novel hum	502	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
428	14.8	74.0	3143	10	AD29747	Novel hum	503	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
429	14.8	74.0	3143	10	AD29747	Novel hum	504	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
430	14.8	74.0	3143	10	AD29747	Novel hum	505	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
431	14.8	74.0	3143	10	AD29747	Novel hum	506	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
432	14.8	74.0	3143	10	AD29747	Novel hum	507	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
433	14.8	74.0	3143	10	AD29747	Novel hum	508	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
434	14.8	74.0	3143	10	AD29747	Novel hum	509	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
435	14.8	74.0	3143	10	AD29747	Novel hum	510	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
436	14.8	74.0	3143	10	AD29747	Novel hum	511	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
437	14.8	74.0	3143	10	AD29747	Novel hum	512	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
438	14.8	74.0	3143	10	AD29747	Novel hum	513	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
439	14.8	74.0	3143	10	AD29747	Novel hum	514	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
440	14.8	74.0	3143	10	AD29747	Novel hum	515	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
441	14.8	74.0	3143	10	AD29747	Novel hum	516	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
442	14.8	74.0	3143	10	AD29747	Novel hum	517	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
443	14.8	74.0	3143	10	AD29747	Novel hum	518	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
444	14.8	74.0	3143	10	AD29747	Novel hum	519	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
445	14.8	74.0	3143	10	AD29747	Novel hum	520	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
446	14.8	74.0	3143	10	AD29747	Novel hum	521	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
447	14.8	74.0	3143	10	AD29747	Novel hum	522	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
448	14.8	74.0	3143	10	AD29747	Novel hum	523	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
449	14.8	74.0	3143	10	AD29747	Novel hum	524	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
450	14.8	74.0	3143	10	AD29747	Novel hum	525	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
451	14.8	74.0	3143	10	AD29747	Novel hum	526	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
452	14.8	74.0	3143	10	AD29747	Novel hum	527	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
453	14.8	74.0	3143	10	AD29747	Novel hum	528	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
454	14.8	74.0	3143	10	AD29747	Novel hum	529	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
455	14.8	74.0	3143	10	AD29747	Novel hum	530	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
456	14.8	74.0	3143	10	AD29747	Novel hum							
457	14.8	74.0	3143	10	AD29747	Novel hum							

C 969	14.2	71.0	578	9	AC121993	AC121993 DNA clone
C 970	14.2	71.0	578	12	ACH69414	ACH69414 Human gen
C 971	14.2	71.0	579	2	AAx01704	AAx01704 Human ant
C 972	14.2	71.0	579	2	AAx01712	AAx01712 Human ant
C 973	14.2	71.0	579	2	AAx01705	AAx01705 Human ant
C 974	14.2	71.0	579	2	AAx01708	AAx01708 Human ant
C 975	14.2	71.0	579	2	AAx01713	AAx01713 Human ant
C 976	14.2	71.0	580	12	AD677004	AD677004 Human CDN
C 977	14.2	71.0	585	4	AAH28816	AAH28816 Protophili
C 978	14.2	71.0	594	8	ACA23424	ACA23424 Prokaryot
C 979	14.2	71.0	598	9	AC121976	AC121976 DNA clone
C 980	14.2	71.0	600	9	AC121977	AC121977 DNA clone
C 981	14.2	71.0	600	14	AD270322	AD270322 Human CDN
C 982	14.2	71.0	603	2	AAV88562	AAV88562 EST clone
C 983	14.2	71.0	603	2	AC121987	AC121987 DNA clone
C 984	14.2	71.0	603	9	AC121996	AC121996 DNA clone
C 985	14.2	71.0	606	11	ABD11974	ABD11974 Pseudomon
C 986	14.2	71.0	618	13	ADT46051	ADT46051 Bacterial
C 987	14.2	71.0	621	9	AC121992	AC121992 DNA clone
C 988	14.2	71.0	621	11	ABD07359	ABD07359 Pseudomon
C 989	14.2	71.0	622	9	AC121981	AC121981 DNA clone
C 990	14.2	71.0	627	6	AB681473	AB681473 Prostate
C 991	14.2	71.0	627	14	AC159924	AC159924 Human col
C 992	14.2	71.0	627	14	AC166578	AC166578 M. xanthu
C 993	14.2	71.0	633	9	AC121980	AC121980 DNA clone
C 994	14.2	71.0	635	9	AC121983	AC121983 DNA clone
C 995	14.2	71.0	641	5	AA891654	AA891654 DNA encod
C 996	14.2	71.0	642	6	AB208504	AB208504 Human leu
C 997	14.2	71.0	649	9	AC122000	AC122000 DNA clone
C 998	14.2	71.0	649	9	AC121999	AC121999 DNA clone
C 999	14.2	71.0	654	11	ADJ12138	ADJ12138 Maize cDN
1000	14.2	71.0	654	11	AC134693	AC134693 Rice abio

ALIGNMENTS

RESULT 1

ID AAF99262 standard; DNA; 20 BP.

XX AAF99262;

DT 12-JUN-2001 (first entry)

XX Immunostimulatory nucleic acid #378.

XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;

XX immunostimulatory; tumour; viral infection; bacterial infection;

XX fungal infection; parasitic infection; cancer; asthma;

XX infectious disease; allergy; immune deficiency; phosphorochioate; ss.

OS Synthetic.

XX WO200122972-A2.

XX 05-APR-2001.

PF 25-SEP-2000; 2000WO-US026383.

XX 25-SEP-1999; 99US-0156113P.

PR 27-SEP-1999; 99US-0156135P.

PR 23-AUG-2000; 2000US-0227436P.

XX (IOWA) UNIV IOWA RES FOUND.

PA (COLE-) COLEY PHARM GMBH.

XX Krieg AM, Schetter C, Vollmer J;

XX MPI, 2001-273485/28.

PT Vaccinating against tumors, infectious diseases, allergies and asthma

XX	Claim 101; Page 46; 338pp; English.
PS	The present invention relates to a method for stimulating an immune
XX	response. The method comprises administering an immunostimulatory nucleic
CC	acid to a non-rodent subject in sufficient quantity to stimulate an
CC	immune response. The present sequence is one such immunostimulatory
CC	nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC	(py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC	against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC	and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC	haemophilus, campylobacter, clostridium, bactericilia coli and/or
CC	staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC	also useful for preventing cancer, asthma, infectious disease, allergy or
CC	immune deficiency. The present sequence can also be used to redirect a
CC	Th2 to a Th1 immune response and to activate immune cells. Note: the
CC	present sequence may have a phosphorochioate backbone
XX	Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
SQ	Query Match 100.0%; Score 20; DB 4; Length 20;
	Best Local Similarity 90.0%; Pred. No. 9.3;
	Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY	1 AGGUAACAGCAGACUACGA 20
DB	1 AGGTACAGCAGACTACGA 20

RESULT 2

ID ABS77907 standard; DNA; 20 BP.

XX ABS77907;

DT 13-DEC-2002 (first entry)

XX Angiogenesis inhibitory oligonucleotide #391.

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;

XX tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;

XX diabetic retinopathy; retinopathy of prematurity; macular degeneration;

XX corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;

XX rubecosis; Osler-Weber Syndrome; myocardial angiogenesis;

XX plaque neovascularisation; telangiectasia; haemophilic joint;

XX angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;

XX scleroderma; hypertrophic scar.

OS Synthetic.

XX WO200253141-A2.

XX 11-JUL-2002.

PF 14-DEC-2001; 2001WO-US048458.

XX 14-DEC-2000; 2000US-025534P.

PR (COLE-) COLEY PHARM GROUP INC.

XX Bratzler RJ;

XX MPI; 2002-566690/60.

XX Inhibiting angiogenesis in a subject, involves administering at least one

XX antiangiogenic nucleic acid molecule to the subject.

XX Claim 2; Page 26; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising

CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth.
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiodioma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention

XX SQ Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 90.0%; Pred. No. 9.3;

Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20
 DB 1 AGGTACAGCCAGACTACGA 20

RESULT 3
 ABL38704 standard; DNA; 20 BP.

XX ABL38704;

DT 16-APR-2002 (first entry)

XX Immunostimulatory nucleic acid SEQ ID NO: 68.

KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
 KW angiogenesis; metastasis; cytostatic; ss.

XX Synthetic.

XX WO200197843-A2.

XX 27-DEC-2001.

XX 22-JUN-2001; 2001WO-US020154.

XX 22-JUN-2000; 2000US-0213346P.

XX (IOWA) UNIV IOWA RES FOUND.

XX Weiner G, Hartmann G;

XX WPI; 2002-154611/20.

PT Treating or preventing cancer, such as basal cell carcinoma, comprises
 PT administering immunostimulatory nucleic acids that induce expression of
 PT cell surface antigens and antibodies to a subject having or at risk of
 PT developing cancer.

XX Disclosure; Page 112; 312pp; English.

CC The present invention relates to methods for treating or preventing
 CC cancer, involving administering to a subject having or at risk of
 CC developing cancer immunostimulatory nucleic acids that induce expression
 CC of cell surface antigens and antibodies. The methods are useful for
 CC treating or preventing cancer such as basal cell carcinoma, bladder
 CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
 CC breast cancer, cervical cancer, colon and rectum cancer, connective
 CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx
 CC cancer, leukemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
 CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
 CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
 CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
 CC present sequence is an immunostimulatory oligonucleotide described in the
 CC exemplification of the invention

SQ Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 90.0%; Pred. No. 9.3;

Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20
 DB 1 AGGTACAGCCAGACTACGA 20

RESULT 4
 ACD99693

XX ACD99693 standard; DNA; 20 BP.

XX ACD99693;

DT 25-SEP-2003 (first entry)

XX Immunostimulatory nucleic acid #379.

KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
 KW anticancer; gene therapy; vaccine; non-allergic inflammatory disease;
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.

XX Synthetic.

XX US2003050268-A1.

XX 13-MAR-2003.

XX 29-MAR-2002; 2002US-00112653.

XX 29-MAR-2001; 2001US-0279642P.

XX (KRIE/) KRIE A. M.

XX (BERG/) BERG D. J.

XX Kriegl AM, Berg DJ;

XX WPI; 2003-521815/49.

PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
 PT disease by administering an immunostimulatory nucleic acid.

XX Disclosure; Page 19; 229pp; English.

CC The invention describes a method of treating non-allergic inflammatory
 CC disease comprising administering to a subject having or at risk of
 CC developing a non-allergic inflammatory disease an immunostimulatory
 CC nucleic acid for prevention or treatment of the disease. The method is
 CC useful for treating non-allergic inflammatory diseases, such as
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
 CC This sequence represents an immunostimulatory nucleic acid

XX SQ Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 20;
 Best Local Similarity 90.0%; Pred. No. 9.3;

Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20
 DB 1 AGGTACAGCCAGACTACGA 20

RESULT 5
 ADB36764

XX ADB36764 standard; DNA; 20 BP.

AC ADB36764;
 XX 04-DEC-2003 (first entry)
 XX Immunostimulatory nucleic acid #378.
 DE Immunostimulatory nucleic acid #378.
 XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
 KM hypo-responsive subject; immunostimulatory.
 XX Synthetic.
 OS US2003087848-A1.
 PN 08-MAY-2003.
 XX 02-FEB-2001; 2001US-00776479.
 PF 03-FEB-2000; 2000US-0179991P.
 PR (BRAT/) BRATZLER R L.
 PA (PETE/) PETERSEN D M.
 PA (FOUR/) FOURON Y.
 XX Bratzler RL, Petersen DM, Fouron Y;
 PI WPI, 2003-657977/62.
 DR Treating and/or preventing allergy or asthma using an immunostimulatory
 PT nucleic acid alone or in combination with an asthma/allergy medicament.
 XX Disclosure; Page 10; 221pp; English.
 XX The invention relates to a method of treating or preventing allergy or
 CC asthma which comprises administering to a subject a poly-G nucleic acid
 CC in an aerosol formulation. The methods and compositions of the present
 CC invention are useful for diagnosing and/or treating asthma and allergy
 CC especially in a hypo-responsive subject. The present sequence represents
 CC an immunostimulatory nucleic acid of the invention.
 XX Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 20; DB 9; Length 20;
 Best Local Similarity 90.0%; Pred. No. 9.3;
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGGUACAGCCAGGACUACGA 20
 DB 1 AGGTACAGCCAGGACTACGA 20
 RESULT 6
 ADU89707
 ID ADU89707 standard; DNA; 20 BP.
 XX ADU89707;
 AC 10-FEB-2005 (first entry)
 DT Allergic response suppressor oligonucleotide #391.
 XX Allergic response suppressor oligonucleotide #391.
 DE ss; antiaesthetic; antiallergic; dermatological; antiinflammatory;
 KM antibacterial; antiviral; immunoglobulin E antagonist; allergy;
 KM immunostimulatory; asthma; rhinitis; urticaria; dermatitis;
 KM bacterial infection; viral infection.
 XX Synthetic.
 OS US2004235774-A1.
 PN 25-NOV-2004.
 PD 23-APR-2004; 2004US-00831778.
 PF

PR 03-FEB-2000; 2000US-0179991P.
 PR 02-FEB-2001; 2001US-00776479.
 XX (BRAT/) BRATZLER R L.
 PA (PETE/) PETERSEN D M.
 PA (FOUR/) FOURON Y.
 XX Bratzler RL, Petersen DM, Fouron Y;
 PI WPI, 2004-833006/82.
 DR Suppressing allergies, including asthma, rhinitis, urticaria and atopic
 PT dermatitis, in a subject, comprises administering a first and second dose
 PT of an immunostimulatory nucleic acid.
 XX Disclosure; SEQ ID NO 391; 235pp; English.
 XX The invention relates to a method of suppressing a symptom of an allergic
 CC response in a subject by administering a first and second dose of an
 CC immunostimulatory nucleic acid that comprises a nucleotide sequence
 CC comprising 5'-cg-3', and where the second dose is administered from 1 day
 CC to 8 weeks after the first dose. The methods and compositions of the
 CC present invention are useful for the treatment or prevention of asthma
 CC and allergy, including rhinitis, urticaria and atopic dermatitis, using
 CC an immunostimulatory nucleic acid alone or in combination with other
 CC medicaments. They can also be used in preventing bacterial and viral
 CC infections. This sequence represents an oligonucleotide used in the
 CC method of the invention.
 XX Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 20; DB 13; Length 20;
 Best Local Similarity 90.0%; Pred. No. 9.3;
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGGUACAGCCAGGACUACGA 20
 DB 1 AGGTACAGCCAGGACTACGA 20
 RESULT 7
 ADW79936
 ID ADW79936 standard; RNA; 20 BP.
 XX ADW79936;
 AC 21-APR-2005 (first entry)
 DT Bacterial immunomodulatory CpG oligoribonucleotide, SEQ ID NO:3.
 XX Bacterial immunomodulatory CpG oligoribonucleotide, SEQ ID NO:3.
 DE Immune modulation; immune stimulation; bacterial infection; infection;
 KM endotoxic shock; antibacterial; antimicrobial; immunomodulator;
 KM immunostimulant; adjuvant; ss.
 XX Bacteria.
 OS Key Location/Qualifiers
 XX misc_feature 18..19
 FT /*tag= a
 FT /note= "CpG dinucleotide"
 XX US2005032731-A1.
 PN 10-FEB-2005.
 PD 15-MAR-2004; 2004US-00800926.
 PF 11-MAY-1993; 93US-00059745.
 PR 20-JAN-1995; 95US-00376175.
 PR 18-AUG-1995; 95US-00517016.
 PR 29-OCT-1996; 96US-00739264.
 PR 17-NOV-1998; 98US-00193653.
 PR 18-JUN-2001; 2001US-00883550.

XX (MARS/) MARSHALL W B.
XX Marshall WE;
PI WPI; 2005-161694/17.
XX
XX Composition for modulating and/or stimulating immune system of animal
PT useful for withstanding microbial infections and lethality of endotoxic
PT shock, comprises low molecular weight oligoribonucleotide from bacteria.
XX
XX Claim 5; SEQ ID NO 3; 17pp; English.
XX
XX The invention relates to a composition for modulating and/or stimulating
CC the immune system of an animal, comprising bacterial oligoribonucleotides
CC (ORN) with a molecular weight of less than 10 kD. The bacterial ORNs are
CC preferably ADW79334-ADW79336, contain Cpg motifs and are resistant to
CC RNase. Bacteria produce RNase-resistant Cpg ORNs in response to stressors
CC such as a change in environment, including the neutral pH they encounter
CC when they colonize animals. The immune systems of animals have co-evolved
CC to recognize such Cpg ORNs as being derived from bacteria, and has
CC adapted a non-toxic alerting response to their release from bacteria. The
CC invention also relates to a method for the preparation of the bacterial
CC ORNs by subjecting bacteria to one or more periods of stress, separating
CC the ORNs and media from the bacteria, and filtering the separated product
CC to remove substances with a molecular weight of more than 10 kD, and a
CC method of using the filtrate to modulate/stimulate the immune system of
CC an animal to withstand microbial infection. The composition and methods
CC of the invention are useful for modulating and/or stimulating the immune
CC system of animals (including humans, poultry and livestock), particularly
CC to withstand microbial infections or the onset of endotoxic shock. The
CC compositions may be administered orally (e.g., as a food supplement) or
CC parentally, and may also be administered as an adjuvant for oral or
CC parenteral vaccines. The compositions may additionally be used topically
CC to protect against ear, nose and vaginal infections. They may further be
CC used to extend the viability of monocytes, thereby improving their
CC ability to mature into macrophages to fight infection, and may be used to
CC downregulate the cytotoxicity of macrophages to prevent them from
CC destroying normal T-cells in people with HIV infections. The composition
CC of the invention contains ORNs released by either harmless or pathogenic
CC bacteria, but is free from bacterial cells. Unlike Cpg
CC oligodeoxyribonucleotides (ODNs), the bacterial Cpg ORNs and compositions
CC containing them are non-toxic. The present sequence represents a
CC specifically claimed bacterial Cpg oligoribonucleotide present in
CC compositions of the invention.
XX
SQ Sequence 20 BP; 7 A; 5 C; 6 G; 0 T; 2 U; 0 Other;
Query Match 100.0%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. NO. 9.3; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;
QY 1 AGGUACAGCCGAGACUACGA 20
1 |||||
1 AGGUACAGCCGAGACUACGA 20
Db 1 AGGUACAGCCGAGACUACGA 20
RESULT 8
ABT40830
ID ABT40830 standard; DNA; 5253 BP.
XX
XX ABT40830;
AC
XX 26-JUN-2003 (first entry)
DT
XX Toxicity modelling related rat gene SEQ ID No 532.
XX
XX Toxic effect; gene expression profile; renal toxicity; toxicity marker;
KW database; drug screening; toxicity assay; rat; ds.
OS Rattus norvegicus.
XX
XX W0200295000-A2.
PN

XX 28-NOV-2002.
PD
XX
XX 22-MAY-2002; 2002WO-US016173.
XX
XX
XX 22-MAY-2001; 2001US-0292335P.
XX 13-JUN-2001; 2001US-0297523P.
XX 19-JUN-2001; 2001US-028925P.
XX 10-JUL-2001; 2001US-0303807P.
XX 10-JUL-2001; 2001US-0303808P.
XX 10-JUL-2001; 2001US-0303810P.
XX 28-AUG-2001; 2001US-0315047P.
XX 27-SEP-2001; 2001US-0324928P.
XX 22-OCT-2001; 2001US-0330462P.
XX 01-NOV-2001; 2001US-0330867P.
XX 21-NOV-2001; 2001US-0331805P.
XX 06-DEC-2001; 2001US-0336144P.
XX 19-DEC-2001; 2001US-0340873P.
XX 21-FEB-2002; 2002US-0357842P.
XX 21-FEB-2002; 2002US-0357843P.
XX 21-FEB-2002; 2002US-0357844P.
XX 15-MAR-2002; 2002US-0364134P.
XX 08-APR-2002; 2002US-0370149P.
XX 08-APR-2002; 2002US-0370206P.
XX 08-APR-2002; 2002US-0370247P.
XX 17-APR-2002; 2002US-0372794P.
XX 21-APR-2002; 2002US-0371679P.
XX
XX (GENE-) GENE LOGIC INC.
XX
XX Mendrick D, Porter M, Johnson K, Higgs B, Caastle A, Blashoff M;
PI WPI; 2003-148464/14.
XX
XX Predicting at least one toxic effect of a compound, useful for toxicity
PT modelling, comprises preparing a gene expression profile of a tissue or
PT cell sample exposed to the compound, and comparing the gene expression
PT profile to a database.
XX
XX Example 4; Page; 446pp; English.
XX
XX The invention relates to a novel method of predicting at least one toxic
CC effect of a compound. The method comprises a gene expression profile of a
CC tissue or cell sample exposed to the compound, and comparing the gene
CC expression profile to a database comprising at least part of the data or
CC information given in the specification. The methods are useful for
CC predicting at least one toxic effect of a compound, predicting the
CC progression of a toxic effect of a compound, predicting the renal
CC toxicity of a compound, or identifying toxicity markers in tissues or
CC cells exposed to known renal toxin. The genes are useful as toxicity
CC markers in drug screening and toxicity assays, in monitoring disease or
CC physiological states, or disease progression. This polynucleotide
CC represents a rat DNA sequence relating to the toxic effect database
CC described in the specification. NOTE: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from the World Intellectual Property
CC Organization
XX
SQ Sequence 5253 BP; 1380 A; 1379 C; 1440 G; 1054 T; 0 U; 0 Other;
Query Match 90.0%; Score 18; DB 10; Length 5253;
Best Local Similarity 88.9%; Pred. NO. 1.2e+02;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGUAACAGCCGAGACUACG 19
2 |||||
2 GGUAACAGCCGAGACUACG 19
Db 2679 GGUAACAGCCGAGACUACG 2696
RESULT 9
ADV39876
ID ADV39876 standard; cDNA; 5253 BP.
XX

AC	ADV39876;
DT	10-FEB-2005 (first entry)
XX	
DE	Rat cardiotoxicity marker gene, SEQ ID NO:742.
XX	
KW	Toxicology screening; drug screening; cardiotoxicity, drug-induced;
KW	expression profile; gene expression; myocarditis; heart arrhythmia;
KW	tachycardia; myocardial ischemia; angina; hypertension; hypotension;
KW	dyspnea; cardiogenic shock; cardiovascular disease; gene; ss.
XX	
OS	Rattus norvegicus.
XX	
PN	WO200406334-A2.
XX	
PD	29-JUL-2004.
XX	
PF	08-JAN-2004; 2004WO-US000240.
XX	
PR	08-JAN-2003; 2003US-00338044.
XX	
PA	(GENE-) GENE LOGIC INC.
XX	
PI	Mendrick DL, Porter MW, Johnson KR, Higgs B, Caetle A;
PT	Fleahoff M;
DR	WPI; 2004-561893/54.
XX	
DR	DDBI; AB012214.
XX	
PS	Predicting a toxic effect of a compound by obtaining a gene expression
PT	profile of a tissue or cell sample exposed to the compound and comparing
PT	the gene expression profile to a database comprising all of the data
PT	given in the specification.
XX	
PS	Example 1; SEQ ID NO 742; 520pp; English.
XX	
CC	The invention relates to a method of predicting at least one toxic effect
CC	of a compound by obtaining a gene expression profile of a tissue or cell
CC	sample exposed to the compound and comparing the gene expression profile
CC	to a database of toxicity prediction genes which are differentially
CC	expressed on exposure to known toxins. The tissue or cell sample is
CC	preferably derived from heart tissue, and the predicted toxic effect is
CC	especially a cardiotoxic effect such as myocarditis, arrhythmias,
CC	tachycardia, myocardial ischemia, angina, hypertension, hypotension,
CC	dyspnea, cardiogenic shock or other specific heart pathologies. The
CC	invention is based on the elucidation of global changes in gene
CC	expression in tissues or cells exposed to known toxins, particularly
CC	cardiotoxins, and the identification of individual genes (toxicity
CC	markers) that are differentially expressed on toxin exposure. The
CC	invention also relates to methods for predicting the progression of a
CC	compound's toxic effects, for predicting the cardiotoxicity of a
CC	compound, for identifying an agent that modulates the onset or
CC	progression of a toxic response, and for predicting which cellular
CC	pathways a particular compound will modulate. The invention further
CC	relates to sets of at least two hybridization probes specific for
CC	toxically prediction genes), and solid supports and kits comprising them.
CC	The method of the invention is useful in toxicologic screening for
CC	predicting the toxic effects (especially cardiotoxic effects) of
CC	compounds such as pharmaceutical agents or environmental pollutants.
CC	Sequences ADV39135-ADV41830 represent cardiotoxicity marker
CC	polynucleotides of rat origin whose expression is altered on exposure to
CC	at least one cardiotoxin. Note: The sequence data for this patent did not
CC	form part of the printed specification, but was obtained in electronic
CC	format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX	
XX	
SQ	Sequence 5253 BP; 1380 A; 1379 C; 1440 G; 1054 T; 0 U; 0 Other;
Query Match	90.0%; Score 18; DB 13; Length 5253;
Best Local Similarity	88.9%; Pred. NO. 1.2e+02;
Matches 16; Conservative	2; Mismatches 0; Indels 0; Gaps 0
GGUACGCGCAGACUACG 19	

```

Db      2679  GGTACGAGCCAGGACTACG 2696

RESULT 10
AAZ50957
ID      AAZ50957 standard; DNA; 720 BP.
AC
XX      AAZ50957;
AC
XX
XX      05-JUN-2000 (first entry)
XX
XX
XX      Pseudomonas aeruginosa LasR response regulator ORF.
DE
XX
XX      luxI, chemical inducer; response regulator protein; inducible promoter;
XX      gene switch; pest control; gene therapy; transgenic plant; mango; melon;
XX      soybean; lethal protein; treatment; cancer; LasR; OddHL;
XX      N-(3-oxododecanolyl)-L-homoserine lactone; ds.
XX
XX      Pseudomonas aeruginosa.
OS
XX
XX      Key
XX      Location/Qualifiers
XX      CDS
XX          1..720
XX          /*tag= a
XX          /product= "LasR response regulator protein"
XX          /note= "Induced by autoinducer, N-(3-oxododecanolyl) -L-
XX          homoserine lactone"
XX
XX      WO200009704-A1.
XX
XX      24-FEB-2000.
XX
XX      12-AUG-1999; 99WO-GB002653.
XX
XX      13-AUG-1998; 98GB-00017704.
XX
XX      (ZENB ) ZENECA LTD.
XX
XX      Martinez A, Jepsen I, Fray RG;
XX
XX      WPI; 2000-224341/19.
XX      P-PSDB; AAY70035.
XX
XX      Inducing target gene expression in plants such as melons, mangoes,
XX      soybean, via a gene switch operably linked to a foreign gene.
XX
XX      Example 3; Page 74-75; 78pp; English.
XX
XX      The patent discloses a method of initiating transcription of a target
XX      gene in a eukaryotic cell, by applying a chemical inducer capable of
XX      binding to the response protein produced by the eukaryotic cell itself,
XX      to form an inducing complex which binds to and induces the inducible
XX      promoter operably linked to the target gene. The gene switch is useful
XX      for externally regulating the target gene expression. This method is
XX      useful for selectively controlling pests in the fields, in gene therapy
XX      and to produce transgenic plants like melons, mangoes and soybean. It
XX      can be used to switch on genes which produce lethal proteins, that can be
XX      employed in the treatment of cancer. The present sequence is the
XX      Pseudomonas aeruginosa response regulator protein, LasR encoding DNA.
XX      LasR is a positive transcriptional activator, that responds to signals
XX      from the LasI inducer gene, that directs the synthesis of autoinducer, N-
XX      (3-oxododecanolyl)-L-homoserine lactone (OddHL).
XX
XX      Sequence 720 BP; 145 A; 200 C; 227 G; 148 T; 0 U; 0 Other;
SQ

Query Match      84.0%; Score 16.8; DB 3; Length 720;
Best Local Similarity 85.0%; Pred. No. 4e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0

1  AGGACAGCCAGGACTACGA 20
|  |||||:|||||
|  |||||:|||||
124 AAAGCAGCCAGGACTACGA 143

```

RESULT 11
ABD09355
ID ABD09355 standard; DNA; 735 BP.
XX
XX ABD09355;
AC
XX
XX 29-JUL-2004 (first entry)
DT
XX
XX Pseudomonas aeruginosa polynucleotide #7959.
DE
XX
XX Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KM antibacterial.
XX
XX Pseudomonas aeruginosa.
OS
XX US651795-B1.
PN
XX 22-APR-2003.
PD
XX 18-FEB-1999; 99US-00252991.
PF
XX 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;
PI WPI; 2003-615309/58.
DR P-PSDB; ABO75784.
XX
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnosis, prophylaxis and treatment of
XX pathological conditions resulting from bacterial infection.
XX
XX Disclosure; SEQ ID NO 7959; 455bp; English.
XX
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
XX Sequence 735 BP; 150 A; 203 C; 232 G; 150 T; 0 U; 0 Other;
SQ
Query Match 84.0%; Score 16.8; DB 11; Length 735;
Best Local Similarity 85.0%; Pred. No. 4e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGGUACAGCCAGACUACGA 20
DB 139 AAGGACAGCCAGACUACGA 158

RESULT 12
ABD33090
ID ABD33090 standard; DNA; 145068 BP.
XX
XX ABD33090;
AC
XX
XX 18-NOV-2004 (first entry)
DT
XX

DE Murine cancer-associated (CA) gene MD07-006.
XX
XX Mouse; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
KM ds; cancer; cytostatic.
XX
XX Mus musculus.
OS
XX WO2004058146-A2.
PN
XX 15-JUL-2004.
PD
XX 15-DEC-2003; 2003WO-US040081.
PF
XX 17-DEC-2002; 2002US-00322281.
PR
XX (SAGR-) SAGRES DISCOVERY INC.
XX
XX Morris DW, Malandro MS;
PI WPI; 2004-499109/47.
DR
XX
XX Novel human cancer associated protein encoded within open reading frame
PT of cancer associated gene, useful as targets for diagnosing cancer.
XX
XX Disclosure; SEQ ID NO 33; 182bp; English.
XX
XX The invention relates to cancer-associated proteins (CAP) and the cancer-
CC associated (CA) nucleic acids encoding them. The invention also relates
CC to a method for treating cancers involving administering to a patient an
CC inhibitor of CAP, and a method of screening for anticancer activity in a
CC potential drug involving providing a cell that expresses a CA gene,
CC contacting a tissue sample derived from a cancer cell with an anticancer
CC drug candidate and monitoring the effect of the anticancer drug candidate
CC on expression of the CA gene. The CAP proteins are useful for detecting
CC cancer associated with expression of a CAP protein in a test cell sample
CC and for screening for a bioactive agent capable of modulating the
CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing
CC cancer, involving determining the expression of a CA nucleic acid in a
CC tissue. This sequence represents a murine CA gene of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
SQ
Sequence 145068 BP; 38358 A; 33586 C; 33004 G; 36708 T; 0 U; 3412 Other;
Query Match 84.0%; Score 16.8; DB 13; Length 145068;
Best Local Similarity 85.0%; Pred. No. 5.7e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGGUACAGCCAGACUACGA 20
DB 50545 AGGTACTGCCAGACACGCA 50564

RESULT 13
AAF10633
ID AAF10633 standard; cDNA; 246 BP.
XX
XX AAF10633;
AC
XX
XX 13-MAR-2001 (first entry)
DT
XX
XX Fusarium venenatum EST SEQ ID NO:3156.
DE
XX
XX Multiple gene expression; filamentous fungal cell; EST;
KM expressed sequence tag; Fusarium venenatum; Aspergillus niger;
KM Aspergillus oryzae; Trichoderma reesei; identification; recombination;
KM culture condition; environmental stress; spore morphogenesis;
XX metabolic pathway engineering; catabolic pathway engineering; ss-
XX Fusarium venenatum.
OS
XX
XX WO200056762-A2.

XX 28-SEP-2000.
 PD 22-MAR-2000; 2000MO-US007781.
 XX 22-MAR-1999; 99US-00273623.
 PR 22-MAR-1999; 99US-00273623.
 XX (NOVO) NOVO NORDISK BIOTECH INC.
 PA (NOVO) NOVO NORDISK AS.
 PI Berka RM, Rey MW, Shuster JR, Kaupinen S, Clausen IG, Olsen PB;
 DR WPI; 2000-594572/56.
 XX Monitoring differential expression of genes in filamentous fungal cells
 PT uses fluorescence-labeled nucleic acids isolated from the cells and a
 PT substrate of expressed sequence tags.
 PS Claim 86; Page 1507; 3161pp; English.
 XX The present invention describes a method for monitoring differential
 CC expression of genes in a first filamentous fungal (FF) cell relative to
 CC expression of the same genes in one or more second filamentous fungal
 CC cells. The method uses fluorescence-labeled nucleic acids isolated from
 CC cells. The method uses a substrate of expressed sequence tags (EST). The ESTs
 CC are used in the methods for monitoring differential expression of genes
 CC in a first filamentous fungal (FF) cell relative to expression of the
 CC same genes in one or more second filamentous fungal cells. Monitoring the
 CC global expression of genes from FF cells allows the production potential
 CC of the microorganisms to be improved. New genes may be discovered,
 CC possible functions of unknown open reading frames can be identified and
 CC gene copy number variation and stability can be monitored. The expression
 CC of genes can be used to study how FF cells adapt to changes in culture
 CC conditions, environmental stress, spore morphogenesis, recombination,
 CC metabolic or catabolic pathway engineering. Using ESTs provides several
 CC advantages over genomic or random cDNA clones including elimination of
 CC redundancy as one spot on an array equals one gene or open reading frame,
 CC and organization of the microarrays based on function of the gene
 CC products to facilitate analysis of the results. AA07478 to AAF11247
 CC represents ESTs from *Fusarium venenatum*; AAF11248 to AAF11853 represents
 CC ESTs from *Aspergillus niger*; AAF11854 to AAF14878 represents ESTs from
 CC *Aspergillus oryzae*; and AAF14879 to AAF15337 represents ESTs from
 CC *Trichoderma reesei*, which are all specifically claimed in the present
 CC invention.
 CC XX Sequence 246 BP; 67 A; 55 C; 64 G; 60 T; 0 U; 0 Other;
 SQ
 CC Query Match 82.0%; Score 16.4; DB 3; Length 246;
 CC Best Local Similarity 83.3%; Pred. No. 5, 8e+02;
 CC Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GUAACGCCAGACUACGA 20
 DB 154 GTACACCGAGACTACGA 171
 RESULT 14
 ADU54674
 ID ADU54674 standard; cDNA; 246 BP.
 AC ADU54674;
 DT 10-FEB-2005 (first entry)
 XX *Fusarium venenatum* CCL-3 EST, SEQ ID NO:3156.
 DE Gene expression; biochip; microarray; hybridization; EST;
 KW expressed sequence tag; ss.
 XX *Fusarium venenatum*; CCL-3.
 OS
 XX US2004229367-A1.
 PN
 XX

PD 18-NOV-2004.
 XX 29-AUG-2003; 2003US-00653047.
 XX 22-MAR-1999; 99US-00273623.
 PR 22-MAR-2000; 2000US-00533559.
 XX (NOVO) NOVOZYMES BIOTECH INC.
 PA (NOVO) NOVOZYMES INC AS.
 PI Berka RM, Rey MW, Shuster JR, Kaupinen S, Clausen IG, Olsen PB;
 DR WPI; 2004-832481/82.
 XX Monitoring differential expression of genes in a filamentous fungal cell
 PT relative to expression of the genes in second filamentous fungal cells,
 PT comprises using microarrays containing *Fusarium venenatum* expressed
 PT sequence tags.
 XX Claim 1; SEQ ID NO 3156; 274pp; English.
 XX The invention relates to a method for monitoring the differential
 CC expression of genes in a first filamentous fungal cell relative to the
 CC same genes in one or more second filamentous fungal cells. The method
 CC involves differentially labeling nucleic acids from the first and second
 CC fungal cells with fluorescent reporter dyes, and adding the mixture of
 CC fluorescently labeled polynucleotides to a substrate containing an array
 CC of *Fusarium venenatum* expressed sequence tags (ESTs) selected from
 CC ADU51519-ADU55288 under conditions that permit hybridization. Relative
 CC expression of genes in the fungal cells is determined by fluorescence;
 CC the fluorescent signal emitted when labeled nucleic acids from the first
 CC fungal cell bind to the ESTs in the array differs in color from that
 CC emitted when labeled nucleic acids from the second fungal cell hybridize.
 CC When both sets of labeled nucleic acids are produced. The filamentous fungal
 CC combined fluorescence emission color is produced. The filamentous fungal
 CC cells used in the method are chosen from *Acromonium*, *Aspergillus*,
 CC *Fusarium*, *Hemicola*, *Mucor*, *Myceliophthora*, *Neurospora*, *Penicillium*,
 CC *Thielavia*, *Tolyposcidium*, and *Trichoderma* cells, preferably *Fusarium*,
 CC *venenatum*, *Aspergillus niger*, or *Aspergillus oryzae*. The method of the
 CC invention is useful for monitoring the expression of a plurality of genes
 CC in filamentous fungal cells, in order to improve the cells' protein
 CC production capacity when such organisms are used for the industrial
 CC production of proteins (e.g., enzymes). The present sequence represents
 CC an EST derived from *Fusarium venenatum* CCL-3 (a morphological mutant of
 CC strain ATCC 20334) which is specifically claimed for use in the method of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from the US patent office at
 CC seqdata.uspto.gov/sequence.html?DocID=US20040222367.
 CC XX Sequence 246 BP; 67 A; 55 C; 64 G; 60 T; 0 U; 0 Other;
 SQ
 CC Query Match 82.0%; Score 16.4; DB 13; Length 246;
 CC Best Local Similarity 83.3%; Pred. No. 5, 8e+02;
 CC Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GUAACGCCAGACUACGA 20
 DB 154 GTACACCGAGACTACGA 171
 RESULT 15
 ADZ92677
 ID ADZ92677 standard; cDNA; 246 BP.
 AC ADZ92677;
 DT 11-AUG-2005 (first entry)
 XX *Fusarium venenatum* expressed sequence tag cDNA SEQ ID NO 3156.
 DE differential expression; gene expression; filamentous fungus;
 KW expressed sequence tag; EST; variation; microarray; ss.
 XX

XX OS Fusarium venenatum.
 XX XX US6902867-B1.
 XX XX 07-JUN-2005.
 XX XX 22-MAR-2000; 2000US-00533559.
 XX XX 22-MAR-1999; 99US-00273623.
 XX PA (NOVO) NOVOZYMES BIOTECH INC.
 XX PA (NOVO) NOVOZYMES AS.
 XX PI Berka RM, Rey MM, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
 XX DR WPI; 2005-401635/41.
 XX PT Monitoring differential expression of genes in first filamentous fungal
 PT cell relative to that of genes in second fungal cells, comprises
 PT hybridizing fluorescence labeled nucleic acids from the cells to an array
 PT of expressed sequence tags.
 XX PS Disclosure; SEQ ID NO 3156; 264pp; English.
 XX CC The invention relates to a method of monitoring (M1) differential
 CC expression of multiple genes in a first filamentous fungal cell relative
 CC to expression of the same genes in one or more second filamentous fungal
 CC cells, comprises adding fluorescence labeled nucleic acids isolated from
 CC the cells to a substrate containing an array of Aspergillus oryzae
 CC expressed sequence tag (EST) of AD293898-AD296922, and examining the
 CC array under fluorescence excitation conditions. (M1) is useful for
 CC monitoring global expression of several genes from a filamentous fungal
 CC cell, discovering new genes, identifying possible functions of unknown
 CC open reading frames and monitoring gene copy number variation and
 CC stability. In (M1), one spot on an array equals one gene or open reading
 CC frame, extensive follow-up characterization is unnecessary since sequence
 CC information is available and EST microarrays can be organized based on
 CC function of the gene products. This sequence corresponds to an EST
 CC sequence of the invention. (Note: this sequence is not given in the
 CC printed specification but can be obtained in electronic form from the
 CC USPTO web site uspto.gov/sequence.html, Document ID: 6902867B1).
 XX SQ Sequence 246 BP; 67 A; 55 C; 64 G; 60 T; 0 U; 0 Other;
 OY Query Match 82.0%; Score 16.4; DB 14; Length 246;
 Db Best Local Similarity 83.3%; Pred. No. 5.8e+02;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OY 3 GUACAGCCAGGACUACGA 20
 Db 154 GTACACCGGAGCTACGA 171
 XX RESULT 16
 XX ADX13768
 XX ID ADX13768 standard; cDNA; 1308 BP.
 XX AC ADX13768;
 XX DT 21-APR-2005 (first entry)
 XX DE Plant full length insert polynucleotide seqid 8343.
 XX KW plant protectant; plant growth regulator; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content; gene; ss.

OS Unidentified.
 XX XX US2004034888-A1.
 XX XX 19-FEB-2004.
 XX XX 28-APR-2003; 2003US-00425114.
 XX XX 06-MAY-1999; 99US-00304517.
 XX XX 05-NOV-2001; 2001US-00985678.
 XX PA (LHU//) LIU J.
 XX PA (ZHO//) ZHOU Y.
 XX PA (KOVA//) KOVALIC D K.
 XX PA (SCRE//) SCREEN S E.
 XX PA (TABA//) TABASKA J E.
 XX PA (CAOY//) CAO Y.
 XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX DR WPI; 2004-180133/17.
 XX PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX PS Claim 1; SEQ ID NO 8343; 15pp; English.
 XX CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.
 XX SQ Sequence 1308 BP; 376 A; 282 C; 278 G; 372 T; 0 U; 0 Other;
 OY Query Match 82.0%; Score 16.4; DB 13; Length 1308;
 Db Best Local Similarity 83.3%; Pred. No. 6.5e+02;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OY 2 GGUACAGCCAGGACUACG 19
 Db 44 GATACAGCCAGGACTACG 61
 XX RESULT 17
 XX ADA03035/C
 XX ID ADA03035 standard; DNA; 31632 BP.
 XX AC ADA03035;
 XX DT 06-NOV-2003 (first entry)
 XX DE Mouse Rorc carcinoma associated gene, SEQ ID NO:1553.
 XX KW mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast;
 KW prostate; lymphoma; leukemia; cytostatic; gene therapy; drug screening;
 KW gene; ds.

OS Mus sp.
 XX WO2003057146-A2.
 XX 17-JUL-2003.
 PD
 XX 26-DEC-2002; 2002MO-US041414.
 XX 26-DEC-2001; 2001US-00035832.
 PR
 XX (SAGR-) SAGRES DISCOVERY.
 PA
 XX Morris DW;
 PI
 XX WPI; 2003-587068/55.
 DR
 XX New recombinant nucleic acid encoding carcinoma associated protein,
 PT useful for preparing compositions for treating carcinomas.
 PT
 XX Claim 1; SEQ ID NO 1553; 245pp; English.
 PS
 XX The invention relates to recombinant carcinoma associated (CA) nucleic
 CC acid sequences from mouse and human (ADA01482-ADA03094), and to
 CC recombinant carcinoma associated proteins (CAP) encoded by them. The
 CC invention also encompasses expression vectors and host cells comprising a
 CC CA nucleic acid, a polypeptide (especially an antibody) that specifically
 CC binds to the protein, and a block comprising CA nucleic acid or
 CC fragments thereof. The sequences of the invention were identified using
 CC oncogenic retroviruses, which insert into the genome of the host organism
 CC at random. Many of these do not carry transduced host oncogenes or
 CC pathogenic trans-acting viral genes, meaning that cancer incidence is a
 CC direct consequence of the effects of proviral integration into host
 CC protooncogenes. The CA nucleic acid sequences can be used to diagnose
 CC carcinoma (especially breast cancer, prostate cancer, lymphoma or
 CC leukemia) or a propensity to carcinoma by determination of the sequence
 CC of a CA gene, or by determination of CA gene expression in particular
 CC tissues. CA nucleic acids, proteins and antibodies are also useful as
 CC therapeutic agents and in screening and evaluating drug candidates. The
 CC present sequence represents a specifically claimed murine CA nucleic acid
 CC sequence of the invention. Note: The complete sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX Sequence 31632 BP; 7931 A; 8130 C; 7983 G; 7588 T; 0 U; 0 Other;
 SQ
 XX
 XX Query Match 82.0%; Score 16.4; DB 9; Length 31632;
 XX Best Local Similarity 83.3%; Pred. No. 8e+02;
 XX Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUAC 18
 DB 26940 AGGTACAGCCAGGCTAC 26923

RESULT 18
 ADA6319/c
 ID ADA6319 standard; DNA; 31632 BP.
 XX
 XX ADA6319;
 AC
 XX 20-NOV-2003 (first entry)
 DT
 XX
 XX Mouse Rorc gene genomic DNA sequence.
 DE
 XX carcinoma-associated gene; CA gene; Rorc gene; MCG15938 gene; BAT1 gene;
 KM Igga1 gene; IGGA1 gene; Zp29 gene; hCG27579 gene; Kcnj9 gene;
 KM KCMJ9 gene; Pp3CC gene; Pp3CC gene; MCG9110 gene; hCG27579 gene;
 KM cancer cell; lymphatic cell; breast cell; prostate cell; epithelial cell;
 KM carcinoma-associated protein; CAP; cytostatic; gene therapy; anticancer;
 KM vaccine; carcinoma; lymphoma carcinoma; lymphatic cancer; breast cancer;
 KM prostate cancer; DNA vaccine; animal model; mouse; murine; ds; Rorc.

OS Mus sp.
 XX WO2003053224-A2.
 XX 03-JUL-2003.
 PD
 XX 20-DEC-2002; 2002MO-US041776.
 XX 20-DEC-2001; 2001US-00034650.
 PR
 XX (SAGR-) SAGRES DISCOVERY.
 PA
 XX Morris DW, Engelhard EK;
 PI
 XX WPI; 2003-569168/53.
 DR
 XX Novel recombinant carcinoma-associated nucleic acid, useful for
 PT evaluating the effect of a candidate carcinoma drug, and for diagnosing
 PT carcinoma.
 PT
 XX Claim 1; Page 51-55; 229pp; English.
 PS
 XX This invention relates to a novel recombinant carcinoma-associated (CA)
 CC nucleic acid comprising a fully defined genomic, mRNA or coding sequences
 CC of mouse Rorc gene or human RORC gene, mouse MCG15938 or human gene BAT1,
 CC mouse Igga1 gene or human IGGA1 gene, mouse Zp29 gene or human
 CC hCG27579 gene, mouse Kcnj9 gene or human KCMJ9 gene, mouse Pp3CC gene or
 CC human Pp3CC gene, mouse MCG9110 gene or human hCG27579 gene, as given in
 CC the specification. CA genes are genes which are preferably expressed in
 CC cancer cells, preferably lymphatic, breast, prostate or epithelial cells.
 CC A compound which modifies the expression of the CA genes or bind to
 CC carcinoma-associated proteins (CAP) may have cytostatic activity and the
 CC sequences of the invention may enable the use of gene therapy or a
 CC development of an anticancer vaccine. Therefore the invention may be
 CC useful for diagnosis and treatment of carcinomas, especially lymphoma
 CC carcinoma, breast cancer and prostate cancer. The CA genes may also be
 CC useful as DNA vaccines and for generating animal models of carcinomas.
 CC The present sequence is that of the mouse Rorc gene genomic DNA sequence
 CC of the invention.
 CC
 XX Sequence 31632 BP; 7931 A; 8128 C; 7985 G; 7588 T; 0 U; 0 Other;
 SQ
 XX
 XX Query Match 82.0%; Score 16.4; DB 9; Length 31632;
 XX Best Local Similarity 83.3%; Pred. No. 8e+02;
 XX Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUAC 18
 DB 26940 AGGTACAGCCAGGCTAC 26923

RESULT 19
 ADB72773/c
 ID ADB72773 standard; DNA; 31632 BP.
 XX
 XX ADB72773;
 AC
 XX 04-DEC-2003 (first entry)
 DT
 XX
 XX Mouse Rorc gene.
 DE
 XX mouse; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
 KM cancer; neoplasm; adenocarcinoma; sarcoma; gene.
 XX
 XX Mus sp.
 OS
 XX WO2003008583-A2.
 PN
 XX 30-JAN-2003.
 PD
 XX 26-DEC-2001; 2001MO-US051291.
 PF
 XX 02-MAR-2001; 2001US-00798586.

23-OCT-2001; 2001US-00004113.
PR 08-NOV-2001; 2001US-00052482.
PR 30-NOV-2001; 2001US-00997722.
PR 20-DEC-2001; 2001US-00034650.
PA (SAGR-) SAGRES DISCOVERY.
XX Morris DW, Engelhard BK;
XX WPI; 2003-239337/23.
DR
XX
XX New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
PT cancers, neoplasm, adenocarcinoma, or sarcomas.
XX
XX Claim 1; SEQ ID NO 601; 2304bp; English.
XX
XX The invention relates to a novel recombinant nucleic acid comprising a
CC nucleotide sequence selected from any of the 660 sequences fully defined
CC in the specification. A polynucleotide of the invention has cytostatic
CC activity, and may have a use in gene therapy, or in a vaccine. The
CC recombinant nucleic acids and polypeptides are useful for treating
CC carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
CC sarcomas. The present sequence represents a mouse gene of the invention.
XX
SQ Sequence 31632 BP; 7931 A; 8130 C; 7983 G; 7588 T; 0 U; 0 Other;
Query Match 82.0%; Score 16.4; DB 10; Length 31632;
Best Local Similarity 83.3%; Pred. No. 8e+02; Indels 0; Gaps 0;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 AGGUAACGCCAGACUAC 18
DB 26940 AGGTACAGCCAGGCTAC 26923
RESULT 20
ADA02933
ID ADA02933 standard; DNA; 96599 BP.
XX
AC ADA02933;
XX
DT 06-NOV-2003 (first entry)
XX
XX Mouse Braf carcinoma associated gene, SEQ ID NO:1451.
XX
XX Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast;
XX prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
XX gene; ds.
XX
XX Mus sp.
XX
XX WO2003057146-A2.
XX
XX 17-JUL-2003.
XX
XX 26-DEC-2002; 2002WO-US041414.
XX
XX 26-DEC-2001; 2001US-00035832.
XX
XX (SAGR-) SAGRES DISCOVERY.
XX
XX Morris DW;
XX
XX WPI; 2003-587068/55.
XX
XX New recombinant nucleic acid encoding carcinoma associated protein,
XX useful for preparing compositions for treating carcinomas.
XX
XX Claim 1; SEQ ID NO 1451; 245bp; English.
XX
XX The invention relates to recombinant carcinoma associated (CA) nucleic
CC acid sequences from mouse and human (ADA01482-ADA03094), and to
CC recombinant carcinoma associated proteins (CAP) encoded by them. The

invention also encompasses expression vectors and host cells comprising a
CC CA nucleic acid, a polypeptide (especially an antibody) that specifically
CC binds to the protein, and a biochip comprising CA nucleic acid or
CC fragments thereof. The sequences of the invention were identified using
CC oncogenic retroviruses, which insert into the genome of the host organism
CC at random. Many of these do not carry transduced host oncogenes or
CC pathogenic trans-acting viral genes, meaning that cancer incidence is a
CC direct consequence of the effects of proviral integration into host
CC protooncogenes. The CA nucleic acid sequences can be used to diagnose
CC carcinoma (especially breast cancer, prostate cancer, lymphoma or
CC leukaemia) or a propensity to carcinoma by determination of the sequence
CC of a CA gene, or by determination of CA gene expression in particular
CC tissues. CA nucleic acids, proteins and antibodies are also useful as
CC therapeutic agents and in screening and evaluating drug candidates. The
CC present sequence represents a specifically claimed murine CA nucleic acid
CC sequence of the invention. Note: The complete sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
XX ftp://wipo.int/pub/published_pct_sequences.
SQ Sequence 96599 BP; 28457 A; 18209 C; 18968 G; 30477 T; 0 U; 488 Other;
Query Match 82.0%; Score 16.4; DB 9; Length 96599;
Best Local Similarity 83.3%; Pred. No. 8.6e+02; Indels 0; Gaps 0;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 AGGUAACGCCAGACUAC 18
DB 28454 AGGTACAGCCAGGCTAC 28471
RESULT 21
ADB72671
ID ADB72671 standard; DNA; 96599 BP.
XX
AC ADB72671;
XX
DT 04-DEC-2003 (first entry)
XX
XX Mouse Braf gene.
XX
XX mouse; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
XX cancer; neoplasm; adenocarcinoma; sarcoma; gene.
XX
XX Mus sp.
XX
XX WO2003008583-A2.
XX
XX 30-JAN-2003.
XX
XX 26-DEC-2001; 2001WO-US051291.
XX
XX 02-MAR-2001; 2001US-00798586.
XX
XX 23-OCT-2001; 2001US-00004113.
XX
XX 08-NOV-2001; 2001US-00052482.
XX
XX 30-NOV-2001; 2001US-00997722.
XX
XX 20-DEC-2001; 2001US-00034650.
XX
XX (SAGR-) SAGRES DISCOVERY.
XX
XX Morris DW, Engelhard BK;
XX
XX WPI; 2003-239337/23.
XX
XX New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
XX cancers, neoplasm, adenocarcinoma, or sarcomas.
XX
XX Claim 1; SEQ ID NO 499; 2304bp; English.
XX
XX The invention relates to a novel recombinant nucleic acid comprising a
CC nucleotide sequence selected from any of the 660 sequences fully defined
CC in the specification. A polynucleotide of the invention has cytostatic
CC activity, and may have a use in gene therapy, or in a vaccine. The

XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656860/75.
 DR WPI; 2001-656860/75.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PI interactions.
 XX Claim 1; SEQ ID NO 12493; 21pp + Sequence Listing; English.
 PS The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signaling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins (AB57737-
 CC AB82072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 4972 BP; 1255 A; 1057 C; 1134 G; 1526 T; 0 U; 0 Other;
 Query Match 80.0%; Score 16; DB 4; Length 4972;
 Best Local Similarity 87.5%; Pred. No. 1.1e+03;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GUACAGCCAGAGACUAC 18
 DB 2160 GTACAGCCAGAGACTAC 2145
 RESULT 27
 ABL09902/c
 ID ABL09902 standard; cDNA; 4989 BP.
 XX ABL09902;
 AC 26-MAR-2002 (first entry)
 DT 26-MAR-2002 (first entry)
 XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 24188.
 KM Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 XX Drosophila melanogaster.
 OS WO200171042-A2.
 PN 27-SEP-2001.
 PD 23-MAR-2001; 2001WO-US009231.
 PF 23-MAR-2001; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656860/75.
 DR P-PSDB; ABB65799.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PI interactions.
 XX Claim 1; SEQ ID NO 24188; 21pp + Sequence Listing; English.
 PS The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signaling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins (AB57737-
 CC AB82072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 4989 BP; 1258 A; 1059 C; 1140 G; 1532 T; 0 U; 0 Other;
 Query Match 80.0%; Score 16; DB 4; Length 4989;
 Best Local Similarity 87.5%; Pred. No. 1.1e+03;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GUACAGCCAGAGACUAC 18
 DB 2160 GTACAGCCAGAGACTAC 2145
 RESULT 28
 ADQ97596
 ID ADQ97596 standard; DNA; 90616 BP.
 XX ADQ97596;
 AC 07-OCT-2004 (first entry)
 DT 07-OCT-2004 (first entry)
 XX Mouse cancer associated sequence MD10-012, SEQ ID 573.
 DR Mouse cancer associated sequence MD10-012, SEQ ID 573.
 XX Cyrostatic; Gene Therapy; cancer; leukemia; lymphoma; Mouse; de.
 KW Mus musculus.
 OS WO2004060304-A2.
 PN 22-JUL-2004.
 PD 22-DEC-2003; 2003WO-US041389.
 PF 27-DEC-2002; 2002US-00330773.
 PR (SAGR-) SAGRES DISCOVERY INC.
 XX Morris DW, Malandro MS;
 PI WPI; 2004-543781/52.
 DR New isolated cancer associated nucleic acids comprising at least 10
 PT contiguous nucleotides, useful for diagnosing, preventing and/or treating
 PT cancers such as leukemia and lymphoma.
 XX Claim 1; SEQ ID NO 573; 199pp; English.
 PS The present invention relates to cancer associated sequences (ADQ97025-
 CC ADQ98004). The sequences are useful for the diagnosis, prevention and/or
 CC treatment of cancer, such as leukemia and lymphoma. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 90616 BP; 22442 A; 19414 C; 20208 G; 27923 T; 0 U; 629 Other;
 Query Match 80.0%; Score 16; DB 12; Length 90616;
 Best Local Similarity 87.5%; Pred. No. 1.3e+03;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GUACAGCCAGAGACUAC 18
 DB 39970 GTACAGCCAGAGACTAC 39985

RESULT 29
ID ADC85298
XX ADC85298 standard; DNA; 96599 BP.
XX
AC ADC85298;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human Bgr2 coding sequence.
XX
DE Cytostatic; gene therapy; vaccine; cancer; carcinoma-associated gene; CA;
XX secreted; transmembrane; intracellular; ds.
XX
OS Homo sapiens.
XX
PN WO2003045230-A2.
XX
PD 05-JUN-2003.
XX
PF 02-DEC-2002; 2002WO-US038582.
XX
PR 30-NOV-2001; 2001US-00997722.
XX
PA (SAGR-) SAGRES DISCOVERY.
XX
PI Morris DW, Engelhard EK;
XX WPI; 2003-513603/48.
XX
DR New recombinant nucleic acid comprising a nucleotide sequence of any of
XX PT candidates for diagnosing or treating carcinomas.
XX
PS Claim 1; SEQ ID NO 84; 983bp; English.
XX
CC The invention relates to a recombinant nucleic acid comprising a
XX CC nucleotide sequence selected from any of the fully defined carcinoma-
XX CC associated (CA) genes from the 50 tables given in the specification. The
XX CC CA proteins are secreted, transmembrane or intracellular proteins. The
XX CC recombinant nucleic acids are useful for screening for drug candidates
XX CC for diagnosing or treating carcinomas. Sequences given in ADC85215-
XX CC ADC85514 represent CA genes of the invention.
XX
SQ Sequence 96599 BP; 27390 A; 19000 C; 20559 G; 29350 T; 0 U; 300 Other;
XX
Query Match 80.0%; Score 16; DB 10; Length 96599;
Best Local Similarity 87.5%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
OY 3 GUACAGCCAGGACTAC 18
DB 91765 GTACAGCCAGGACTAC 91780
XX
RESULT 30
ID ADA02819
XX ADA02819 standard; DNA; 96600 BP.
XX
AC ADA02819;
XX
DT 06-NOV-2003 (first entry)
XX
DE Mouse Sos1 carcinoma associated gene, SEQ ID NO:1337.
XX
XX Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast;
XX KM prostate; lymphoma; leukaemia; cytosolic; gene therapy; drug screening;
XX KM gene; ds.
XX
OS Mus sp.
XX
PN WO2003057146-A2.
XX
PD 17-JUL-2003.
XX

XX
XX 26-DEC-2002; 2002WO-US041414.
XX
XX 26-DEC-2001; 2001US-00035832.
XX
XX (SAGR-) SAGRES DISCOVERY.
XX
XX Morris DW;
XX WPI; 2003-587068/55.
XX
XX New recombinant nucleic acid encoding carcinoma associated protein,
XX PT useful for preparing compositions for treating carcinomas.
XX
PS Claim 1; SEQ ID NO 1337; 245bp; English.
XX
XX The invention relates to recombinant carcinoma associated (CA) nucleic
XX CC acid sequences from mouse and human (ADA01482-ADA03094), and to
XX CC recombinant carcinoma associated proteins (CAP) encoded by them. The
XX CC invention also encompasses expression vectors and host cells comprising a
XX CC CA nucleic acid, a polypeptide (especially an antibody) that specifically
XX CC binds to the protein, and a biochip comprising CA nucleic acid or
XX CC fragments thereof. The sequences of the invention were identified using
XX CC oncogenic retroviruses, which insert into the genome of the host organism
XX CC at random. Many of these do not carry transduced host oncogenes or
XX CC pathogenic trans-acting viral genes, meaning that cancer incidence is a
XX CC direct consequence of the effects of proviral integration into host
XX CC protooncogenes. The CA nucleic acid sequences can be used to diagnose
XX CC carcinoma (especially breast cancer, prostate cancer, lymphoma or
XX CC leukaemia) or a propensity to carcinoma by determination of the sequence
XX CC of a CA gene, or by determination of CA gene expression in particular
XX CC tissues. CA nucleic acids, proteins and antibodies are also useful as
XX CC therapeutic agents and in screening and evaluating drug candidates. The
XX CC present sequence represents a specifically claimed murine CA nucleic acid
XX CC sequence of the invention. Note: The complete sequence data for this
XX CC patent did not form part of the printed specification, but was obtained
XX CC in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 96600 BP; 27391 A; 19001 C; 20558 G; 29350 T; 0 U; 300 Other;
XX
Query Match 80.0%; Score 16; DB 9; Length 96600;
Best Local Similarity 87.5%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
OY 3 GUACAGCCAGGACTAC 18
DB 91766 GTACAGCCAGGACTAC 91781
XX
RESULT 31
ID ADB72557
XX ADB72557 standard; DNA; 96600 BP.
XX
AC ADB72557;
XX
DT 04-DEC-2003 (first entry)
XX
DE Mouse Sos1 gene.
XX
XX mouse; ds; cytosolic; gene therapy; vaccine; carcinoma; lymphomas;
XX KM cancer; neoplasm; adenocarcinoma; sarcoma; gene.
XX
OS Mus sp.
XX
PN WO2003006583-A2.
XX
PD 30-JAN-2003.
XX
PF 26-DEC-2001; 2001WO-US051291.
XX
PR 02-MAR-2001; 2001US-00798586.
XX
PR 23-OCT-2001; 2001US-00004113.
XX

PR 08-NOV-2001; 2001US-00052482.
 PR 30-NOV-2001; 2001US-00997722.
 PR 20-DEC-2001; 2001US-00034650.
 XX
 PA (SAGR-) SAGRES DISCOVERY.
 XX
 PI Morris DW, Engelhard EK;
 XX WPI; 2003-239337/23.
 DR
 PT New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
 PT cancer, neoplasm, adenocarcinoma, or sarcomas.
 XX
 PS Claim 1; SEQ ID NO 385; 2304pp; English.
 XX
 CC The invention relates to a novel recombinant nucleic acid comprising a
 CC nucleotide sequence selected from any of the 660 sequences fully defined
 CC in the specification. A polynucleotide of the invention has cytostatic
 CC activity, and may have a use in gene therapy, or in a vaccine. The
 CC recombinant nucleic acids and polypeptides are useful for treating
 CC carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
 CC sarcomas. The present sequence represents a mouse gene of the invention.
 XX
 SQ Sequence 96600 BP; 27391 A; 19001 C; 20558 G; 29350 T; 0 U; 300 Other;
 Query Match 80.0%; Score 16; DB 10; Length 96600;
 Best Local Similarity 87.5%; Pred. No. 1.3e+03;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GUNACGCCAGACUAC 18
 DB 91766 GTACAGCCAGACTAC 91781
 RESULT 32
 ADM74414
 ID ADM74414 standard; DNA; 96600 BP.
 XX
 AC ADM74414;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Murine carcinoma associated (CA) nucleic acid #43.
 XX
 KM Mouse; carcinoma associated nucleic acid; CA nucleic acid; gene; ds;
 KM carcinoma associated protein; CAP; carcinoma; leukaemia; lymphoma;
 KM cytosolic.
 XX
 OS Mus musculus.
 XX
 PN US2004072154-A1.
 XX
 PD 15-APR-2004.
 XX
 PF 30-NOV-2001; 2001US-00997722.
 XX
 PR 22-DEC-2000; 2000US-00747377.
 PR 02-MAR-2001; 2001US-00798586.
 XX
 PA (MORR/) MORRIS D W.
 PA (ENGEL/) ENGELHARD E K.
 XX
 PI Morris DW, Engelhard EK;
 XX WPI; 2004-328562/30.
 DR
 XX New carcinoma associated gene or protein, useful for preparing a
 PT composition for diagnosing or treating carcinoma e.g., leukemia or
 PT lymphoma.
 XX
 PS Claim 1; SEQ ID NO 85; 29pp; English.
 XX
 CC The invention relates to new recombinant nucleic acids. The invention

CC also relates to a host cell comprising a recombinant nucleic acid or
 CC expression vector, an expression vector comprising a recombinant nucleic
 CC acid, a recombinant protein, a method of screening for drug candidates, a
 CC method of screening for a bioactive agent capable of binding to a
 CC carcinoma associated protein (CAP) encoded by a nucleotide sequence, a
 CC method of screening for a bioactive agent capable of modulating the
 CC activity of a CAP, a method of evaluating the effect of a candidate
 CC carcinoma drug, a method of diagnosing carcinoma, a method for inhibiting
 CC the activity of a CAP, a method of treating carcinomas, a method of
 CC neutralising the effect of a CAP and a method of diagnosing carcinoma or
 CC propensity to carcinoma. A method of evaluating the effect of a candidate
 CC carcinoma drug comprises administering the drug to a patient, removing a
 CC cell sample from the patient and determining alterations in the
 CC expression or activation of a gene comprising the nucleotide sequence. A
 CC method of diagnosing carcinoma comprises determining the expression of
 CC one or more genes comprising the nucleic acid sequence in a first tissue
 CC type of a first individual and comparing the expression of the gene from
 CC a second normal tissue type from the first individual or a second
 CC unaffected individual, where a difference in the expression indicates
 CC that the first individual has carcinoma. A method of inhibiting the
 CC activity of a CAP comprises binding an inhibitor to the CAP. Treating
 CC carcinomas comprises administering to a patient an inhibitor of CAP.
 CC Neutralising the effect of a CAP comprises contacting an agent specified
 CC for the CAP. The polypeptide specifically binds to the protein encoded by
 CC the nucleic acid. It comprises an antibody that specifically binds to the
 CC protein encoded by the nucleic acid. The nucleic acids are useful for
 CC preparing a composition for diagnosing or treating carcinoma e.g.,
 CC leukaemia or lymphoma. This sequence represents a murine carcinoma
 CC associated (CA) nucleic acid of the invention. Note: The sequence data
 CC for this patent did not form part of the printed specification but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 96600 BP; 27391 A; 19001 C; 20558 G; 29350 T; 0 U; 300 Other;
 Query Match 80.0%; Score 16; DB 12; Length 96600;
 Best Local Similarity 87.5%; Pred. No. 1.3e+03;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GUNACGCCAGACUAC 18
 DB 91766 GTACAGCCAGACTAC 91781
 RESULT 33
 ADP74214/C
 ID ADP74214 standard; DNA; 144411 BP.
 XX
 AC ADP74214;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Equine herpesvirus 4 genome gm deletion mutant #2.
 XX
 KM virucide; vaccine; Equine Herpes Virus; EHV; gm; vaccine;
 KM EHV-associated condition; Equine herpesvirus 4; EHV4; ds; mutant; mutein.
 XX
 OS Equine herpesvirus 4.
 XX
 PN US2004109873-A1.
 XX
 PD 10-JUN-2004.
 XX
 PF 21-JUL-2003; 2003US-00624149.
 XX
 PR 19-JUL-2002; 2002US-01033064.
 PR 14-AUG-2002; 2002US-0403282P.
 PR 11-APR-2003; 2003US-01017008.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.
 PA Neubauer A, Ziegler C;
 XX

XX WPI; 2004-440311/41.
XX
XX
XX New recombinant equine herpes (EHV) virus free of heterologous elements,
PT and where protein gm has been deleted, useful as a vaccine for treating
PT or preventing EHV infections.
XX
XX Claim 18; Page; 156pp; English.
XX
XX The invention describes a new recombinant Equine Herpes Virus (EHV) where
CC the protein gm is absent, and the EHV is free of heterologous elements.
CC Also described are: a nucleic acid coding for an EHV defined above; a
CC vaccine preparation comprising the EHV or nucleic acid; obtaining a
CC recombinant EHV; and a cell line for use in the method, where the gene
CC encoding the protein gm is transfected into the cell line, and the cell
CC line expresses gm. The vaccine comprising the EHV or nucleic acid
CC encoding EHV is useful for treating and/or preventing EHV-associated
CC condition, and for monitoring the therapeutic success. The recombinant
CC EHV is useful as a vaccine against EHV infections. This sequence
CC represents an Equine herpesvirus 4 genome in which nucleotides 92681-
CC 93865, comprising regions of the gm gene, have been deleted.
SQ Sequence 144411 BP; 35893 A; 36645 C; 36246 G; 35627 T; 0 U; 0 Other;
Query Match 80.0%; Score 16; DB 12; Length 144411;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGUACAGCCAGACTA 17
DB 76346 GGTACAGCCAGACTA 76331
RESULT 34
ADP74213/C
ID ADP74213 standard; DNA; 144486 BP.
XX
XX ADP74213;
XX
XX 26-AUG-2004 (first entry)
XX
XX Equine herpesvirus 4 genome gm deletion mutant #3.
XX
XX virucide; vaccine; Equine Herpes Virus; EHV; gm; vaccine;
XX EHV-associated condition; Equine herpesvirus 4; EHV4; ds; mutant; mutein.
XX
XX Equine herpesvirus 4.
XX
XX Synthetic.
XX
XX US2004109873-A1.
XX
XX 10-JUN-2004.
XX
XX 21-JUN-2003; 2003US-00624149.
XX
XX 19-JUL-2002; 2002DE-01033064.
XX 14-AUG-2002; 2002US-0403282P.
XX 11-APR-2003; 2003DE-01017008.
XX
XX (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.
XX
XX Neubauer A, Ziegler C;
XX
XX WPI; 2004-440311/41.
XX
XX New recombinant equine herpes (EHV) virus free of heterologous elements,
PT and where protein gm has been deleted, useful as a vaccine for treating
PT or preventing EHV infections.
XX
XX Claim 19; Page; 156pp; English.
XX
XX The invention describes a new recombinant Equine Herpes Virus (EHV) where
CC the protein gm is absent, and the EHV is free of heterologous elements.

CC Also described are: a nucleic acid coding for an EHV defined above; a
CC vaccine preparation comprising the EHV or nucleic acid; obtaining a
CC recombinant EHV; and a cell line for use in the method, where the gene
CC encoding the protein gm is transfected into the cell line, and the cell
CC line expresses gm. The vaccine comprising the EHV or nucleic acid
CC encoding EHV is useful for treating and/or preventing EHV-associated
CC condition, and for monitoring the therapeutic success. The recombinant
CC EHV is useful as a vaccine against EHV infections. This sequence
CC represents an Equine herpesvirus 4 genome in which nucleotides 92715-
CC 93824, comprising regions of the gm gene, have been deleted.
SQ Sequence 144486 BP; 35916 A; 36662 C; 36259 G; 35649 T; 0 U; 0 Other;
Query Match 80.0%; Score 16; DB 12; Length 144486;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGUACAGCCAGACTA 17
DB 76346 GGTACAGCCAGACTA 76331
RESULT 35
ADP74213/C
ID ADP74213 standard; DNA; 145444 BP.
XX
XX ADP74213;
XX
XX 26-AUG-2004 (first entry)
XX
XX Equine herpesvirus 4 genome gm deletion mutant #1.
XX
XX virucide; vaccine; Equine Herpes Virus; EHV; gm; vaccine;
XX EHV-associated condition; Equine herpesvirus 4; EHV4; ds; mutant; mutein.
XX
XX Equine herpesvirus 4.
XX
XX Synthetic.
XX
XX US2004109873-A1.
XX
XX 10-JUN-2004.
XX
XX 21-JUN-2003; 2003US-00624149.
XX
XX 19-JUL-2002; 2002DE-01033064.
XX 14-AUG-2002; 2002US-0403282P.
XX 11-APR-2003; 2003DE-01017008.
XX
XX (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.
XX
XX Neubauer A, Ziegler C;
XX
XX WPI; 2004-440311/41.
XX
XX New recombinant equine herpes (EHV) virus free of heterologous elements,
PT and where protein gm has been deleted, useful as a vaccine for treating
PT or preventing EHV infections.
XX
XX Claim 17; Page; 156pp; English.
XX
XX The invention describes a new recombinant Equine Herpes Virus (EHV) where
CC the protein gm is absent, and the EHV is free of heterologous elements.
CC Also described are: a nucleic acid coding for an EHV defined above; a
CC vaccine preparation comprising the EHV or nucleic acid; obtaining a
CC recombinant EHV; and a cell line for use in the method, where the gene
CC encoding the protein gm is transfected into the cell line, and the cell
CC line expresses gm. The vaccine comprising the EHV or nucleic acid
CC encoding EHV is useful for treating and/or preventing EHV-associated
CC condition, and for monitoring the therapeutic success. The recombinant
CC EHV is useful as a vaccine against EHV infections. This sequence
CC represents an Equine herpesvirus 4 genome in which nucleotides 92681-
CC 92731 and 93765-93865, comprising regions of the gm gene, have been
CC deleted.

```
XX Sequence 145444 BP; 36178 A; 36893 C; 36497 G; 35876 T; 0 U; 0 Other;
SQ
Query Match 80.0%; Score 16; DB 12; Length 145444;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGUACAGCCAGACUA 17
Db 76346 GTTACAGCCAGACTA 76331

RESULT 36
ADP74202/c
ID ADP74202 standard; DNA; 145596 BP.
XX
AC ADP74202;
XX
DT 26-AUG-2004 (first entry)
XX
DE Equine herpesvirus 4 genome segid 2.
XX
KM virucide; vaccine; Equine Herpes Virus; EHV; gm; vaccine;
KM EHV-associated condition; Equine herpesvirus 4; EHV4; ds.
XX
OS Equine herpesvirus 4.
XX
FN US2004109873-A1.
XX
PD 10-JUN-2004.
XX
PF 21-JUL-2003; 2003US-00624149.
XX
PR 19-JUL-2002; 2002DE-01033064.
PR 14-AUG-2002; 2002US-0403282P.
PR 11-APR-2003; 2003DE-01017008.
XX
PA (BOEH ) BOEHRINGER INGELHEIM VETMEDICA GMBH.
XX
PI Neubauer A, Ziegler C;
XX
DR WPI; 2004-440311/41.
XX
PT New recombinant equine herpes (EHV) virus free of heterologous elements,
PT or where protein gm has been deleted, useful as a vaccine for treating
PT or preventing EHV infections.
XX
PS Disclosure; SEQ ID NO 2; 156pp; English.
XX
CC The invention describes a new recombinant Equine Herpes Virus (EHV) where
CC the protein gm is absent, and the EHV is free of heterologous elements.
CC Also described are: a nucleic acid coding for an EHV defined above; a
CC vaccine preparation comprising the EHV or nucleic acid; obtaining a
CC recombinant EHV; and a cell line for use in the method, where the cell
CC encoding the protein gm is transfected into the cell line, and the cell
CC line expresses gm. The vaccine comprising the EHV or nucleic acid
CC encoding EHV is useful for treating and/or preventing EHV-associated
CC condition, and for monitoring the therapeutic success. The recombinant
CC EHV is useful as a vaccine against EHV infections. This sequence
CC represents the Equine herpesvirus 4 genome.
XX
SQ Sequence 145596 BP; 36213 A; 36932 C; 36529 G; 35922 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 12; Length 145596;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGUACAGCCAGACUA 17
Db 76346 GTTACAGCCAGACTA 76331

RESULT 37
```

```
ADZ13116/c
ID ADZ13116 standard; DNA; 241748 BP.
XX
AC ADZ13116;
XX
DT 16-JUN-2005 (first entry)
XX
DE Murine cancer-associated genomic DNA #54.
XX
KM Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
KM cytostatic; gene; ds.
XX
OS Mus sp.
XX
FN WO2005031001-A2.
XX
PD 07-APR-2005.
XX
PF 23-SEP-2004; 2004WO-US031617.
XX
PR 23-SEP-2003; 2003US-00669920.
XX
PA (CHIR ) CHIRON CORP.
XX
PI Morris DW, Malandro MS;
XX
DR WPI; 2005-273395/28.
XX
PT Nucleic acid array useful for detecting cancer associated nucleic acid,
PT comprises two or more nucleic acid probes.
XX
PS Disclosure; SEQ ID NO 636; 198pp; English.
XX
CC The invention relates to a nucleic acid array for detecting a cancer
CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
CC The invention also relates to a peptide array comprising two or more
CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
CC that binds to a polypeptide, an isolated antibody or its fragment which
CC binds to a polypeptide, which is prepared by immunizing a host animal
CC with a composition comprising the polypeptide or its antigen binding
CC fragment and collecting cells from the host expressing antibodies against
CC the antigen or its antigen binding fragment, a composition comprising the
CC antibody and a carrier, a method of screening for anticancer activity, a
CC method of detecting a CA nucleic acid, a method of inhibiting expression of a CA
CC nucleic acid in a cell. The CA nucleic acid are useful for detecting CA
CC absence of cancer cells in an individual which involves contacting cells
CC from the individual with the antibody and detecting a complex of a CA
CC protein from the cancer cells and the antibody, where the detection of
CC the complex correlates with the presence of cancer cells in the
CC individual. The composition is useful for inhibiting growth of cancer
CC cells in an individual or for delivering a therapeutic agent to cancer
CC cells in an individual. The invention is also useful for diagnosing
CC cancer, for treating cancer and for inhibiting expression of a CA gene in
CC a cell. This sequence represents murine cancer-associated genomic DNA of
CC the invention.
XX
SQ Sequence 241748 BP; 59664 A; 56662 C; 57444 G; 61211 T; 0 U; 6767 Other;

Query Match 80.0%; Score 16; DB 14; Length 241748;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGUACAGCCAGACUA 18
Db 42387 GTTACAGCCAGACTAC 42372

RESULT 38
ABD15945/c
ID ABD15945 standard; DNA; 411 BP.
XX
```


AC ABD15945;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polynucleotide #14549.
XX
KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
XX antibacterial.
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
XX
PR 27-JUL-1998; 98US-0094190P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
PI Rubenfield MJ, Nolling J, DeLoughery C, Bush D;
DR WPI; 2003-615309/58.
DR P-PSDB; ABO82374.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
XX Disclosure; SEQ ID NO 14549; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 411 BP; 56 A; 128 C; 170 G; 57 T; 0 U; 0 Other;
XX
Query Match 79.0%; Score 15.8; DB 11; Length 411;
Best Local Similarity 78.9%; Pred. No. 1.2e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGGUNACGCCGAGACTUACG 19
DB 346 AGCTACAGCCTGAGACTACG 328
XX
RESULT 39
ABD16211
ID ABD16211 standard; DNA; 537 BP.
XX
XX ABD16211;
AC
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polynucleotide #14815.
XX
XX Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
XX antibacterial.

XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
XX
PR 27-JUL-1998; 98US-0094190P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
PI Rubenfield MJ, Nolling J, DeLoughery C, Bush D;
DR WPI; 2003-615309/58.
DR P-PSDB; ABO82640.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
XX Disclosure; SEQ ID NO 14815; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 537 BP; 76 A; 226 C; 160 G; 75 T; 0 U; 0 Other;
XX
Query Match 79.0%; Score 15.8; DB 11; Length 537;
Best Local Similarity 78.9%; Pred. No. 1.2e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGGUNACGCCGAGACTUACG 19
DB 162 AGCTACAGCCTGAGACTACG 180
XX
RESULT 40
ABV15922/C
ID ABV15922 standard; cDNA; 542 BP.
XX
XX ABV15922;
AC
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 15913.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US005171.
XX

```
XX 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JB;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 2668; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the efficacy
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX determining whether prostate cancer has metastasized in a patient; (h)
XX assessing the aggressiveness or indolence of prostate cancer in a patient
XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
XX Sequence 542 BP; 130 A; 111 C; 124 G; 173 T; 0 U; 4 Other;
XX
XX Query Match 79.0%; Score 15.8; DB 5; Length 542;
XX Best Local Similarity 78.9%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 AGGUAAGCCAGGACUACG 19
XX |||:|||||||:|
XX 90 AGGTAGGCCAGACTATG 72
XX
XX
XX RESULT 41
XX ABV45722/C
XX ID ABV45722 standard; cDNA; 592 BP.
XX
XX ABV45722;
XX
XX 16-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 45713.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX MO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US005171.
XX
XX 17-FEB-2000; 2000US-0183319P.
XX 16-MAR-2000; 2000US-0189862P.
XX 25-MAY-2000; 2000US-0207454P.
XX 09-JUN-2000; 2000US-0211314P.
XX 18-JUL-2000; 2000US-0219007P.
XX 13-DEC-2000; 2000US-0255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
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XX Schlegel R, Endege WO, Monahan JB;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 9040; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the efficacy
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX determining whether prostate cancer has metastasized in a patient; (h)
XX assessing the aggressiveness or indolence of prostate cancer in a patient
XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
XX Sequence 592 BP; 141 A; 124 C; 142 G; 185 T; 0 U; 0 Other;
XX
XX Query Match 79.0%; Score 15.8; DB 5; Length 592;
XX Best Local Similarity 76.9%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 AGGUAAGCCAGGACUACG 19
XX |||:|||||||:|
XX 136 AGGTAGGCCAGACTATG 118
XX
XX
XX RESULT 42
XX AAS89740/C
XX ID AAS89740 standard; cDNA; 693 BP.
XX
XX AAS89740;
XX
XX 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #25544.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX MO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSB-) HYSBQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX P-PSDB; ABG25553.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 1; SEQ ID NO 25544; 103pp; English.
XX
```

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping.
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostic, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC
SQ Sequence 693 BP, 141 A, 192 C, 218 G, 142 T, 0 U, 0 Other;
Query Match 79.0%; Score 15.8; DB 5; Length 693;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 2 GGUACAGCCAGACTUACGA 20
DB 186 GGCACAGCCAGACTUACGA 168
RESULT 43
ABL04139/c
ID ABL04139 standard; cDNA, 978 BP.
XX
AC ABL04139;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 6899.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
XX
PT 11-JUL-2000; 2000US-00614150.
XX
PA (PERK) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers BW;
XX
DR WPI; 2001-655660/75.
XX
DR P-PSDB; ABB60036.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions.
XX
PS Claim 1; SEQ ID NO 6899; 21bp + Sequence listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
CC ABBS72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
CC
SQ Sequence 978 BP, 213 A, 253 C, 234 G, 278 T, 0 U, 0 Other;
Query Match 79.0%; Score 15.8; DB 4; Length 978;
Best Local Similarity 78.9%; Pred. No. 1.2e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 AGUACAGCCAGACTUACG 19
DB 236 AGGTATAGCCAGACTUACG 218
RESULT 44
ADS14617
ID ADS14617 standard; DNA, 1023 BP.
XX
AC ADS14617;
XX
DT 16-DEC-2004 (first entry)
XX
DE Pseudomonas aeruginosa quorum sensing controlled gene PA2514, SEQ ID 172.
XX
KW Cytostatic; Anti-HIV; Antimicrobial; Immunosuppressive;
KW quorum sensing signalling; bacterium; quorum sensing controlled gene;
KW biofilm-associated disease; cystic fibrosis; AIDS; middle ear infection;
KW acne; periodontal disease; gene; ds; PA2514.
XX
OS Pseudomonas aeruginosa.
XX
PN WO2004083385-A2.
XX
PD 30-SEP-2004.
XX
PF 11-MAR-2004; 2004WO-US007467.
XX
PR 14-MAR-2003; 2003US-00389647.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Greenberg EP, Schuster M, Iostroh C;
XX
DR WPI; 2004-709932/69.
XX
PT Identifying a modulator of quorum sensing signalling in bacteria, useful
XX for treating a biofilm-associated disorder, comprises contacting the cell
XX with a quorum sensing signal molecule in the presence and absence of a
XX test compound.
XX
PS Disclosure; SEQ ID NO 172; 233bp; English.
XX
XX The present invention relates to a method for identifying a modulator of
XX quorum sensing signalling in bacteria. The method comprises: providing a
XX cell that comprises a quorum sensing controlled gene (ADS1446-ADS14798),
XX where the cell is responsive to a quorum sensing signal molecule such
XX that a detectable signal is generated; contacting the cell with a quorum
XX sensing signal molecule in the presence and absence of a test compound;
XX and detecting a change in the detectable signal. The method and modulator
XX identified by the method are useful for treating a biofilm-associated
XX disease or disorder, e.g. cystic fibrosis, AIDS, middle ear infections,
XX acne, periodontal disease, catheter-associated infections, and medical
XX device-associated infections. Note: The sequence data for this patent was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1023 BP, 142 A, 392 C, 329 G, 160 T, 0 U, 0 Other;

Query Match 79.0%; Score 15.8; DB 13; Length 1023;
 Best Local Similarity 78.9%; Pred. No. 1.2e+03;
 Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGUAACGCCGAGACUACG 19
 ID AGCTACAGCCTGAGACTACG 184
 DB

RESULT 45

ABD16472
 ID ABD16472 standard; DNA; 1044 BP.
 XX
 AC ABD16472;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Pseudomonas aeruginosa polynucleotide #15076.
 XX
 XX Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
 KM antibacterial.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN US6551795-B1.
 XX
 PD 22-APR-2003.
 XX
 PF 18-FEB-1999; 99US-00252991.
 XX
 PR 18-FEB-1998; 98US-0074788P.
 XX
 PR 27-JUL-1998; 98US-0094190P.
 XX

PA (GENE-) GENOME THERAPEUTICS CORP.
 XX
 XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 PI
 DR WPI; 2003-615309/58.
 DR P-PSDB; ABO82901.

PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX
 PS Disclosure; SEQ ID NO 15076; 455bp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa-derived peptides or polypeptides, as target
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences ABD01397-
 CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 CC
 XX

Sequence 1044 BP; 142 A; 404 C; 336 G; 162 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 11; Length 1044;
 Best Local Similarity 78.9%; Pred. No. 1.2e+03;
 Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGUAACGCCGAGACUACG 19
 ID AGCTACAGCCTGAGACTACG 202
 DB

RESULT 46
 AAZ61623
 ID AAZ61623 standard; cDNA; 1057 BP.
 XX
 AC AAZ61623;
 XX
 DT 27-MAR-2000 (first entry)
 XX
 DE cDNA encoding rat skin cell secreted protein, SEQ ID NO:18.
 XX
 XX Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;
 KM embryonic skin cell; keratinocyte stem cell; transit amplifying cell;
 KM secreted; transmembrane; inflammation; cancer; neurological disease;
 KM angiogenesis; tumour vascularisation; growth disorder;
 KM developmental disorder; skin wound; hair follicle disorder;
 KM anti-inflammatory; cytostatic; neuroprotective; vulnery; se.
 XX
 OS Rattus sp.
 XX
 PN WO9955865-A1.
 XX
 PD 04-NOV-1999.
 XX
 PF 29-APR-1999; 99WO-NZ000051.
 XX
 PR 29-APR-1998; 98US-00069726.
 XX
 PR 09-NOV-1998; 98US-00188930.
 XX

PA (GENE-) GENESIS RES & DEV CORP LTD.
 XX
 XX Strachan L, Sleeman M, Watson JD, Onrust R, Kumble A, Murlison JG;
 PI
 DR WPI; 2000-072177/06.
 XX
 PT Novel polynucleotides useful for the treatment of various conditions
 PT including wounds and cancer.
 XX
 PS Claim 1; Page 69-70; 235bp; English.

XX The invention relates to novel nucleic acid sequences derived from rat
 CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
 CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying
 CC cells. Polypeptides of the invention may be used to treat inflammation,
 CC cancer and neurological diseases. The proteins may be used to stimulate
 CC the growth and motility of keratinocytes, to inhibit the growth of cancer
 CC cells, to modulate angiogenesis and tumour vascularisation, to modulate
 CC skin inflammation, to modulate epithelial cell growth and to inhibit
 CC binding of HIV-1 to leukocytes. The invention may also be used to treat
 CC growth and developmental defects, skin wounds and hair follicle
 CC disorders. Sequences AAZ61606-261832 represent cDNA sequences derived
 CC from several mouse, rat or human skin cell types. Sequences AAZ61606-
 CC 261649, AAZ61725-261765, AAZ61802-261811 and AAZ61826 encode proteins
 CC with an N-terminal signal sequence, indicating that the proteins are
 CC secreted. Sequences AAZ61650-261668, AAZ61766-261780, AAZ61812-261817 and
 CC AAZ61827-261829 encode proteins with one or more putative transmembrane
 CC domains
 CC
 XX

Sequence 1057 BP; 223 A; 315 C; 295 G; 224 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 3; Length 1057;
 Best Local Similarity 84.2%; Pred. No. 1.2e+03;
 Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUAACGCCGAGACUACGA 20
 ID GCTACAGCCGAGCAACGA 1040
 DB

RESULT 47
 AAC99556
 ID AAC99556 standard; cDNA; 1057 BP.
 XX

AC AAC99556;
XX
DT 08-MAR-2001 (first entry)
XX
DE Skin cell cDNA, SEQ ID NO: 18.
XX
XX Rat; skin cell; cytostatic; antiinflammatory; anti-HIV; nootropic;
KM neuroprotective; vulnary; immunomodulatory; vaccine;
KM keratinocyte growth stimulation; cancer; angiogenesis inhibition;
KM inflammation; neurological disease; ss.
XX
OS Rattus sp.
XX
PN WO20069884-A2.
XX
PD 23-NOV-2000.
XX
XX 15-MAY-2000; 2000MO-NZ000075.
XX
XX 14-MAY-1999; 99US-00312283.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD;
PI Murison JG;
XX
XX WPI: 2001-007495/01.
XX
XX P-PSDB; AAB55898.
XX
XX New isolated polynucleotide used in the identification of genetic
PT disorders and encoding polypeptides used for treating inflammatory
PT disease, cancer and neurological diseases.
XX
XX Claim 1; Page 81; 352pp; English.
XX
XX The present polynucleotide encodes a polypeptide which is expressed in
CC mammalian skin cells. The polypeptide is useful for stimulating
CC keratinocyte growth and motility, inhibiting the growth of cancer cells,
CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of
CC tumors, modulating skin inflammation, stimulating the growth of
CC epithelial cells, inhibiting the binding of human immunodeficiency virus
CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and
CC neurological diseases. The polynucleotide can be used as a marker, in the
CC identification of genetic disorders, and for the design of
CC oligonucleotides for examining expression patterns
XX
SQ Sequence 1057 BP; 223 A; 315 C; 295 G; 224 T; 0 U; 0 Other;
XX
Query Match 79.0%; Score 15.8; DB 4; Length 1057;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 2 GGUACAGCCAGACUACGA 20
DB 1022 GCTACAGCCAGACGA 1040
XX
RESULT 48
ABL34708
ID ABL34708 standard; cDNA; 1057 BP.
XX
AC ABL34708;
XX
DT 04-APR-2002 (first entry)
XX
XX Rat cDNA isolated from skin cells SEQ ID NO: 18.
XX
XX Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
KM developmental defect; inflammatory disease; dermatological; vulnary;
KM immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;
KM ss.
XX
OS Rattus sp.

XX
XX WO200190357-A1.
XX
XX 29-NOV-2001.
XX
XX 24-MAY-2001; 2001MO-NZ000099.
XX
XX 24-MAY-2000; 2000US-0206650P.
XX
XX 25-JUL-2000; 2000US-0221232P.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG;
XX Kumble KD;
XX
XX WPI: 2002-122020/16.
XX
XX New polynucleotides and polypeptides encoded by the polynucleotides
PT isolated from skin cells, useful for treating skin wounds, cancers,
PT growth and developmental defects, inflammatory diseases, or for
PT modulating immune responses.
XX
XX Claim 1; Page 83; 466pp; English.
XX
XX The present invention provides the protein and coding sequences of cDNAs
CC isolated from human, murine and rat skin cell libraries. The sequences
CC can be used in the development of therapeutic agents useful in the
CC treatment of skin diseases, including skin wounds, cancer, growth
CC defects, developmental defects and inflammatory diseases. The proteins
CC have important roles in the induction of hair growth, cell proliferation
CC and cell-cell interaction, in maintaining tissue integrity, in wound
CC healing and in modulating immune responses. The present sequence is a
CC cDNA of the invention
XX
SQ Sequence 1057 BP; 223 A; 315 C; 295 G; 224 T; 0 U; 0 Other;
XX
Query Match 79.0%; Score 15.8; DB 6; Length 1057;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 2 GGUACAGCCAGACUACGA 20
DB 1022 GCTACAGCCAGACGA 1040
XX
RESULT 49
ABD16075/C
ID ABD16075 standard; DNA; 1452 BP.
XX
AC ABD16075;
XX
DT 29-JUL-2004 (first entry)
XX
XX Pseudomonas aeruginosa polynucleotide #14679.
XX
XX Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KM antibacterial.
XX
XX Pseudomonas aeruginosa.
XX
XX US6551795-B1.
XX
XX 22-APR-2003.
XX
XX 18-FEB-1999; 99US-00252891.
XX
XX 18-FEB-1998; 98US-0074788P.
XX
XX 27-JUL-1998; 98US-0094190P.
XX
XX (GENE-) GENOME THERAPEUTICS CORP.
XX
XX Rubenfeld MJ, Nollng J, Deloughery C, Bush D;
XX

DR WPI; 2003-615309/58.
 P-PSDB; ABO82504.
 XX Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide,
 PT useful as molecular targets for diagnostic, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX
 PS Disclosure; SEQ ID NO 14679; 455bp; English.
 CC The invention relates to *Pseudomonas aeruginosa* polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-*P. aeruginosa* drugs, as templates for recombinant
 CC production of *P. aeruginosa*-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of *P. aeruginosa*-caused
 CC infection, and in detection of *P. aeruginosa* sequences or other sequences
 CC of *Pseudomonas* species using biochip technology. Sequences ABD01397-
 CC ABD17967 represent *P. aeruginosa* polynucleotides of the invention. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 1452 BP; 220 A; 453 C; 559 G; 220 T; 0 U; 0 Other;
 Query Match 79.0%; Score 15.8; DB 11; Length 1452;
 Best Local Similarity 78.9%; Pred. No. 1.3e+03;
 Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AGGUAAGCCAGGACUACG 19
 ||:|||||:|||||
 Db 693 AGCTACAGCTGACTGACG 675
 RESULT 50
 AAC99799
 ID AAC99799 standard; cDNA; 1890 BP.
 XX AAC99799;
 AC
 XX 08-MAR-2001 (first entry)
 DT
 XX
 DE Skin cell cDNA, SEQ ID NO: 447.
 XX
 XX Rat; skin cell; cytostatic; antiinflammatory; anti-HIV; nootropic;
 KW neuroprotective; vulnery; immunomodulatory; vaccine;
 KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;
 KW inflammation; neurological disease; ss.
 XX
 XX *Rattus* sp.
 OS
 XX W0200069884-A2.
 PN
 XX 23-NOV-2000.
 PD
 XX 15-MAY-2000; 2000WO-NZ000075.
 PF
 XX 14-MAY-1999; 99US-00312283.
 PR
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 PA
 XX Watson JD, Strachan L, Orrust R, Sleeman M, Kumble KD;
 PI Murison JG;
 PI
 XX WPI; 2001-007495/01.
 DR
 XX
 PT New isolated polynucleotide used in the identification of genetic
 PT disorders and encoding polypeptides used for treating inflammatory
 PT disease, cancer and neurological diseases.
 XX

PS Claim 1; Page 338-339; 352pp; English.
 XX The present polynucleotide encodes a polypeptide which is expressed in
 CC mammalian skin cells. The polypeptide is useful for stimulating
 CC keratinocyte growth and motility, inhibiting the growth of cancer cells,
 CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of
 CC tumours, modulating skin inflammation, stimulating the growth of
 CC epithelial cells, inhibiting the binding of human immunodeficiency virus
 CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and
 CC neurological diseases. The polynucleotide can be used as a marker, in the
 CC identification of genetic disorders, and for the design of
 CC oligonucleotides for examining expression patterns
 XX
 SQ Sequence 1890 BP; 388 A; 611 C; 463 G; 428 T; 0 U; 0 Other;
 Query Match 79.0%; Score 15.8; DB 4; Length 1890;
 Best Local Similarity 84.2%; Pred. No. 1.3e+03;
 Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 GGUACAGCCAGGACUACGA 20
 ||:|||||:|||||
 Db 881 GCTACAGCCAGGACUACGA 899
 Search completed: March 18, 2006, 18:55:40
 Job time : 463.923 secs


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c 972 15.2 76.0 694 10 CW002144
c 973 15.2 76.0 695 2 BF404570
c 974 15.2 76.0 698 6 CB620278
975 15.2 76.0 699 5 BM485981
976 15.2 76.0 702 7 CM270366
977 15.2 76.0 703 5 BM258660
978 15.2 76.0 703 5 BM4847824
c 979 15.2 76.0 703 9 CC971392
980 15.2 76.0 704 3 B1640898
981 15.2 76.0 704 9 CC636479
982 15.2 76.0 704 10 C2779238
983 15.2 76.0 705 8 DN263841
c 984 15.2 76.0 706 10 AG281534
985 15.2 76.0 707 2 BG631938
986 15.2 76.0 709 2 BF492519
987 15.2 76.0 709 2 BF502369
988 15.2 76.0 709 3 B1386781
989 15.2 76.0 710 3 DR690050
c 990 15.2 76.0 714 6 CF679766
c 991 15.2 76.0 715 9 AZ098631
c 992 15.2 76.0 717 10 AG550929
c 993 15.2 76.0 718 7 CK446426
994 15.2 76.0 719 6 CD636053
c 995 15.2 76.0 719 6 DN426666
c 996 15.2 76.0 719 8 DN426666
c 997 15.2 76.0 720 8 BU560241
998 15.2 76.0 722 8 DT086197
c 999 15.2 76.0 723 1 AM128196
c1000 15.2 76.0 723 1 AM128196

```

ALIGNMENTS

```

RESULT 1
LOCUS BU280879
DEFINITION 603599710F1 CSBQCHN54 Gallus gallus CDNA clone CHEST572d4 5', mRNA
sequence.
ACCESSION BU280879
VERSION BU280879.1 GI:25730333
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Archaeopteryx; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Phasiantidae; Aves; Neognathae; Galliformes; Phasianidae;
Phasianidae; Gallus.
1 (bases 1 to 864)
Boardman, P. B., Sanz-Ezquerro, J., Overton, I. M., Burt, D. W., Bosch, E.,
Fong, W. T., Tickle, C., Brown, W. R. A., Wilson, S. A. and Hubbard, S. J.
A Comprehensive Collection of Chicken cDNAs
J. Cur. Biol. 12 (22), 1965-1969 (2002)
12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(MIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1..864
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="CHEST572d4"
/sex="Female"
/issue_type="not cerebrum or cerebellum"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="CSBQCHN54"

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ORIGIN
Query Match 95.0%; Score 19; DB 5; Length 864;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
1 AGGTACGACCGACGACG 19
|||||
186 AGGTACGACCGACGACG 204

```

/note="Organ: brain; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand reaction, double-stranded cDNA. Following this first strand reaction, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research (1996) 791, except that a significantly longer reannealing hybridization was used."

```

RESULT 2
LOCUS AGS09048
DEFINITION 747 bp DNA linear GSS 22-DEC-2004
Mus musculus molossinus DNA, clone:MSMg01-412D14.TU, genomic survey
sequence.
ACCESSION AGS09048
VERSION AGS09048.1 GI:48216461
KEYWORDS GSS.
SOURCE Mus musculus molossinus (Japanese wild mouse)
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1
Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,
Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriuchi, K. and
Shirotani, T.
Contribution of Asian mouse subspecies Mus musculus molossinus to
genomic constitution of strain C57BL/6J, as defined by BAC-end
sequence-SNP analysis
Genome Res. 14 (12), 2439-2447 (2004)
15574823
2 (bases 1 to 747)
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan
1-7-22 Suenho-chou, Tsukuba-Ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kunya Abe (abe@tc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyada, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@tc.riken.jp
PRIMERS
Sequencing : TU
LIBRARY : DBAC3.6
Vector : BcoRI
R Site 1 : BcoRI
R Site 2 : BcoRI.
Location/Qualifiers
1..747
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"

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ORIGIN

Query Match 90.0%; Score 18; DB 10; Length 747;
 Best Local Similarity 88.9%; Pred. No. 5.9e+02;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GTACAGCCGAGACUACGA 20
 |||||
 Db 432 GTACAGCCGAGACTACGA 449

/db_xref="taxon:57486"
 /clone="MSMG01-412D14.TJ"
 /sex="male"
 /tissue_type="mixture of kidney and spleen"
 /clone_lib="MSMG01 Mouse Male BAC Library"

RESULT 3
 AA855258 331 bp mRNA linear EST 06-MAR-1998
 LOCUS vW70d11.r1 StrataGene mouse heart (#937316) Mus musculus cDNA clone
 DEFINITION IMAGE:1260284 5', mRNA sequence.
 AA855258
 VERSION AA855258.1 GI:2942796
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lemon, G., Soares, B., Wilson, R., and Waterston, R.
 The WashU-HMNI Mouse EST Project
 Unpublished (1996)
 JOURNAL CONTACT: Marra M/Mouse EST Project
 COMMENT WashU-HMNI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LML; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:662836

FEATURES
 source
 location/Qualifiers
 1..331
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="NIH Swiss"
 /db_xref="taxon:10090"
 /clone="IMAGE:1260284"
 /sex="pooled"
 /tissue_type="heart"
 /dev_stage="13 day embryos"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="StrataGene mouse heart (#937316)"
 /note="Organ: heart; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. 93 pooled NIH/Swiss 13 day embryo hearts. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTTT TTT TTT TTT TTT TTT 3' "

ORIGIN

Query Match 87.0%; Score 17.4; DB 1; Length 331;
 Best Local Similarity 89.5%; Pred. No. 1.1e+03;
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGACAGCCGAGACUACG 19
 |||||
 Db 267 AGGACAGCCGAGACTACG 285

RESULT 4
 A1463924 332 bp mRNA linear EST 09-MAR-1999
 LOCUS vW70d11.y1 StrataGene mouse heart (#937316) Mus musculus cDNA clone
 DEFINITION IMAGE:1260284 5', mRNA sequence.
 A1463924
 VERSION A1463924.1 GI:4317954
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
 The WashU-NCI Mouse EST Project 1999
 Unpublished (1999)
 JOURNAL CONTACT: Marra M/WashU-NCI Mouse EST Project 1999
 COMMENT Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LML; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:662836

FEATURES
 source
 location/Qualifiers
 1..332
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="NIH Swiss"
 /db_xref="taxon:10090"
 /clone="IMAGE:1260284"
 /sex="pooled"
 /tissue_type="heart"
 /dev_stage="13 day embryos"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="StrataGene mouse heart (#937316)"
 /note="Organ: heart; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. 93 pooled NIH/Swiss 13 day embryo hearts. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTTT TTT TTT TTT TTT TTT 3' "

ORIGIN

Query Match 87.0%; Score 17.4; DB 1; Length 332;
 Best Local Similarity 89.5%; Pred. No. 1.1e+03;
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGACAGCCGAGACUACG 19
 |||||
 Db 268 AGGACAGCCGAGACTACG 286

RESULT 5
 CE251666/c

LOCUS CE251666 632 bp DNA linear GSS 26-SEP-2003
 DEFINITION tigr-gss-dog-17000335911441 Dog library Canis familiaris genomic,
 genomic survey sequence.
 ACCESSION CE251666
 VERSION CE251666.1 GI:35948584
 KEYWORDS GSS.
 SOURCE
 ORGANISM Canis familiaris (dog)
 Canis familiaris
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 Canis.
 1 (bases 1 to 632)
 Kirkness,B.F., Batina,V., Halpern,A.L., Levy,S., Remington,K.,
 Ruesch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
 Venter,J.C.
 The dog genome: survey sequencing and comparative analysis
 Science 301 (5641), 1898-1903 (2003)
 14512627
 JOURNAL
 PUBMED
 COMMENT Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Buiaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.
 Location/Qualifiers
 1..632
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN
 Query Match 87.0%; Score 17.4; DB 9; Length 632;
 Best Local Similarity 84.2%; Pred. No. 1.1e+03;
 Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGACGACCGAGACGACG 19
 |||:|||||:|||||:|||||
 530 AGGTACGACGACGACGACTAG 512

Db

RESULT 6
 BH898697 706 bp DNA linear GSS 31-OCT-2002
 MB61p10C9 Mission Bay (San Diego, CA) uncultured virus community
 sequence.
 unclutured marine virus genomic clone MB61p10C9, genomic survey
 sequence.
 BH898697
 BH898697.1 GI:24432823
 GSS.
 uncultured marine virus
 unclutured marine virus
 viruses; environmental samples.
 1 (bases 1 to 706)
 Breitbart,M., Salamon,P., Andresen,B., Mahaffy,J.M., Segall,A.M.,
 Mead,D., Azam,F. and Rohwer,F.
 Genomic analysis of uncultured marine viral communities
 Proc. Natl. Acad. Sci. U.S.A. 99 (22), 14250-14255 (2002)
 12384570
 JOURNAL
 PUBMED
 COMMENT Contact: Rohwer F
 Biology Dept.
 San Diego State University
 5500 Campanile Dr, San Diego, CA 92102, USA
 Tel: 6195941336
 Fax: 619595676
 Email: forest@sunstroke.sdsu.edu
 Class: shotgun.
 Location/Qualifiers

source
 1..706
 /organism="uncultured marine virus"
 /mol_type="genomic DNA"
 /db_xref="taxon:186617"
 /clone="MB61p10C9"
 /clone_lib="Mission Bay (San Diego, CA) uncultured virus
 community"
 /note="Vector: pSMART; Sample from Mission Bay (San Diego,
 CA). Marine viruses were isolated from 200 liters of
 surface seawater using a combination of differential
 filtration and density-dependent gradient centrifugation.
 linker-amplified shotgun libraries were constructed by
 randomly shearing the total marine viral community DNA,
 end-repeating, ligating dsDNA linkers to the ends, and
 amplifying the fragments using Vent DNA polymerase. The
 resulting fragments were ligated into the pSMART vector
 and electroporated into MC12 cells (Lucigen, Middleton,
 WI)."

ORIGIN
 Query Match 87.0%; Score 17.4; DB 9; Length 706;
 Best Local Similarity 84.2%; Pred. No. 1.2e+03;
 Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGACGACCGAGACGACG 19
 |||:|||||:|||||:|||||
 664 AGGTACGACGACGACGACTAG 646

Db

RESULT 7
 CG307131 847 bp DNA linear GSS 26-AUG-2003
 CG307131
 LOCUS
 DEFINITION OG2BX53TH ZM 0.7-1.5 KB Zea mays genomic clone ZMMBMA0759110,
 genomic survey sequence.
 ACCESSION CG307131
 VERSION CG307131.1 GI:34224291
 KEYWORDS GSS.
 SOURCE Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 847)
 Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
 Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
 Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
 Consortium for Maize Genomics
 Unpublished (2002)
 Other GSSs: OG2BX53TV
 Contact: Cathy Whitelaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TR
 Class: methylation filtered.
 Location/Qualifiers
 1..847
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMMBMA0759110"
 /clone_lib="ZM_0.7-1.5_KB"
 /note="Vector: pBCK-K; Site 1: HincII; 0.7-1.5 kb
 methylation filtered genomic DNA library"

ORIGIN
 Query Match 87.0%; Score 17.4; DB 10; Length 847;
 Best Local Similarity 84.2%; Pred. No. 1.2e+03;
 Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;


```

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

COMMENT
source

FEATURES
source

ORIGIN

Query Match      87.0%; Score 17.4; DB 11; Length 993;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy      2  GGUACAGCCGAGACTUACGA 20
      |||:|||||:|||||:|||||
Db      503  GGTACAGCCGAGACTACCA 521

RESULT 10
BE379071
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BE379071      1016 bp      mRNA      linear      EST 21-JUL-2000
60123694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608974 5'
mRNA sequence.
BE379071
BE379071.1  GI:9324436
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 1016)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection. (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMU at:
http://image.lmhl.gov
Plate: LCM262 row: k column: 23
High quality sequence stop: 602.
Location/Qualifiers
1..1016
/organism="Homo sapiens"

```

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="3608974"
/issue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 44"
/note="Organ: uterus; Vector: pOT87; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 87.0%; Score 17.4; DB 2; Length 1016;
Best Local Similarity 89.5%; Pred. No. 1.2e+03;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGTACAGCCAGACGAC 19
DB 830 AGGACAGCCAGACGACTACG 848

RESULT 11
AI757758/c 427 bp mRNA linear EST 18-JAN-2000
LOCUS ETEBTEA3403.Y1 Bimertia S5-2 Sporozoite stage Bimertia tenella cDNA
DEFINITION 5', mRNA sequence.
ACCESSION AI757758
VERSION AI757758.1 GI:5151481
KEYWORDS EST.
SOURCE Bimertia tenella
ORGANISM Bimertia tenella
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriidae; Eimeriidae;
Bimertia.

REFERENCE 1 (bases 1 to 427)
AUTHORS Liberatori P., Diaz C., Tang K., Marra M., Hillier L., Kucaba T., Martin J., Wylie T., Underwood K., Steptoe M., Theising B., Allen M., Bowers Y., Person B., Swaller T., Gibbons M., Page D., Harvey N., Schurk R., Ritter E., Kohn S., Florence N., Shin T., Jackson Y., Cardenas M., McCann R., Waterston R., Wilson R. and Sibley D.
TITLE WashU-Merck Bimertia tenella project
JOURNAL Unpublished (1999)
COMMENT Contact: David Sibley, Ph.D.
WashU-Merck Bimertia tenella project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 266 1800
Fax: 314 266 1810
Email: estewartson.wustl.edu
Contact David Sibley (toxosec@orcim.wustl.edu) for further information relating to organism, libraries, or clone availability.
Seq primer: -40RP from Gibco
High quality sequence stop: 418.
Location/Qualifiers

FEATURES
source
1..427
/organism="Bimertia tenella"
/mol_type="mRNA"
/strain="1S18"
/db_xref="taxon:5802"
/dev_stage="Sporozoite"
/lab_host="SOLR B. coli"
/clone_lib="Bimertia S5-2 Sporozoite stage"
/note="Vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Sporozoites were obtained from in vitro sporulated and excysted oocysts of B. tenella grown in chickens.
cDNA was synthesized from poly mRNA using an oligo-dt primer containing a XhoI site. Following second strand synthesis, EcoRI adapters were ligated to the cDNA and products were size-selected on Sephacryl S500. cDNAs were digested with EcoRI/XhoI and cloned into lambda zap II

(Stratagene). Clones were converted to phagemids by mass excision using Exaseist helper phage and SOLR cells (Stratagene). Insert sizes range from 1.2-2.9 kb."

ORIGIN

Query Match 85.0%; Score 17; DB 1; Length 427;
Best Local Similarity 88.2%; Pred. No. 1.7e+03;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTACAGCCAGACGAC 17
DB 33 AGTACAGCCAGACGACTA 17

RESULT 12

CE109731 488 bp DNA linear GSS 24-SEP-2003
LOCUS tigr-gss-dog-17000324505919 Dog library Canis familiaris genomic,
DEFINITION genomic survey sequence.
ACCESSION CE109731
VERSION CE109731.1 GI:35176616
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

REFERENCE 1 (bases 1 to 488)
AUTHORS Kirtness R.F., Bafna V., Halpern A.L., Levy S., Remington K., Kirsch D.B., Delcher A.L., Pop M., Wang M., Fraser C.M. and Venter J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
PUBMED 14512627

COMMENT Contact: Kirtness RF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirtness@tigr.org
Class: shotgun.
Location/Qualifiers

FEATURES
source
1..488
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BclXI; Libraries were prepared from peripheral blood"

ORIGIN

Query Match 85.0%; Score 17; DB 9; Length 488;
Best Local Similarity 88.2%; Pred. No. 1.7e+03;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTACAGCCAGACGAC 17
DB 226 AGTACAGCCAGACGACTA 242

RESULT 13

BG336492 1097 bp mRNA linear EST 27-FEB-2001
LOCUS BG336492
DEFINITION 602405476P1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4541146 5',
mRNA sequence.
ACCESSION BG336492
VERSION BG336492.1 GI:13142930
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel.: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

```

/organism="Homo sapiens"
/mol_type="genomic DNA"

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/db_xref="GDB:7562015"
/db_xref="taxon:9606"
/clone="RPC1-11-162H24"
/bex="Male"
/cell_type="Lymphocytes"
/clone_id="RPC1-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC11 Human Male BAC library"
ORIGIN

Query Match      84.0%; Score 16.8; DB 9; Length 427;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy      1 AGGATACAGCCAGGACTACGA 20
      |||:|||||||:|
Db      104 AGGTATACGACGAGTATAGA 123

RESULT 16
LOCUS      AJ691440      432 bp      mRNA      linear      EST 29-JUN-2004
ACCESSION      AJ691440      KN261 Bos taurus cDNA clone KN261-024_H05, mRNA sequence.
VERSION      AJ691440.1      GI:49424048
KEYWORDS
SOURCE      EST.
ORGANISM      Bos taurus (cow)
            Buleri, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE      1 (bases 1 to 432)
AUTHORS      Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE      Development of cDNA and EST resources for studying reproduction and
            embryo development in pigs and cattle
JOURNAL      Unpublished (2004)
COMMENT      Contact: Anderson SI
            Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross match with the -minscore 20
            and -mismatch 12 options. Vector:pBluescriptII(SK-) R. Site1: EcoRI;
            R. Site2: SmaI 5' Seq Primer T3 Normalised library constructed from
            bovine ovary. Clones available from UK Centre for Functional
            Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK.
            EH25 9PS, www.arkgenomics.org.
FEATURES
            source
            1..432
            /organism="Bos taurus"
            /mol_type="mRNA"
            /db_xref="taxon:9913"
            /clone="KN261-024_H05"
            /tissue_type="ovary"
            /clone_id="KN261"
            /note="Vector: pBluescriptII(SK-); Site_1: EcoRI; Site_2:
            SmaI; Single pass sequencing. Normalised library
            constructed from bovine ovary."
ORIGIN

Query Match      84.0%; Score 16.8; DB 1; Length 432;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy      1 AGGATACAGCCAGGACTACGA 20
      |||:|||||||:|
Db      341 AGGTATACGACGAGTATAGA 360

RESULT 17
LOCUS      BY471445      527 bp      mRNA      linear      EST 02-JAN-2004
ACCESSION      BY471445      RIKEN full-length enriched, melanocyte mus musculus cDNA
DEFINITION

```

accession
 clone G270099g11 3', mRNA sequence.
 BY474745
 keywORDS
 BY474745.1 GI:26805854
 SOURCE
 EST.
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
 REFERENCE
 1 (bases 1 to 527)
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nishida, I., Otsu, N., Saito, R., Suzuki, H., Yamanka, I., Miyawaka, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schirral, L. M., Kanapin, A., Matsuda, H., Batalov, S., Batzel, K. W., Blake, J. A., Brad, D., Brusic, V., Chothia, C., Corbett, L. E., Cousin, S., Datta, E., Dragan, T. A., Fletcher, C. F., Forrest, A., Frizer, K. S., Gaasterland, T., Gariboldi, M., Glessi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Korochkin, I. V., Lee, Y., Lehman, B., Lyons, P. A., Maglott, D. R., Maltsev, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Naito, K., Okido, T., Pavan, W. J., Petosa, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sanderlin, A., Schneider, C., Sempke, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Williams, L. G., Wyshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yang, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Okada, T., Kono, H., Nakamura, M., Sakakura, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Aizawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kigawa, I., Miyazaki, A., Sakai, K., Saeki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 2004, 563-573 (2002)
 12466851
 COMMENT
 CONTACT: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/
 Aizawa, K., Akimura, T., Aikawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Kono, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numata, R., Ohno, M., Sakai, K., Sakakura, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Cells were provided by Drs. William J Pavan, Stacie Loftus, and Denise Larson (Division of Intramural Research Genetic Disease

Research Branch National Human Genome Research Institute, National Institutes of Health (NIH) Building: 49, Room 4A62 49 Convent Drive MSC 4472 Bethesda, Maryland U.S.A.) whose assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

Source

```
1. .527
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="Taxon:10090"
/cclone="G2700099G11"
/cell_type="melanocyte"
/clone_lib="RIKEN full-1
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ORIGIN

Query Match	84.0%;	Score 16.8;	DB 5;	Length 527;
Best Local Similarity	85.0%;	Pred. No. 2.2e+03;		
Matches 17; Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0;

```

Qy      1 AGUACAGCCAGGACUACGA 20
         ||| ||| ||| : |||
Db      213 AGGAACAGGCGACTACGA 194

```

RESULT 18
BF825833

LOCUS	644 bp	mRNA	linear	EST 13-JAN-2001
DEFINITION	MR2-HN0036-171100-002-a01	HN0036 Homo sapiens cDNA,	mRNA sequence.	
ACCESSION	AF825623			

ACCESSION	BF825833
VERSION	BF825833.1
REVISION	GI:12168549

SOURCE	Homo sapiens (human)
--------	----------------------

ORGANISM

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCES

TITLE
JOURNAL
PUBMED
COMMENT

O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922

Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPSP/ICR Human Cancer Genome Project. This entry can be seen in the following URL
<http://www.ludwig.org.br/scripts/getcm12.pl?tl=RR2et2=RR2-HN0036-171100-002-601et3=2000-11-17et4=1>
 Seq primer: puc 18 forward
 High quality sequence start: 3
 High quality sequence stop: 618.

FEATURES

SOURCE

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_strage="Adult"
/clone_lib="NR0036"
/note="Organ: head_normal, Vector: puc18, Site_1: SmaI,
Site_2: SmaI, A mini-library was made by cloning products

```

derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research). . . profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match	84.0%	Score 16.8;	DB 2;	Length 644;
Best Local Similarity	80.0%;	Pred. No. 2.3e+03;		
Matches 16;	Conservative 2;	Mismatches 2;	Indels 0;	Gaps 0;

```

Qy      1 AGTACAGCCAGGACUACGA 20
         |||:|||||||: ||
Db      407 AGGTACAGCCAGGACTGAGA 426

```

RESULT 19	LOCUS	DEFINITION	ACCESSION
AZ941856/c	AC941856	644 bp DNA linear	GSS 26-APR-2001
	2M0201G17R	Mouse 10kb plasmid U0GCG2M library Mus musculus genomic	
	clone U0GCG2M0201G17 R,	genomic survey sequence.	
	2M041856/c		

VERSION AZ941856.1 GI:13804673
KEYWORDS GSS.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

**JOURNAL
COMMENT**

Contact: Robert B. Weiss
University of Utah
Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0201 row: G column: 17
Seq primer: CACACAGGAAACAGCATGACG
Class: Plasmid ends
High quality sequence stop: 644.

FEATURES
SOURCE

`/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGM0201617"
 /sex="Female"
 /lab_host="R. coli strain XL10-Gold, T1-resistant, F-"
 /clone_1fb="Mouse 10kb plasmid UGCG2M library"
 /note="Vector: pMD229; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnareqs/). The DNA
 was hydrothermally sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD22 (g147321a19b AF128072.1), a copy-number`

RESULT 25
CG269100/c 784 bp DNA linear GSS 25-AUG-2003
DEFINITION OGA40TV ZM 0.7-1.5_KB Zea mays genomic clone ZMMBMA0586H07,
genomic survey sequence.
ACCESSION CG269100
VERSION CG269100.1 GI:34181241
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 784)
White, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Frazer, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nurnberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGA40TV
Contact: Cathy White, cwhite@tigr.org
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitec@tigr.org
Seq primer: TF
Classes: methylation filtered.
Location/Qualifiers
1..784
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_id="ZMMBMA0586H07"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 84.0%; Score 16.8; DB 10; Length 784;
Best Local Similarity 85.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
CY 1 AGGUAACGCCAGACUACGA 20
|||||
468 AGGTACAGCCAGAACACGA 449

RESULT 26
CG269110 865 bp DNA linear GSS 25-AUG-2003
DEFINITION OGA40TV ZM 0.7-1.5_KB Zea mays genomic clone ZMMBMA0586H07,
genomic survey sequence.
ACCESSION CG269110
VERSION CG269110.1 GI:34181251
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 865)
White, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Frazer, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nurnberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGA40TV
Contact: Cathy White, cwhite@tigr.org
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843
Fax: 301-838-0208
Email: whitec@tigr.org
Seq primer: TF
Classes: methylation filtered.
Location/Qualifiers
1..865
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_id="ZMMBMA0586H07"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 84.0%; Score 16.8; DB 10; Length 865;
Best Local Similarity 85.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
CY 1 AGGUAACGCCAGACUACGA 20
|||||
366 AGGTACAGCCAGAACACGA 385

RESULT 27
CG252727 936 bp DNA linear GSS 25-AUG-2003
DEFINITION OGMH23TV ZM 0.7-1.5_KB Zea mays genomic clone ZMMBMA0577D21,
genomic survey sequence.
ACCESSION CG252727
VERSION CG252727.1 GI:34154817
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 936)
White, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Frazer, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nurnberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGMH23TV
Contact: Cathy White, cwhite@tigr.org
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitec@tigr.org
Seq primer: TF
Classes: methylation filtered.
Location/Qualifiers
1..936
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_id="ZMMBMA0577D21"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 84.0%; Score 16.8; DB 10; Length 936;
Best Local Similarity 85.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
CY 1 AGGUAACGCCAGACUACGA 20
|||||
366 AGGTACAGCCAGAACACGA 385

RESULT 28
BZ553930/c 940 bp DNA linear GSS 17-DEC-2002
LOCUS pacel-60_4436.xl pacel-60 Pseudomonas aeruginosa genomic clone
DEFINITION pacel-60_4436, genomic survey sequence.
ACCESSION BZ553930
VERSION BZ553930.1 GI:27160619
KEYWORDS GSS.
SOURCE Pseudomonas aeruginosa
ORGANISM Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 940)
Spencer,D.H., Raymond,C.K., Smith,E.B., Sims,E.B., Hastings,M.,
Burns,J.L., Kaul,R. and Olsen,M.V.
Whole-Genome-Sequence Variation among multiple isolates of
Pseudomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: ckraymond@u.washington.edu
Class: shotgun.
FEATURES
source
location/Qualifiers
1..940
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="1-60"
/db_xref="taxon:287"
/clone="pacel-60_4436"
/clone_lib="pacel-60"
/note="clinical isolate 1-60 whole genomic shotgun
library."

ORIGIN
Query Match 84.0%; Score 16.8; DB 9; Length 940;
Best Local Similarity 85.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACAGCCGAGACTACGA 20
Db 240 AAGGACAGCCGAGACTACGA 221

RESULT 29
BZ214228/c 965 bp mRNA linear EST 06-NOV-2000
LOCUS BZ214228
DEFINITION 601848401F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4079137 5',
mRNA sequence.
ACCESSION BZ214228
VERSION BZ214228.1 GI:11107814
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Buthera; Euarchoontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 965)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA library Preparation: CLONTECH Laboratories, Inc.
cDNA library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

found through the I.M.A.G.E. Consortium/ILNL at:
<http://image.lnl.gov>
Plate: LHC937 row: b column: 02
High quality sequence stop: 8.
location/Qualifiers
1..965
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4079137"
/tissue_type="from acute myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 55"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site: 1: S11 (ggccgcctggcc); Site 2: S11
(ggccatcggcc); Double-stranded cDNA was prepared from
cell line RNA. 5' and 3' adaptors were used in cloning as
follows: 5' adaptor sequence: 5'-CACGGCATTATGACC-3' and
3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCGCGGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

ORIGIN
Query Match 84.0%; Score 16.8; DB 2; Length 965;
Best Local Similarity 85.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACAGCCGAGACTACGA 20
Db 631 AGGACAGCCGAGACTACGA 612

RESULT 30
BZ563339 1062 bp DNA linear GSS 17-DEC-2002
LOCUS BZ563339
DEFINITION pac82-164_4207.y2 pac82-164 Pseudomonas aeruginosa genomic clone
ACCESSION BZ563339
VERSION BZ563339.1 GI:27166999
KEYWORDS GSS.
SOURCE Pseudomonas aeruginosa
ORGANISM Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 1062)
Spencer,D.H., Raymond,C.K., Smith,E.B., Sims,E.B., Hastings,M.,
Burns,J.L., Kaul,R. and Olsen,M.V.
Whole-Genome-Sequence Variation among multiple isolates of
Pseudomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: ckraymond@u.washington.edu
Class: shotgun.
FEATURES
source
location/Qualifiers
1..1062
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="2-164"
/db_xref="taxon:287"
/clone="pac82-164_4207"
/clone_lib="pac82-164"
/note="clinical isolate 2-164 whole genomic shotgun
library."

ORIGIN

Query Match	84.0%;	Score 16.8;	DB 9;	Length 1062;
Best Local Similarity	85.0%;	Pred. No. 2.4e+03;		
Matches 17;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	AGGUAACGCCAGACUACGA 20		
Db	120	AAAGCAGACCGACGACTACGA 139		
RESULT 31				
LOCUS	CL023089	1210 bp	DNA	linear
DEFINITION	CH216-15N1.RM1.1.CH216 Xenopus tropicalis genomic clone CH216-15N1,			
	genomic survey sequence.			
ACCESSION	CL023089			
VERSION	CL023089.1	GI:40464902		
KEYWORDS	GSF.			
SOURCE	Xenopus tropicalis (western clawed frog)			
ORGANISM	Xenopus tropicalis			
	Bufoctata; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;			
	Xenopodinae; Xenopus; Silurana.			
	1 (bases 1 to 1210)			
REFERENCES	Kremliak, C., Carter, J., McPherson, J., Warren, W., Graves, T.,			
AUTHORS	Martin, E. and Wilson, R.			
TITLE	A physical map of the xenopus tropicalis genome			
JOURNAL	Unpublished (2003)			
COMMENT	Contact: Richard K Wilson Genome Sequencing Center Washington University School of Medicine Email: submissions@watson.wustl.edu Insert length: 175000 Std Error: 0.00 Seq primer: RM1 TACGACTCATTATAGGAGA Class: BAC ends High quality sequence start: 147 High quality sequence stop: 495. Location/Qualifiers			
FEATURES	source			
	1..1210			
	/organism="Xenopus tropicalis"			
	/mol_type="genomic DNA"			
	/strain="Nigerian frog"			
	/db_xref="taxon:8364"			
	/clone="CH216-15N1"			
	/sex="male"			
	/cell_line="Stock 248 F7A2, inbred N7"			
	/clone_1lb="CH216"			
	/note="Vector: pTARBAC2.1; CHOKI-216 Xenopus tropicalis BAC library"			
ORIGIN				
Query Match	84.0%;	Score 16.8;	DB 10;	Length 1210;
Best Local Similarity	80.0%;	Pred. No. 2.5e+03;		
Matches 16;	Conservative 2;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	AGGUAACGCCAGACUACGA 20		
Db	212	AGGTACAGCCAGAGGCTACGA 231		
RESULT 32				
LOCUS	DN675670	1217 bp	mRNA	linear
DEFINITION	CFM67-H01.Y1d-8 SHGC-CFM Gasterosteus aculeatus cDNA clone			
ACCESSION	DN675670			
VERSION	DN675670.1	GI:61995849		
KEYWORDS	EST.			
SOURCE	Gasterosteus aculeatus (three spined stickleback)			
ORGANISM	Gasterosteus aculeatus			
	Bufoctata; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
	Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;			
	Acanthomorpha; Acanthopterygii; Perciforma; Gasterosteiformes;			

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Gasterosteidae; Gasterosteus.
1 (bases 1 to 1217)
Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M.,
Schmutz,J. and Myers,R.M.
Expressed sequence tags from Gasterosteus aculeatus
Unpublished (2003)
Contact: Grimwood, Jane
Stanford Human Genome Center
Stanford University School of Medicine
975 S California Ave, Palo Alto, CA 94304, USA
Tel: 650 320 5917
Fax: 650 320 5801
Email: jane@hgsc.stanford.edu
Plate: 87

FEATURES
Source

High quality sequence stop: 855.
Location/Qualifiers
1..1217
/organism="Gasterosteus aculeatus"
/mol_type="mRNA"
/strain="Corner Creek sticklebacke, WA USA"
/db_xref="taxon:69293"
/clone="CFW87-H01"
/sex="mixed male and female"
/tissue_type="gills"
/dev_stage="adult"
/lab_host="DH10B (T1 phage resistant)"
/clone_1lb="SHGC-CFW"
/note="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACGAGTTCTGATCGCAGCGGCCGCC(T)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxAATC' where is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at:
http://www.openbiosystems.com/cdna_library_construction_fa_q.php#8 The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems:
<http://www.openbiosystems.com/stickleback>"

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 1217;
Best Local Similarity 80.0%; Fred.No. 2.5e+03;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0.

Dy 1 AGNUGAGCCAGAGCUACGA 20
|||:|||||:|||||:|||
Db 446 AAGTCAGCCAGACTTACGA 465

RESULT 33
AKO50767/c

LOCUS 3033 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus 9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:ID030018D2 Product:unclassified, full insert sequence.
ACCESSION AKO50767
VERSION AKO50767.1 GI:26094105
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1

AUTHORS Carrincci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE

AUTHORS 2
Carrincci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE

AUTHORS 3
Shibata, K., Itoh, M., Atzawa, K., Nagaoaka, S., Sasaki, N., Carrincci, P., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiyagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawaj, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplexed sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE

AUTHORS 4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
PUBMED 11076861
REFERENCE

AUTHORS 5
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 11076861
REFERENCE

AUTHORS Adachi, J., Atzawa, K., Akimura, T., Arakawa, T., Bono, H., Carrincci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hoti, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawaj, J., Kojima, Y., Kondo, S., Komno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Ohsato, N., Okazaki, Y., Saito, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Saeki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeki, Y., Tanaka, T., Tomaru, A., Toya, T., Yasuniishi, A., Muramatsu, M., and Hayashizaki, Y.

TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001)

COMMENT Yoshitake Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

CNA library was prepared and sequenced in Mouse Genome Encyclopaedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues

Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers

1. .3033

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:D030018D22"
/db_xref="taxon:10090"
/clone="D030018D22"
/issue type="whole body"
/clone_lib="RIKEN full-length enriched mouse cDNA library"

FEATURES
SOURCE

```
misc_feature      /dev stage="9 days embryo"
                  1..3033
ORIGIN            /note="unclassified"

Query Match          84.0%; Score 16.8; DB 4; Length 3033;
Best Local Similarity 85.0%; Pred. No. 2.8e+03;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY                1 AGGACAGCCAGCACTACGA 20
                   ||| ||||| ||||| |||
                   2232 AGGACAGCCAGCACTACGA 2213

RESULT 34
A2106943
LOCUS              A2106943             176 bp    DNA        linear   GSS 09-MAY-2000
DEFINITION         RPCI-23-453P19.TJ RPCI-23 Mus musculus genomic clone
VERSION            RPCI-23-453P19, genomic survey sequence.
KEYWORDS           A2106943
ACCESSION          A2106943
SOURCE            GI:7759999
ORGANISM          Mus musculus
                  Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 176)
Zhao,S., Nieman,M., Feldblum,T., Malek,J., Shatsman,S.,
Akhtar,B., Levins,M., McGann,S., Tesgaye,G., Geer,K., Krol,M., de
Jong,P. and Fraser,C.M.:
Mouse, BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSEs: RPCI-23-453P19.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel.: 301 838 0200
Fax: 301 838 0208
Email: szhaoc@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pjeter@ed.jong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.html)
or from Resee ch Genetics (info@ressee.com). BAC end page:
http://www.tigr.org/tdb/bac\_end/mouse/bac\_end\_intro.html
Plate: 453 row: P column: 19
Seq primer: SP6
Class: BAC ends.
FEATURES
Source            Location/Qualifiers
                  1..176
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="RPCI-23-453P19"
                    /sex="Female"
                    /lab_host="DH10B"
                    /clone_id="DH10B"
                    /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
EcORI; Site 2: EcORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcORI and EcORI MethIase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
ORIGIN
Query Match       82.0%; Score 16.4; DB 9; Length 176;
Best Local Similarity 83.3%; Pred. No. 3e+03;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```


RESULT 37
BG408882 307 bp mRNA linear EST 13-MAR-2001
LOCUS 9b81c06.y1 Moss EST library PGK Physcomitrella patens cDNA clone
DEFINITION PEP SOURCE ID: PGP CopyA-100612 5' similar to TR:081361 081361 40S
RIBOSOMAL PROTEIN S8. ; mRNA sequence.
ACCESSION BG408882
VERSION BG408882.1 GI:13315227
KEYWORDS EST.
SOURCE Physcomitrella patens
ORGANISM Physcomitrella patens
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
1 (bases 1 to 307)
AUTHORS Quatrano, R., Bashardes, S., Cove, D., Cuming, A., Knight, C.,
Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T.,
Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Steptoe, M., Gibbons, M., Harvey, N., Rittner, E.,
Jackson, Y., McCann, R., Waterson, R. and Wilson, R.
Leeds/Wash U Moss EST Project
Unpublished (1995)
COMMENT Contact: Ralph Quatrano
Leeds/Wash U Moss EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watscn.wustl.edu
Libraries were constructed by Dr. Stavros Bashardes as part of the
Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
trace please contact: Celia Knight (c.d.knight@leeds.ac.uk)
Trace considered overall poor quality
Seq primer: -40RP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..307
/organism="Physcomitrella patens"
/mol_type="mRNA"
/db_xref="taxon:3218"
/clone="PEP SOURCE ID: PGP CopyA-100612"
/tissue_type="gametophore: 30 day old tissue,
ammonium-grown"
/lab_host="DH10B"
/clone_lib="Moss EST library PGP"
/note="Vector: PAMPI; Construction of the cDNA library was
performed by Dr. W. Gregg Clark using a modification of
the cDNA synthesis protocol developed in the laboratory of
Dr. Michael Lovett by Dr. Yulia Korshunova (personal
communication). First polyA + RNA was isolated from total
gametophore RNA using oligo dT magnetic beads. Following
this, first strand cDNA synthesis was performed on the
bead-bound polyA + RNA, during which an oligonucleotide
anchor sequence was incorporated onto the 5'-ends of the
cDNA. PCR amplification was then used to synthesize the
second strand, to amplify the double stranded DNA, and to
incorporate dUTP containing sequences into the ends of the
double stranded cDNA. This DNA was size selected and
cloned into PAMPI using the CloneAMP PAMPI System (Life
Technologies, GibcoBRL) for cloning amplification products
by a non-restriction site dependant process. The cloning
was directional based on sequence asymmetry introduced at
the ends during PCR amplification. The 3' cDNA ends are
proximal to the NotI site of the multiple cloning site in
PAMPI. This annealing mixture was transformed into
ampicillin resistant growth. The resulting clones (about
330,000) were pooled to make the library."

82.0%; Score 16.4; DB 2; Length 307;

ORIGIN
Query Match

Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Oy 2 GGUACAGCCAGGACUACG 19
||:|||||||:
84 GGTAACAGCCAGGACTACG 101
Db
RESULT 38
BP427629 308 bp mRNA linear EST 24-MAY-2004
LOCUS BP427629
DEFINITION BP427629 Mus musculus cerebellum E18-P56 Mus musculus cDNA clone
FD1374. mRNA sequence.
ACCESSION BP427629
VERSION BP427629.1 GI:47589653
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 308)
AUTHORS Furnichi, T. and Sato, A.
TITLE Gene expression during the postnatal cerebellar development
JOURNAL Unpublished (2004)
COMMENT Contact: Teiichi Furnichi
Laboratory for Molecular Neurogenesis
RIKEN Brain Science Institute
2-1 Hirotsawa, Wako, Saitama 351-0198, Japan
Tel: 81-48-467-5906
Fax: 81-48-467-6079
Email: mol-neurogenesis@brain.riken.go.jp, URL:
http://www.brain.riken.go.jp/labs/lmn/index.html.
Location/Qualifiers
1..308
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="FD1374"
/sex="mixed"
/tissue_type="cerebellum"
/dev_stage="E18-P56"
/clone_lib="Mus musculus cerebellum E18-P56"
ORIGIN
Query Match 82.0%; Score 16.4; DB 3; Length 308;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Oy 1 AGGUAACGCCAGGACUAC 18
||:|||||||:
74 AGGTACAGCCAGGCGCTAC 91
Db
RESULT 39
CZ689611 341 bp DNA linear GSS 14-JUN-2005
LOCUS CZ689611
DEFINITION OA_BBA0160P02.r OA_BBA Oryza alta genomic clone OA_BBA0160P02 3',
genomic survey sequence.
ACCESSION CZ689611
VERSION CZ689611.1 GI:70810763
KEYWORDS GSS.
SOURCE Oryza alta
ORGANISM Oryza alta
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 341)
AUTHORS Samtignel, P., Westerman, R., Kim, H., Yu, Y., Watsotaki, M., Yost, D.,
Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C.,
Haffield, J., Soderlund, C., Wing, R. and Jackson, S.A.
TITLE OMAP (Oryza Map Alignment Project) - Purdue University
JOURNAL Unpublished (2004)

COMMENT

Contact: Scott A. Jackson
Jackson Laboratory
Purdue University
915 W. State St., West Lafayette, IN 47907, USA
Tel: 7654963621
Fax: 7654967255

Email: stjackson@purdue.edu
Basecalling by phred version 0.020425.c. This sequence was derived from the raw sequence read by clipping with Lucy version 1.198. Bases 108-448 of the raw sequence (length 1010) were retained after clipping.
Plate: 0160 row: F column: 02
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES

SOURCE

1..341
/organism="Oryza sativa"
/mol_type="genomic DNA"
/db_xref="taxon:52545"
/clone="OA_BBa0160P02"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OA_BBa"
/note="vector: pAG1BAC1, Site_1: HindIII, Site_2: HindIII"

ORIGIN

Query Match 82.0%; Score 16.4; DB 1; Length 341;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
1 AGGACAGCCAGACACTAC 18
|||:|||||:|||||:
269 AGGTACAGCAGACACTAC 286

RESULT 40 373 bp mRNA linear EST 22-MAR-2000
AM598793
LOCUS G88B10.Y1 Moss EST library PPU Physcomitrella patens cDNA clone
DEFINITION PPU_SOURCE ID: PPU61320 5' similar to SM_RS8_ORFSA P49199 408
RIBOSOMAL PROTEIN 88.; mRNA sequence.

ACCESSION AM598793.1 GI:7286306
VERSION AM598793
KEYWORDS EST.
SOURCE Physcomitrella patens
ORGANISM Physcomitrella patens

REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
1 (bases 1 to 373)

Quatrano, R., Bashardes, S., Cove, D., Cumling, A., Knight, C.,
Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T.,
Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B.,
Waller, T., Steptoe, M., Gibbons, M., Harvey, N., Ritter, E.,
Jackson, Y., McCann, R., Waterston, R. and Wilson, R.

Leeds/Mash v Moss EST Project
Unpublished (1999)
Contact: Ralph Quatrano
Leeds/Mash v Moss EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@wustl.wustl.edu
Libraries were constructed by Dr. Stavros Bashardes as part of the
Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
University Genome Sequencing Center for information on obtaining a
clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)

Seq primer: -40RP from Gibco
High quality sequence atop: 262.
Location/Qualifiers
1..373
/organism="Physcomitrella patens"

FEATURES

SOURCE

1..373
/organism="Physcomitrella patens"

/mol_type="mRNA"
/db_xref="taxon:3218"
/clone="PPU_SOURCE_ID: PPU61320"
/tissue_type="protonemata: 7 day old tissue
ammonium-grown"

/lab_host="DH10B"
/clone_lib="Moss EST library PPU"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Construction of the cDNA library was carried out
using Stratagene's 'unizap - cDNA synthesis kit'. cDNA
was constructed using an oligo dt primer/liner that
contains a XhoI site within it. Following ds cDNA
synthesis, EcoRI adapters were ligated to the blunt ends
and sample was digested with XhoI. The result is cDNA
with an EcoRI sticky end on one side and a XhoI sticky
end on the other. This cDNA was ligated directionally in
unizap arms. The vector is designed containing the
pBluescript sequence as well as lambda DNA and cDNA is
cloned within this pBluescript sequence. The vector was
then packaged using Gold giga-packaging extracts. Library
was grown in XL1Blue MRF' cells and amplified. The library
was excised by mass excision using Stratagene's 'Mass
excision kit' that uses exsacit as a helper phage that
releases the pBluescript sequence and circularizes it as
single stranded plasmids that are then packaged (by helper
phage) and secreted out of the host cell as phagemids.
SOLR cells were transformed with phagemids and the library
was plated out on LB-amp plates to select for
transformants. Approximately 1,000,000 colonies were grown
and recovered. The double stranded plasmid library was
recovered by using Qulagen Midl prep kit. 2 micro grams of
each library were used to transform DH10B cells by
electroporation."

ORIGIN

Query Match 82.0%; Score 16.4; DB 1; Length 373;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
2 GGUACAGCCAGACACTAC 19
|||:|||||:|||||:
330 GGTACAGCCAGACACTAC 347

RESULT 41 385 bp mRNA linear EST 24-SEP-2004
CV320420
LOCUS CM3-CN0094-230101-645-b02 CN0094 Homo sapiens cDNA, mRNA sequence.
DEFINITION CV320420
ACCESSION CV320420.1 GI:52643634
VERSION CV320420.1 GI:52643634

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 385)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Coesa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.U.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

CONTACT: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the RAP8SP/LICR Human Cancer Genome
Project. <http://www.ludwig.org.br>.
Location/Qualifiers

FEATURES

source

1..385

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1lb="CN0094"
/note="Organ: colon normal; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 82.0%; Score 16.4; DB 7; Length 385;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 AGUACAGCCAGACUAC 18
|||:|||||:|||||:|
Db 172 AGTACAGCCAGACTTC 155

RESULT 42 390 bp mRNA linear EST 13-JUN-2005
Bj949932
LOCUS Bj949932 pphf full-length cDNA library Physcomitrella patens subsp.
DEFINITION patens cDNA clone pphf5022 5', mRNA sequence.
ACCESSION Bj949932
VERSION Bj949932.1 GI:67577765
KEYWORDS EST.
SOURCE Physcomitrella patens subsp. patens
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
REFERENCE 1 (bases 1 to 390)
Fujita, T., Nishiyama, T., Shin-i, T., Kohara, Y. and Hasebe, M.
Physcomitrella patens EST at a stage of the first asymmetric cell
division of protoplasts
Unpublished (2005)
CONTACT: Tadao Shin-i
JOURNAL Center For Genetic Resource Information
COMMENT National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp
Protoplasts were isolated from the protonemata, further incubated
at 25C under continuous light for 2-3 days. The regenerated cells,
which were rich in cells at a stage during the first asymmetric
cell division, were collected. Total RNA was extracted for
constructing a full-length cDNA library. The database of the EST
clones is available at the PHYSCOBASE (<http://moss.nibb.ac.jp>).
Location/Qualifiers

1..390
/organism="Physcomitrella patens subsp. patens"
/mol_type="mRNA"
/sub_species="patens"
/db_xref="taxon:145481"
/clone="pphf5022"
/tissue_type="regenerated protoplasts (chloronemata)"
/dev_stage="at the first asymmetric cell division of
protoplasts"
/clone_1lb="pphf full-length cDNA library"
/note="Protonemata were inoculated on BCDATG medium for
every ca. 5 days. Protoplasts were isolated from the

FEATURES

source

ORIGIN

Query Match 82.0%; Score 16.4; DB 3; Length 390;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 2 GUUACAGCCAGACUACG 19
|||:|||||:|||||:|
Db 368 GTTACAGCCAGACTTACG 385

protonemata, further incubated at 25C under continuous
light for 2-3 days. The regenerated cells, which were rich
in cells at a stage during the first asymmetric cell
division, were collected. Total RNA was extracted for
constructing a full-length cDNA library."

RESULT 43 395 bp mRNA linear EST 13-JUN-2005
Bj949577
LOCUS Bj949577 pphf full-length cDNA library Physcomitrella patens subsp.
DEFINITION patens cDNA clone pphf4c21 5', mRNA sequence.
ACCESSION Bj949577
VERSION Bj949577.1 GI:67576753
KEYWORDS EST.
SOURCE Physcomitrella patens subsp. patens
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
REFERENCE 1 (bases 1 to 395)
Fujita, T., Nishiyama, T., Shin-i, T., Kohara, Y. and Hasebe, M.
Physcomitrella patens EST at a stage of the first asymmetric cell
division of protoplasts
Unpublished (2005)
CONTACT: Tadao Shin-i
JOURNAL Center For Genetic Resource Information
COMMENT National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp
Protoplasts were isolated from the protonemata, further incubated
at 25C under continuous light for 2-3 days. The regenerated cells,
which were rich in cells at a stage during the first asymmetric
cell division, were collected. Total RNA was extracted for
constructing a full-length cDNA library. The database of the EST
clones is available at the PHYSCOBASE (<http://moss.nibb.ac.jp>).
Location/Qualifiers

1..395
/organism="Physcomitrella patens subsp. patens"
/mol_type="mRNA"
/sub_species="patens"
/db_xref="taxon:145481"
/clone="pphf4c21"
/tissue_type="regenerated protoplasts (chloronemata)"
/dev_stage="at the first asymmetric cell division of
protoplasts"
/clone_1lb="pphf full-length cDNA library"
/note="Protonemata were inoculated on BCDATG medium for
every ca. 5 days. Protoplasts were isolated from the
protonemata, further incubated at 25C under continuous
light for 2-3 days. The regenerated cells, which were rich
in cells at a stage during the first asymmetric cell
division, were collected. Total RNA was extracted for
constructing a full-length cDNA library."

ORIGIN

Query Match 82.0%; Score 16.4; DB 3; Length 395;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 2 GUUACAGCCAGACUACG 19
|||:|||||:|||||:|

DB 308 GGTAAGCCAGCACTACG 325

RESULT 44
LOCUS B1436739
DEFINITION B1436739 400 bp mRNA linear EST 21-AUG-2001
gcs1e03.y1 Moss EST library PPN Physcomitrella patens cDNA clone
PEP SOURCE ID:PPN180905 5' similar to SW:RS8_MALZE 008069 40S
RIBOSOMAL PROTEIN S8. [1] ; mRNA sequence.

ACCESSION B1436739 GI:15261436
VERSION B1436739.1 GI:15261436
KEYWORDS EST.
SOURCE Physcomitrella patens
ORGANISM Physcomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
1 (bases 1 to 400)
Quatrano, R., Bashlades, S., Cove, D., Cumming, A., Knight, C.,
Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T.,
Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Steptoe, M., Gibbons, M., Harvey, N., Ritter, E.,
Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
Leeds/Wash U Moss EST Project
Unpublished (1999)
Contact: Ralph Quatrano
Leeds/Wash U Moss EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Libraries were constructed by Dr. Stavros Bashlades as part of the
physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
University Genome Sequencing Center for information on obtaining a
clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
Trace considered overall poor quality
High quality sequence stop: 1.
Location/Qualifiers
1..400
/organism="Physcomitrella patens"
/mol_type="mRNA"
/db_xref="taxon:3218"
/clone="PEP SOURCE ID:PPN180905"
/tissue_type="protonemata: 7 day old tissue auxin treated"
/lab_host="DH10B"
/clone_lib="Moss EST library PPN"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Construction of the cDNA library was carried out
using Stratagene's 'UnizAP - cDNA synthesis kit'. cDNA was
constructed using an oligo dt primer/linker that contains
a XhoI site within it. Following de cDNA synthesis,
EcoRI adapters were ligated to the blunt ends and sample
was digested with XhoI. The result is cDNA with an EcoRI
sticky end on one side and a XhoI sticky end on the other.
This cDNA was ligated directionally in UnizAP arms. The
vector is designed containing the pBluescript sequence as
well as lambda DNA and cDNA is cloned within this
pBluescript sequence. The vector was then packaged using
Gold gigaPackaging extracts. Library was grown in XL1Blue
MRP cells and amplified. The library was excised by mass
excision using Stratagene's 'Mass excision kit' that uses
exonuclease as a helper phage that releases the pBluescript
sequence and circularises it as single stranded plasmids
that are then packaged (by helper phage) and secreted out
of the host cell as phagemids. SOLR cells were transformed
with phagemids and the library was plated out on LB-amp
plates to select for transformants. Approximately
1,000,000 colonies were grown and recovered. The double
stranded plasmid library was recovered by using Qiaagen
MidI prep kit. 2 micro grams of each library were used to
transform DH10B cells by electroporation."

ORIGIN

Query Match 82.0%; Score 16.4; DB 3; Length 400;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 93 GGTAAGCCAGCACTACG 110

OR 2 GGTAAGCCAGCACTACG 19

RESULT 45
LOCUS BB819360
DEFINITION BB819360 401 bp mRNA linear EST 19-NOV-2001
musculus cDNA clone G730049G01 3', mRNA sequence.
BB819360
BB819360.1 GI:16991989
VERSION BB819360.1 GI:16991989
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 401)
Akimura, T., Aikawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Imotani, K.,
Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Komno, H., Kouda, M.,
Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R.,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Tanaka, T., Tomaru, A., Toyota, T., Watanabe, A., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (AKimura, T., et al.
2001)
Unpublished (2001)
Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Saitoh-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@ac.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
Matsuyama, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A.
and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--364-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Komno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
Location/Qualifiers
1..401
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="G730049G01"
/tissue_type="lung"
/cell_line="RCB-0558 LLC"
/clone_lib="RIKEN full-length enriched, lung RCB-0558 LLC

RESULT 47

division of protoplasts

JOURNAL
COMMENT

Unpublished (2005)
Contact: Tadao Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tsuhit@genes.nig.ac.jp

Protoplasts were inoculated on BCDATG medium for every ca. 5 days. Protoplasts were isolated from the protoplasts, further incubated at 25C under continuous light for 2-3 days. The regenerated cells, which were rich in cells at a stage during the first asymmetric cell division, were collected. Total RNA was extracted for constructing a full-length cDNA library. The database of the EST clones is available at the PHSCOBASE (<http://mos.nibb.ac.jp>).

FEATURES

source

```
1..406
/organism="Physcomitrella patens subsp. patens"
/mol_type="mRNA"
/sub_species="patens"
/db_xref="taxon:145481"
/clone="pphf4c21"
/cisuse_type="regenerated protoplasts (chloroplasts)"
/dev_stage="at the first asymmetric cell division of protoplasts"
/clone_1lb="pphf full-length cDNA library"
/note="Protoplasts were inoculated on BCDATG medium for every ca. 5 days. Protoplasts were isolated from the protoplasts, further incubated at 25C under continuous light for 2-3 days. The regenerated cells, which were rich in cells at a stage during the first asymmetric cell division, were collected. Total RNA was extracted for constructing a full-length cDNA library."
```

ORIGIN

Query Match 82.0%; Score 16.4; DB 3; Length 406;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGUACGCGGACGACUACG 19
||:|||||:|||||
Db 370 GGUACGCGGACGACUACG 353

RESULT 49
BH405922 413 bp DNA linear GSS 19-APR-2002
LOCUS RPCI-23-114A5.SP6S RPCI-23 Mus musculus genomic clone
DEFINITION RPCI-23-114A5, genomic survey sequence.
ACCESSION BH405922
VERSION BH405922.1 GI:17460837
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 413)
Young, J.M., Friedman, C., Williams, E.M., Ross, J.A., Tomnes-Priddy, L. and Trask, B.J.
Different evolutionary processes shaped the mouse and human olfactory receptor gene families
Hum. Mol. Genet. 11 (5), 535-546 (2002)
11875048
Contact: Young JM
Barbara Trask, Division of Human Biology
Fred Hutchinson Cancer Research Center
1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA 98109-1024, USA.
Tel: 206 667 1471
Fax: 206 667 6524
Email: jayoung@hcr.org
Young, J.M., Swartzell, S., Friedman, C., Tomnes-Priddy, L., Lane, R.P.,

FEATURES
source

Wallace, J.C., Mahairas, G.G., Hood, L., and Trask, B.J. End sequences of mouse BACs containing olfactory receptor genes. Unpublished plates: 114 row: A column: 5
Seq primer: SP6S
Class: BAC ends.
Location/Qualifiers
1..413
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-114A5"
/sex="Female"
/lab_host="DH10B"
/clone_1lb="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACs.6; Site 1: EcoRI, Site 2: EcoRI, Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methyase. Size selected DNA was cloned into the pBACs.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN

Query Match 82.0%; Score 16.4; DB 9; Length 413;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGUACAGCCGACGACUAC 18
||:|||||:|||||
Db 55 AAGTACAGCCGACGACTAC 72

RESULT 50

AZ222766 426 bp DNA linear GSS 14-JUN-2000
LOCUS RPCI-23-46U7.TV RPCI-23 Mus musculus genomic clone RPCI-23-46U7,
DEFINITION genomic survey sequence.
ACCESSION AZ222766
VERSION AZ222766.1 GI:9530815
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 426)
Zhao, S., Nierman, W., Feldblum, T., Malek, J., Shatman, S., Akhtar, B., Levins, M., McGinn, S., Teegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-46U7.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhaoc@igr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@delong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (<http://resgcn.com>). BAC end page: http://www.igr.org/cdb/bac_ends/mouse/bac_end_intro.html
Plate: 46 row: J column: 7
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
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/lab_host="mdu108"

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/db_xref="taxon:10090"
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sex="Female"
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/lab_host="DH10B"
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/clone_11b="RPCI-23"
/note="Organ: Kidney/B
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/mce-organ: mceorg/
ECORI; Site_2: EcorI;

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with a combination of selected DNA was clone

BECCRED DNA WAS CLONED
ECORI SITES. THE LIG

DH10B electrocompetent

82.0%; Score 16.

83.3%; Pred. No.

ORIGIN

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					Gaps 0.
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	: :				
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Search completed: March 18, 2006, 20:03:51
Job time : 1948.08 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:35:23 ; Search time 76.5385 Seconds
(without alignments)
464.468 Million cell updates/sec

Title: US-10-800-926-3

Perfect score: 20

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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	15.8	79.0	411	3	US-09-252-991A-14549 Sequence 14549, A
5	15.8	79.0	537	3	US-09-252-991A-14815 Sequence 14815, A
6	15.8	79.0	576	3	US-09-270-767-11626 Sequence 11626, A
7	15.8	79.0	601	3	US-09-949-016-64678 Sequence 64678, A
8	15.8	79.0	601	3	US-09-949-016-64680 Sequence 64680, A
9	15.8	79.0	601	3	US-09-949-016-64681 Sequence 64681, A
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15	15.8	79.0	2004	3	US-09-312-283C-230 Sequence 230, App
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22	15.4	77.0	260286	3	US-09-949-016-17037 Sequence 17037, A
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26	15.2	76.0	987	3	US-09-270-767-10639 Sequence 10639, A
27	15.2	76.0	1029	3	US-09-270-767-4796 Sequence 4796, Ap
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97	14.8	74.0	24602	3	US-09-902-540-1202 Sequence 1202, Ap


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ALIGNMENTS

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RESULT 1
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; Sequence 7959, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7959
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7959

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QY      1 AGGACGACCCAGCAGCTACGA 20
Db      139 AAGACAGCCAGCAGCTACGA 158

RESULT 2
US-09-533-559-3156
; Sequence 3156, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen

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; APPLICANT: Peter Bjørke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3156
; LENGTH: 246
; TYPE: DNA
; ORGANISM: Fusarium venenatum
US-09-533-559-3156

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; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12904
; LENGTH: 1564
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-12904

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; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14549

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; Patent No. 6551795
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; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 1998-07-27
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; LENGTH: 537
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14815

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Best Local Similarity 78.9%; Pred. No. 3.9e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACAGCCGAGGACG 19
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; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 11626
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US-09-270-767-11626

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; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64679
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-64679

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Best Local Similarity 84.2%; Pred. No. 3.9e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGACAGCCGAGGACTACG 20
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RESULT 8
US-09-949-016-64680
; Sequence 64680, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64680
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-64680

Query Match 79.0%; Score 15.8; DB 3; Length 601;
Best Local Similarity 84.2%; Pred. No. 3.9e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGACAGCCGAGGACTACG 20
DB 309 GGACAGCCGAGGACTACG 327

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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016

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; CURRENT FILING DATE: 2000-04-14
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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
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; ORGANISM: Human
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Query Match          79.0%; Score 15.8; DB 3; Length 601;
Best Local Similarity 84.2%; Pred. No. 3.9e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```

QY      2 GGUACAGCCAGACUACGA 20
DB      118 GGCACAGCCAGACTRAGA 136
```

```

RESULT 10
US-09-252-991A-15076
; Sequence 15076, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15076
; LENGTH: 1044
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-15076
```

```

Query Match          79.0%; Score 15.8; DB 3; Length 1044;
Best Local Similarity 78.9%; Pred. No. 4e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```

QY      1 AGGUACAGCCAGACUACG 19
DB      184 AGCTACAGCCTGGACTACG 202
```

```

RESULT 11
US-09-188-930-18
; Sequence 18, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
```

```

; LENGTH: 1057
; TYPE: DNA
; ORGANISM: Rat
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (45)...(45)
; NAME/KEY: unsure
; LOCATION: (53)...(53)
; NAME/KEY: unsure
; LOCATION: (116)...(116)
; NAME/KEY: unsure
; LOCATION: (118)...(118)
; US-09-188-930-18
```

```

Query Match          79.0%; Score 15.8; DB 3; Length 1057;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```

QY      2 GGUACAGCCAGACUACGA 20
DB      1022 GCTACAGCCAGACACGA 1040
```

```

RESULT 12
US-09-312-283C-18
; Sequence 18, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1057
; TYPE: DNA
; ORGANISM: Mouse
; US-09-312-283C-18
```

```

Query Match          79.0%; Score 15.8; DB 3; Length 1057;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```

QY      2 GGUACAGCCAGACUACGA 20
DB      1022 GCTACAGCCAGACACGA 1040
```

```

RESULT 13
US-09-252-991A-14679/C
; Sequence 14679, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14679
```

LENGTH: 1452
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14679

Query Match 79.0%; Score 15.8; DB 3; Length 1452;
Best Local Similarity 78.9%; Pred. No. 4e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGUACAGCCAGCACTUACG 19
DB 693 AGCTACAGCCTGAGCACTACG 675

RESULT 14
US-09-188-930-230
Sequence 230, Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 230
LENGTH: 2004
TYPE: DNA
ORGANISM: Rat
US-09-188-930-230

Query Match 79.0%; Score 15.8; DB 3; Length 2004;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGCACTUACGA 20
DB 995 GCTACAGCCAGCACTUACGA 1013

RESULT 15
US-09-312-283C-230
Sequence 230, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishnand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 230
LENGTH: 2004
TYPE: DNA
ORGANISM: Mouse
US-09-312-283C-230

Query Match 79.0%; Score 15.8; DB 3; Length 2004;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGCACTUACGA 20
DB 995 GCTACAGCCAGCACTUACGA 1013

RESULT 16
US-09-252-991A-14954
Sequence 14954, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107136.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 14954
LENGTH: 2550
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14954

Query Match 79.0%; Score 15.8; DB 3; Length 2550;
Best Local Similarity 78.9%; Pred. No. 4.1e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGUACAGCCAGCACTUACG 19
DB 680 AGCTACAGCCTGAGCACTACG 698

RESULT 17
US-09-949-016-13629
Sequence 13629, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13629
LENGTH: 93894
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(93894)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13629

Query Match 79.0%; Score 15.8; DB 3; Length 93894;
Best Local Similarity 84.2%; Pred. No. 4.4e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGCACTUACGA 20
DB 80915 GGCACAGCCAGCACTUACGA 80933

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/925,695
FILING DATE: 19920807
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 287402/91
FILING DATE: 09-AUG-1991
PRIOR APPLICATION NUMBER: JP 360441/91
FILING DATE: 05-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Weillacher, Robert G.
REGISTRATION NUMBER: 20,531
REFERENCE/DOCKET NUMBER: 06/87-48009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2811
TELEFAX: (202) 659-1462
TELEX: WUI 64470
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 9511 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-925-695-7

Query Match 77.0%; Score 15.4; DB 3; Length 9511;
Best Local Similarity 73.7%; Pred. No. 6.4e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGGACTUACGA 20
DB 2764 GGTAAAGCCAGGACTUACGA 2746

RESULT 22
US-09-949-016-17037
Sequence 17037, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17037
LENGTH: 260286
TYPE: DNA
ORGANISM: Human
US-09-949-016-17037

Query Match 77.0%; Score 15.4; DB 3; Length 260286;
Best Local Similarity 82.4%; Pred. No. 6.4e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGGACTUACGA 17
DB 105679 AGGTAGCCAGGACTUACGA 105695

RESULT 23
US-09-949-016-12106
Sequence 12106, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12106
LENGTH: 260293
TYPE: DNA
ORGANISM: Human
US-09-949-016-12106

Query Match 77.0%; Score 15.4; DB 3; Length 260293;
Best Local Similarity 82.4%; Pred. No. 6.4e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGGACTUACGA 17
DB 105687 AGGTAGCCAGGACTUACGA 105703

RESULT 24
US-09-252-991A-15084
Sequence 15084, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15084
LENGTH: 546
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15084

Query Match 76.0%; Score 15.2; DB 3; Length 546;
Best Local Similarity 80.0%; Pred. No. 7.4e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGGACTUACGA 20
DB 353 AGCTACCGCCAGGACTUACGA 372

RESULT 25
US-09-105-390-33
Sequence 33, Application US/09105390
Patent No. 6288303
GENERAL INFORMATION:
APPLICANT: Rodriguez, Raymond
TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESS: Dehlinger & Associates

```
/ STREET: 350 Cambridge Ave., Suite 250
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94306
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/105,390
/ FILING DATE: Filed herewith
/ CLASSIFICATION:
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: 60/050,675
/ FILING DATE: 25-JUN-97
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pelichory, Joanne R.
/ REGISTRATION NUMBER: P42,995
/ REFERENCE/DOCKET NUMBER: 2000-0455.30
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-324-0880
/ TELEFAX: 650-324-0960
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 33:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 924 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: Coding Sequence
/ LOCATION: 1...924
/ OTHER INFORMATION:
/ US-09-105-390-33

Query Match          76.0%; Score 15.2; DB 3; Length 924;
Best Local Similarity 85.0%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 AGGUACAGCCGAGACUACGA 20
DB      514 AGGACAGCCGAGACUACGA 533

RESULT 26
US-09-270-767-10699/c
/ Sequence 10699, Application US/09270767
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT APPLICATION NUMBER: US/09/270,767
/ CURRENT FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 10699
/ LENGTH: 987
/ TYPE: DNA
/ ORGANISM: Drosophila melanogaster
/ US-09-270-767-10699

Query Match          76.0%; Score 15.2; DB 3; Length 987;
Best Local Similarity 80.0%; Pred. No. 7.5e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 AGGUACAGCCGAGACUACGA 20
DB      650 AGGACAGCCGAGACUACGA 631

/ STREET: 350 Cambridge Ave., Suite 250
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94306
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: 60/050,675
/ FILING DATE: 25-JUN-97
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pelichory, Joanne R.
/ REGISTRATION NUMBER: P42,995
/ REFERENCE/DOCKET NUMBER: 2000-0455.30
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-324-0880
/ TELEFAX: 650-324-0960
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 33:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 924 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: Coding Sequence
/ LOCATION: 1...924
/ OTHER INFORMATION:
/ US-09-105-390-33

Query Match          76.0%; Score 15.2; DB 3; Length 1029;
Best Local Similarity 80.0%; Pred. No. 7.5e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 AGGUACAGCCGAGACUACGA 20
DB      114 ATGTACAGCTTGACACGA 133

RESULT 27
US-09-270-767-4796
/ Sequence 4796, Application US/09270767
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT APPLICATION NUMBER: US/09/270,767
/ CURRENT FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4796
/ LENGTH: 1029
/ TYPE: DNA
/ ORGANISM: Drosophila melanogaster
/ US-09-270-767-4796

Query Match          76.0%; Score 15.2; DB 3; Length 1029;
Best Local Similarity 80.0%; Pred. No. 7.5e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 AGGUACAGCCGAGACUACGA 20
DB      114 ATGTACAGCTTGACACGA 133

RESULT 28
US-09-270-767-20078
/ Sequence 20078, Application US/09270767
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT APPLICATION NUMBER: US/09/270,767
/ CURRENT FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 20078
/ LENGTH: 1029
/ TYPE: DNA
/ ORGANISM: Drosophila melanogaster
/ US-09-270-767-20078

Query Match          76.0%; Score 15.2; DB 3; Length 1029;
Best Local Similarity 80.0%; Pred. No. 7.5e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 AGGUACAGCCGAGACUACGA 20
DB      114 ATGTACAGCTTGACACGA 133

RESULT 29
US-09-105-390-49
/ Sequence 49, Application US/09105390
/ Patent No. 6286303
/ GENERAL INFORMATION:
/ APPLICANT: Rodriguez, Raymond
/ TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
/ TITLE OF INVENTION: and Genes
/ NUMBER OF SEQUENCES: 66
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Dehlinger & Associates
/ STREET: 350 Cambridge Ave., Suite 250
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94306
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: 60/050,675
/ FILING DATE: 25-JUN-97
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pelichory, Joanne R.
/ REGISTRATION NUMBER: P42,995
/ REFERENCE/DOCKET NUMBER: 2000-0455.30
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-324-0880
/ TELEFAX: 650-324-0960
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 33:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 924 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: Coding Sequence
/ LOCATION: 1...924
/ OTHER INFORMATION:
/ US-09-105-390-33

Query Match          76.0%; Score 15.2; DB 3; Length 1029;
Best Local Similarity 80.0%; Pred. No. 7.5e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 AGGUACAGCCGAGACUACGA 20
DB      114 ATGTACAGCTTGACACGA 133
```

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,390
FILING DATE: Filed herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,675
FILING DATE: 25-JUN-97
ATTORNEY/AGENT INFORMATION:
NAME: Petichory, Joanne R.
REGISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 2000-0455.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 1035 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...1035
OTHER INFORMATION:
US-09-105-390-49

Query Match 76.0%; Score 15.2; DB 3; Length 1035;
Best Local Similarity 85.0%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGUAACGCCAGACUACGA 20
Db 625 AGGACAGCCAGACATCGA 644

RESULT 30
US-09-252-991A-14826
Sequence 14826, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 14826
LENGTH: 1521
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14826

Query Match 76.0%; Score 15.2; DB 3; Length 1521;
Best Local Similarity 80.0%; Pred. No. 7.6e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGUAACGCCAGACUACGA 20
Db 985 AGCTACGCCAGACGACGA 1004

RESULT 31
US-09-252-991A-14538/c
Sequence 14538, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 14538
LENGTH: 1596
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14538

Query Match 76.0%; Score 15.2; DB 3; Length 1596;
Best Local Similarity 80.0%; Pred. No. 7.6e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGUAACGCCAGACUACGA 20
Db 606 AGCTACGCCAGACGACGA 587

RESULT 32
US-09-105-390-1
Sequence 1, Application US/09105390
Patent No. 6288303
GENERAL INFORMATION:
APPLICANT: Rodriguez, Raymond
TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESSES:
ADDRESSER: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,390
FILING DATE: Filed herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,675
FILING DATE: 25-JUN-97
ATTORNEY/AGENT INFORMATION:
NAME: Petichory, Joanne R.
REGISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 2000-0455.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2230 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-105-390-1

Query Match 76.0%; Score 15.2; DB 3; Length 2230;
Best Local Similarity 85.0%; Pred. No. 7.7e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AGGACAGCCAGGACGACGA 20
1817 AGGACAGCCAGGACGACGA 1836
DB

RESULT 33
US-09-949-016-13044
Sequence 13044, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13044
LENGTH: 9319
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(9319)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13044

Query Match 76.0%; Score 15.2; DB 3; Length 9319;
Best Local Similarity 75.0%; Pred. No. 7.9e+02;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGACAGCCAGGACGACGA 20
DB 8946 AGGACAGCCAGGACGACGA 8965

RESULT 34
US-09-949-016-14958/C
Sequence 14958, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14958
LENGTH: 23406
TYPE: DNA
ORGANISM: Human
US-09-949-016-14958

Query Match 76.0%; Score 15.2; DB 3; Length 23406;
Best Local Similarity 80.0%; Pred. No. 8.1e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGACAGCCAGGACGACGA 20
DB 12749 AGCTACAGCCAGGACGACCA 12730

RESULT 35
US-09-949-016-15248
Sequence 15248, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15248
LENGTH: 28283
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(28283)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15248

Query Match 76.0%; Score 15.2; DB 3; Length 28283;
Best Local Similarity 80.0%; Pred. No. 8.1e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGACAGCCAGGACGACGA 20
DB 22011 AGGACAGCTCAGGACGACGA 22030

RESULT 36
US-09-949-016-14213/C
Sequence 14213, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14213
LENGTH: 30456
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(30456)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14213

Query Match 76.0%; Score 15.2; DB 3; Length 30456;
Best Local Similarity 75.0%; Pred. No. 8.1e+02;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGGACTACGA 20
DB 6160 AGTCTCTGCGAGGCTACGA 6141

RESULT 37
US-09-949-016-15420
; Sequence 15420, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15420
; LENGTH: 47375
; TYPE: DNA
; ORGANISM: Human
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (1)...(47375)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15420

Query Match 76.0%; Score 15.2; DB 3; Length 47375;
Best Local Similarity 75.0%; Pred. No. 8.2e+02;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGGACTACGA 20
DB 2718 AGCTACAGCCAGGCTTACGA 2737

RESULT 38
US-09-949-016-11995/c
; Sequence 11995, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11995
; LENGTH: 60304
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11995

Query Match 76.0%; Score 15.2; DB 3; Length 60304;

Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGGACTACGA 20
DB 12691 AGCTACAGCCAGGACTACCA 12672

RESULT 39
US-09-949-016-17264/c
; Sequence 17264, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17264
; LENGTH: 60304
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17264

Query Match 76.0%; Score 15.2; DB 3; Length 60304;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGGACTACGA 20
DB 12691 AGCTACAGCCAGGACTACCA 12672

RESULT 40
US-09-949-016-12361/c
; Sequence 12361, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12361
; LENGTH: 69874
; TYPE: DNA
; ORGANISM: Human
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (1)...(69874)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12361

Query Match 76.0%; Score 15.2; DB 3; Length 69874;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;

Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 AGGACAGCCAGACTGACGA 20
1721 AGGACAGCTGACGACTGCGA 1702

RESULT 41
US-09-949-016-13049/c
Sequence 13049, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13049
LENGTH: 69874
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(69874)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13049

Query Match 76.0%; Score 15.2; DB 3; Length 69874;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGACAGCCAGACTGACGA 20
Db 1721 AGGACAGCTGACGACTGCGA 1702

RESULT 42
US-09-750-580-1/c
Sequence 1, Application US/09750580
Patent No. 6453280
GENERAL INFORMATION:
APPLICANT: Yen, Frances
APPLICANT: Denison, Blake
APPLICANT: Bour, Barbara
APPLICANT: Bihain, Bernard
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
APPLICANT: Ebbets-Reed, Dana
APPLICANT: Salter-Cid, Luisa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITTING NEOPLASTIC CELL GROWTH
FILE REFERENCE: 89.US2.CIP
CURRENT APPLICATION NUMBER: US/09/750,580
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 09/599,362
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: PCT/IB00/0101
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: PCT/IB99/02058
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: US 49/469/099
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 60/113,686
PRIOR FILING DATE: 1998-12-22

PRIOR APPLICATION NUMBER: US 60/141,032
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 81001
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 10946..12946
OTHER INFORMATION: 5/regulatory region
NAME/KEY: exon
LOCATION: 12947..12958
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 13470..13526
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 13641..13752
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 14271..15968
OTHER INFORMATION: exon 4
NAME/KEY: misc_feature
LOCATION: 15969..17969
OTHER INFORMATION: 3/regulatory region
NAME/KEY: allele
LOCATION: 1239
OTHER INFORMATION: 20-828-311 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 12347
OTHER INFORMATION: 17-42-319 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 15241
OTHER INFORMATION: 17-41-250 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 42218
OTHER INFORMATION: 20-841-149 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 45442
OTHER INFORMATION: 20-842-115 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 77058
OTHER INFORMATION: 20-853-415 : polymorphic base C or T
NAME/KEY: primer_bind
LOCATION: 929..949
OTHER INFORMATION: 20-828.pu
NAME/KEY: primer_bind
LOCATION: 1357..1377
OTHER INFORMATION: 20-828.rp complement
NAME/KEY: primer_bind
LOCATION: 12029..12050
OTHER INFORMATION: 17-42.pu
NAME/KEY: primer_bind
LOCATION: 12581..12603
OTHER INFORMATION: 17-42.rp complement
NAME/KEY: primer_bind
LOCATION: 14992..15012
OTHER INFORMATION: 17-41.pu
NAME/KEY: primer_bind
LOCATION: 15460..15482
OTHER INFORMATION: 17-41.rp complement
NAME/KEY: primer_bind
LOCATION: 42070..42090
OTHER INFORMATION: 20-841.pu
NAME/KEY: primer_bind
LOCATION: 42572..42591
OTHER INFORMATION: 20-841.rp complement
NAME/KEY: primer_bind
LOCATION: 45328..45347
OTHER INFORMATION: 20-842.pu
NAME/KEY: primer_bind

Query Match	76.0%	Score 15.2	DB 3	Length 81001
Best Local Similarity	75.0%	Pred. No. 8.2e+02		
Matches 15; Conservative		2; Mismatches 3;	Indels 0;	Gaps 0;

```

RESULT 43
US-09-949-016-14881/c
; Sequence 14881, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH THE DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14881
; LENGTH: 146307
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14881

Query Match      76.0%; Score 15.2; DB 3; Length 146307;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

CY          1 AGGACAGCCAGCAGACTCAGA 20
||| ||||||||| : ||
Db          39701 AGGCACAGCCAGCAGACTCAGA 39682

RESULT 44
US-09-949-016-14882/c
; Sequence 14882, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14882
; LENGTH: 146307
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14882

Query Match      76.0%; Score 15.2; DB 3; Length 146307;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

CY          1 AGGACAGCCAGCAGACTCAGA 20
||| ||||||||| : ||
Db          39701 AGGCACAGCCAGCAGACTCAGA 39682

```

39701 AGGCACAGCCAGACTCAGA 39682
 39701 AGGCACAGCCAGACTCAGA 39682

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; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14883
; LENGTH: 146307
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14883

Query Match          76.0%; Score 15.2; DB 3; Length 146307;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGACAGCCAGGACTCAGA 20
DB 39701 AGGACAGCCAGGACTCAGA 39682

RESULT 46
US-09-949-016-14884/c
; Sequence 14884, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14884
; LENGTH: 146307
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14884

Query Match          76.0%; Score 15.2; DB 3; Length 146307;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGACAGCCAGGACTCAGA 20
DB 39701 AGGACAGCCAGGACTCAGA 39682

RESULT 47
US-09-949-016-14885/c
; Sequence 14885, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
```

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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14885
; LENGTH: 146307
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14885

Query Match          76.0%; Score 15.2; DB 3; Length 146307;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGACAGCCAGGACTCAGA 20
DB 39701 AGGACAGCCAGGACTCAGA 39682

RESULT 48
US-09-949-016-14886/c
; Sequence 14886, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14886
; LENGTH: 146307
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14886

Query Match          76.0%; Score 15.2; DB 3; Length 146307;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGACAGCCAGGACTCAGA 20
DB 39701 AGGACAGCCAGGACTCAGA 39682

RESULT 49
US-09-949-016-14887/c
; Sequence 14887, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
```


; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 14887
; LENGTH: 146307
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14887

Query Match 76.0%; Score 15.2; DB 3; Length 146307;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 AGGACAGCCAGGACTCAGA 20
Db 39701 AGGACAGCCAGGACTCAGA 39682

RESULT 50
US-09-949-016-14888/C
; Sequence 14888, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 14888
; LENGTH: 146307
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14888

Query Match 76.0%; Score 15.2; DB 3; Length 146307;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 AGGACAGCCAGGACTCAGA 20
Db 39701 AGGACAGCCAGGACTCAGA 39682

Search completed: March 18, 2006, 18:40:11
Job time : 103.538 secs

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391	14.8	74.0	1327	6	US-10-165-124A-170	Sequence 170, App
392	14.8	74.0	1327	6	US-10-165-124A-170	Sequence 170, App
393	14.8	74.0	1327	6	US-10-145-087A-170	Sequence 170, App
394	14.8	74.0	1327	6	US-10-017-086A-170	Sequence 170, App
395	14.8	74.0	1327	6	US-10-164-829A-170	Sequence 170, App
396	14.8	74.0	1327	6	US-10-164-829A-170	Sequence 170, App
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426	14.8	74.0	1327	8	US-10-918-851-170	Sequence 170, App
427	14.8	74.0	1327	8	US-10-805-667-170	Sequence 170, App
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459	14.8	74.0	1327	10	US-10-821-122A-729S	Sequence 170, App
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976 14.2 71.0 277 7 US-10-424-599-9946 Sequence 9946, Ap
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979 14.2 71.0 342 8 US-10-425-115-179790 Sequence 179790, A
980 14.2 71.0 367 8 US-10-425-115-19742 Sequence 19742, A
981 14.2 71.0 378 6 US-10-029-386-16309 Sequence 16309, A
982 14.2 71.0 385 9 US-10-950-009-169 Sequence 169, App
983 14.2 71.0 392 7 US-10-424-599-40113 Sequence 40113, A
984 14.2 71.0 408 3 US-09-803-713-1908 Sequence 1908, Ap
985 14.2 71.0 408 3 US-10-779-543-15178 Sequence 15178, A
986 14.2 71.0 423 4 US-09-925-065A-855911 Sequence 855911, A
987 14.2 71.0 423 9 US-10-779-543-13240 Sequence 13240, A
988 14.2 71.0 425 8 US-10-425-115-159641 Sequence 159641, A
989 14.2 71.0 435 3 US-09-876-889-1170 Sequence 1170, App
990 14.2 71.0 435 8 US-10-425-115-110738 Sequence 110738, A
991 14.2 71.0 447 8 US-10-425-115-13568 Sequence 13568, A
992 14.2 71.0 455 9 US-10-450-763-16178 Sequence 16178, A
993 14.2 71.0 458 8 US-10-425-115-43280 Sequence 43280, A
994 14.2 71.0 459 3 US-09-918-995-15779 Sequence 15779, A
995 14.2 71.0 460 5 US-10-198-846-6132 Sequence 6132, Ap
996 14.2 71.0 461 3 US-09-864-761-4406 Sequence 4406, Ap
997 14.2 71.0 472 3 US-09-918-995-13974 Sequence 13974, A
998 14.2 71.0 476 9 US-10-956-157-5119 Sequence 5119, Ap
999 14.2 71.0 476 9 US-10-956-157-10354 Sequence 10354, A
1000 14.2 71.0 480 4 US-09-925-065A-498925 Sequence 498925, A

ALIGNMENTS

RESULT 1

US-09-888-326-68
; Sequence 68, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AMS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 68
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-888-326-68

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.2;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACAGCCAGGACUACGA 20
DB 1 AGGTACAGCCAGGACTACGA 20

RESULT 2

US-09-776-479-391
; Sequence 391, Application US/09776479
; Publication No. US20030087846A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.

; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 391
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-391

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.2;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACAGCCAGGACUACGA 20
DB 1 AGGTACAGCCAGGACTACGA 20

RESULT 3

US-09-776-479-391
; Sequence 391, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 391
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-391

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.2;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACAGCCAGGACUACGA 20
DB 1 AGGTACAGCCAGGACTACGA 20

RESULT 4

US-10-112-653-379
; Sequence 379, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Kriegl, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060 (AMS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29

PRIOR APPLICATION NUMBER: US 60/279,642
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 379
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-379

Query Match 100.0%; Score 20; DB 5; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.2;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGUACAGCCAGACUACGA 20
|||:|||||:|||||:|||||
Db 1 AGGTACAGCCAGACTACGA 20

RESULT 5
US-10-017-995-391
Sequence 391, Application US/10017995
Publication No. US20030055014A1
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
FILE REFERENCE: C1037/7025 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/017,995
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 60/255,534
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 391
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-10-017-995-391

Query Match 100.0%; Score 20; DB 5; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.2;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGUACAGCCAGACUACGA 20
|||:|||||:|||||:|||||
Db 1 AGGTACAGCCAGACTACGA 20

RESULT 6
US-10-314-578-391
Sequence 391, Application US/103314578
Publication No. US20030212026A1
GENERAL INFORMATION:
APPLICANT: Kries, Arthur M.
APPLICANT: Schetter, Christian
APPLICANT: Vollmer, Jorg
TITLE OF INVENTION: Immunostimulatory Nucleic Acids
FILE REFERENCE: C1039/7035 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/314,578
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 60/156,113
PRIOR FILING DATE: 1999-09-25
PRIOR APPLICATION NUMBER: US 60/156,135
PRIOR FILING DATE: 1999-09-27
PRIOR APPLICATION NUMBER: US 60/227,436
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 1145
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 391

LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-10-314-578-391

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.2;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGUACAGCCAGACUACGA 20
|||:|||||:|||||:|||||
Db 1 AGGTACAGCCAGACTACGA 20

RESULT 7
US-10-831-778-391
Sequence 391, Application US/10831778
Publication No. US20040235774A1
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
APPLICANT: Petersen, Deanna M.
APPLICANT: Fouron, Yves
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
TITLE OF INVENTION: Treatment of Asthma and Allergy
FILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/831,778
CURRENT FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 391
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-10-831-778-391

Query Match 100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.2;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGUACAGCCAGACUACGA 20
|||:|||||:|||||:|||||
Db 1 AGGTACAGCCAGACTACGA 20

RESULT 8
US-10-800-926-3
Sequence 3, Application US/10800926
Publication No. US20050032731A1
GENERAL INFORMATION:
APPLICANT: MARSHALL, WILLIAM E.
TITLE OF INVENTION: OLIGORIBONUCLEOTIDES ALERT THE IMMUNE SYSTEM OF ANIMALS
FILE REFERENCE: P01936US06
CURRENT APPLICATION NUMBER: US/10/800,926
CURRENT FILING DATE: 2004-03-15
PRIOR APPLICATION NUMBER: 09/883,550
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 09/193,653
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 08/739,264
PRIOR FILING DATE: 1996-10-29
PRIOR APPLICATION NUMBER: 08/517,016
PRIOR FILING DATE: 1995-08-18
PRIOR APPLICATION NUMBER: 08/376,175
PRIOR FILING DATE: 1995-01-20
PRIOR APPLICATION NUMBER: 08/059,745
PRIOR FILING DATE: 1993-05-11

NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 3
LENGTH: 20
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-800-926-3

Query Match 100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20
DB 1 AGGUACAGCCAGACUACGA 20

RESULT 9
US-10-152-319A-532
Sequence 532, Application US/10152319A
Publication No. US20040072160A1

GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Higgs, Brandon
APPLICANT: Castle, Arthur
APPLICANT: Slashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,808
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/315,047
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: US 60/324,928
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/330,867
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/330,462
PRIOR FILING DATE: 2001-10-22
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2221
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 532
LENGTH: 5253
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. AB012214
US-10-152-319A-532

Query Match 90.0%; Score 18; DB 7; Length 5253;
Best Local Similarity 88.9%; Pred. No. 30;

Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGUAACAGCCAGACUACGA 19
DB 2679 GGTAACAGCCAGACTACG 2696

RESULT 10
US-10-425-115-14343
Sequence 14343, Application US/10425115
Publication No. US2004021472A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 14343
LENGTH: 281
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MHT4577_113070C.1
US-10-425-115-14343

Query Match 84.0%; Score 16.8; DB 8; Length 281;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20
DB 160 AGGTACAGCCAGACTACGA 179

RESULT 11
US-09-925-065A-693333/c
Sequence 693333, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 693333
LENGTH: 605
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-693333

Query Match 84.0%; Score 16.8; DB 4; Length 605;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20
DB 398 AGGCACAGCCAGACTACGA 379

RESULT 12

US-09-925-065A-73830
; Sequence 73830, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73830
; LENGTH: 740
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-73830

Query Match 84.0%; Score 16.8; DB 4; Length 740;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGUAAGCCGAGACTUACA 20
 |||:|||||||:|:|
DB 66 AGGTACAGCCAGCGCTACGA 85

RESULT 13
US-10-322-281-33
; Sequence 33, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 145068
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(145068)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-33

Query Match 84.0%; Score 16.8; DB 7; Length 145068;
Best Local Similarity 85.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGUAAGCCGAGACTUACA 20
 |||:|||||||:|:|
DB 50545 AGGTACTGCGCAGACACACA 50564

RESULT 14
US-10-653-047-3156
; Sequence 3156, Application US/10653047
; Publication No. US20040229367A1

GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Ray
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjørke Olsen
; TITLE OF INVENTION: Methods for Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/10/653,047
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/533,559
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/273,623
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3156
; LENGTH: 246
; TYPE: DNA
; ORGANISM: Fusarium venenatum
US-10-653-047-3156

Query Match 82.0%; Score 16.4; DB 8; Length 246;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GUACAGCCGAGACUACA 20
 |||:|||||||:|:|
DB 154 GTACAGCCGAGACTUACA 171

RESULT 15
US-09-925-065A-369463
; Sequence 369463, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 369463
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-369463

Query Match 82.0%; Score 16.4; DB 4; Length 586;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGUAAGCCGAGACUAC 18
 |||:|||||||:|:|
DB 39 AGGTAGCCGAGACTAC 56

RESULT 16
US-10-425-114-8343

```
Sequence 8343, Application US/10425114
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Tabaska, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 8343
LENGTH: 1308
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 700748540_FLI
US-10-425-114-8343

Query Match      82.0%; Score 16.4; DB 7; Length 1308;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 GGUACGCCAGCAGCAGC 19
DB      44 GATACGCCAGCAGCAGC 61

RESULT 17
US-10-034-650-1/c
Sequence 1, Application US/10034650
GENERAL INFORMATION:
APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000128
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 09/474,377
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 31632
TYPE: DNA
ORGANISM: Mus musculus
US-10-034-650-1

Query Match      82.0%; Score 16.4; DB 6; Length 31632;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 AGGUACGCCAGCAGCAGC 18
DB      26940 AGGTACGCCAGCAGCCTAC 26923

RESULT 18
US-09-997-722-199
Sequence 199, Application US/09997722
GENERAL INFORMATION:
APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
```

```
FILE REFERENCE: A-71171/RMS/DCF
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PatentIn version 3.1
SEQ ID NO 199
LENGTH: 96599
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc feature
LOCATION: (9652)..(10001)
OTHER INFORMATION: "n" at positions 4189 through 4208 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (9652)..(10001)
OTHER INFORMATION: "n" at positions 9652 through 10001 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (27805)..(27824)
OTHER INFORMATION: "n" at positions 27805 through 27824 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (54062)..(54139)
OTHER INFORMATION: "n" at positions 54062 through 54139 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (88386)..(88405)
OTHER INFORMATION: "n" at positions 88386 through 88405 can be any base.
US-09-997-722-199

Query Match      82.0%; Score 16.4; DB 3; Length 96599;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 AGGUACGCCAGCAGCAGC 18
DB      28454 AGGTACGCCAGCAGCCTAC 28471

RESULT 19
US-10-085-117-250
Sequence 250, Application US/10085117
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: 529452000121
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 250
LENGTH: 168749
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: variation
LOCATION: (1)..(168749)
OTHER INFORMATION: n = any nucleotide
US-10-085-117-250

Query Match      82.0%; Score 16.4; DB 6; Length 168749;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

Qy 1 AGUACGCCAGGACUAC 18
|||:|||||:|||||:|
Db 89636 AGGACACTGACGACTAC 89653

RESULT 20
US-11-097-143-27752
; Sequence 27752, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27752
; LENGTH: 2550
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-27752

Query Match 80.0%; Score 16; DB 10; Length 2550;
Best Local Similarity 87.5%; Pred. No. 3.2e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GUACGCCAGGACUAC 18
|||:|||||:|||||:|
Db 1447 GTACGCCAGGACTAC 1462

RESULT 21
US-11-097-143-12095
; Sequence 12095, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383

PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12095
; LENGTH: 2668
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-12095

Query Match 80.0%; Score 16; DB 10; Length 2668;
Best Local Similarity 87.5%; Pred. No. 3.2e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GUACGCCAGGACUAC 18
|||:|||||:|||||:|
Db 1565 GTACGCCAGGACTAC 1580

RESULT 22
US-11-097-143-27751/C
; Sequence 27751, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27751
; LENGTH: 4972
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-27751

Query Match 80.0%; Score 16; DB 10; Length 4972;
Best Local Similarity 87.5%; Pred. No. 3.2e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GUACGCCAGGACUAC 18
|||:|||||:|||||:|
Db 2160 GTACGCCAGGACTAC 2145

RESULT 23
US-11-097-143-12094/C
; Sequence 12094, Application US/11097143

```
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLO000728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12094
LENGTH: 4989
TYPE: DNA
ORGANISM: DROSOPHILA
US-11-097-143-12094

Query Match      80.0%; Score 16; DB 10; Length 4989;
Best Local Similarity 87.5%; Pred. No. 3.2e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 GUACAGCCGAGACTAC 18
DB      2160 GTACAGCCGAGACTAC 2145

RESULT 24
US-09-997-722-85
Sequence 85, Application US/09997722
Publication No. US20040072154A1
GENERAL INFORMATION:
APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71171/RMS/DCP
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PatentIn version 3.1
SEQ ID NO 85
LENGTH: 96600
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc feature
LOCATION: (7785)..(7808)
OTHER INFORMATION: "n" at positions 7789 through 7808 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (9978)..(9997)
OTHER INFORMATION: "n" at positions 9978 through 9997 can be any base.
FEATURE:
```

```
NAME/KEY: misc feature
LOCATION: (14125)..(14144)
OTHER INFORMATION: "n" at positions 14125 through 14144 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (20780)..(20799)
OTHER INFORMATION: "n" at positions 20780 through 20799 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (27757)..(27816)
OTHER INFORMATION: "n" at positions 27797 through 27816 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (31149)..(31168)
OTHER INFORMATION: "n" at positions 31149 through 31168 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (33786)..(33805)
OTHER INFORMATION: "n" at positions 33786 through 33805 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (34873)..(34892)
OTHER INFORMATION: "n" at positions 34873 through 34892 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (45961)..(45980)
OTHER INFORMATION: "n" at positions 45961 through 45980 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (50121)..(50140)
OTHER INFORMATION: "n" at positions 50121 through 50140 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (53877)..(53896)
OTHER INFORMATION: "n" at positions 53877 through 53896 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (55271)..(55290)
OTHER INFORMATION: "n" at positions 55271 through 55290 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (57012)..(57031)
OTHER INFORMATION: "n" at positions 57012 through 57031 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (60915)..(60934)
OTHER INFORMATION: "n" at positions 60915 through 60934 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (63387)..(63406)
OTHER INFORMATION: "n" at positions 63387 through 63406 can be any base.
US-09-997-722-85

Query Match      80.0%; Score 16; DB 3; Length 96600;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 GUACAGCCGAGACTAC 18
DB      91766 GTACAGCCGAGACTAC 91781

RESULT 25
US-10-624-149A-2/c
Sequence 2, Application US/10624149A
Publication No. US20040109873A1
GENERAL INFORMATION:
APPLICANT: Neubauer, Antoine
APPLICANT: Ziegler, Christina
TITLE OF INVENTION: GM-Negative EBV-Mutants without Heterologous Elements
FILE REFERENCE: 1/1372
CURRENT APPLICATION NUMBER: US/10/624,149A
CURRENT FILING DATE: 2003-07-21
```



```
/ PRIOR APPLICATION NUMBER: 60/403,282
/ PRIOR FILING DATE: 2002-08-14
/ PRIOR APPLICATION NUMBER: DE 10233064
/ PRIOR FILING DATE: 2002-07-19
/ PRIOR APPLICATION NUMBER: DE 10317008
/ PRIOR FILING DATE: 2003-04-11
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: Patentin Version 3.0
/ SEQ ID NO: 2
/ LENGTH: 145597
/ TYPE: DNA
/ ORGANISM: Equine herpesvirus 4
/ PUBLICATION INFORMATION:
/ AUTHORS: Telford, B.A.
/ AUTHORS: Watson, M.S.
/ AUTHORS: Perry, J.
/ AUTHORS: Cullinane, A.A.
/ AUTHORS: Davison, A.J.
/ TITLE: The DNA sequence of equine herpesvirus-4
/ JOURNAL: J. Gen. Virol.
/ VOLUME: 79
/ ISSUE: 5
/ PAGES: 1197-1203
/ DATE: MAY-1998
/ DATABASE ACCESSION NUMBER: NC 001844, NCBI
/ DATABASE ENTRY DATE: 2000-08-01
/ US-10-624-149A-2
```

```
Query Match      80.0%; Score 16; DB 7; Length 145597;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      2  GGUACAGCCAGACUA 17
Db      76347  GGTACAGCCAGACTA 76332
```

```
RESULT 26
US-09-925-065A-132060/C
/ Sequence 132060, Application US/09925065A
/ Publication No. US20050228172A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 132060
/ LENGTH: 364
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-925-065A-132060
```

```
Query Match      79.0%; Score 15.8; DB 4; Length 364;
Best Local Similarity 78.9%; Pred. No. 4.3e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      2  GGUACAGCCAGACUA 20
Db      93  GGTGACGCCAGGCTACGA 75
```

```
RESULT 27
US-09-925-065A-290634/C
/ Sequence 290634, Application US/09925065A
/ Publication No. US20050228172A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 290634
/ LENGTH: 533
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-925-065A-290634
```

```
Query Match      79.0%; Score 15.8; DB 4; Length 533;
Best Local Similarity 78.9%; Pred. No. 4.2e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      1  AGUACAGCCAGACUACG 19
Db      347  AAGTACAGCCAGGACTAG 329
```

```
RESULT 28
US-09-925-065A-290636/C
/ Sequence 290636, Application US/09925065A
/ Publication No. US20050228172A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 290636
/ LENGTH: 533
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-925-065A-290636
```

```
Query Match      79.0%; Score 15.8; DB 4; Length 533;
Best Local Similarity 78.9%; Pred. No. 4.2e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1 AGGACAGCCGAGACTGAC 19
 ||:|||||||:|
 Db 347 AAGTACAGCCAGACTAG 329

RESULT 29

US-10-357-930-15913/C
 ; Sequence 15913, Application US/10357930
 ; Publication No. US20040259086A1

GENERAL INFORMATION:

APPLICANT: Schlegel, Robert
 APPLICANT: Endege, Wilson

APPLICANT: Monahan, John

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 TITLE OF INVENTION: HUMAN PROSTATE CANCER

FILE REFERENCE: MRI-007BCN

CURRENT APPLICATION NUMBER: US/10/357, 930

PRIOR FILING DATE: 2003-02-04

PRIOR APPLICATION NUMBER: 09/785, 276

PRIOR FILING DATE: 2003-02-16

PRIOR APPLICATION NUMBER: 60/183, 319

PRIOR FILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: 60/189, 862

PRIOR FILING DATE: 2000-03-16

PRIOR APPLICATION NUMBER: 60/207, 454

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 60/211, 314

PRIOR FILING DATE: 2000-06-09

PRIOR APPLICATION NUMBER: 60/219, 007

PRIOR FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: 60/255, 281

PRIOR FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 62232

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 15913

LENGTH: 542

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

LOCATION: 502_516, 518, 525

OTHER INFORMATION: n = A,T,C or G

US-10-357-930-15913

Query Match 79.0%; Score 15.8; DB 8; Length 542;

Best Local Similarity 78.9%; Pred. No. 4.2e+02;

Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGACAGCCGAGACTGAC 19
 ||:|||||||:|
 Db 90 AAGTACAGCCAGACTAG 72

RESULT 30

US-09-925-065A-813093
 ; Sequence 813093, Application US/09925065A
 ; Publication No. US2005028172A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.
 TITLE OF INVENTION: Identification and Mapping of Single
 TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
 FILE REFERENCE: 108827.135
 CURRENT APPLICATION NUMBER: US/09/925, 065A
 PRIOR FILING DATE: 2001-08-08
 PRIOR APPLICATION NUMBER: US 60/243, 096
 PRIOR FILING DATE: 2000-10-24
 PRIOR APPLICATION NUMBER: US 60/252, 147
 PRIOR FILING DATE: 2000-11-20
 PRIOR APPLICATION NUMBER: US 60/250, 092
 PRIOR FILING DATE: 2000-11-30
 PRIOR APPLICATION NUMBER: US 60/261, 766
 PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289, 846
 PRIOR FILING DATE: 2001-05-09
 NUMBER OF SEQ ID NOS: 957086
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 813093
 LENGTH: 572
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-925-065A-813093

Query Match 79.0%; Score 15.8; DB 4; Length 572;

Best Local Similarity 84.2%; Pred. No. 4.2e+02;

Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGACAGCCGAGACTAGA 20
 ||:|||||||:|
 Db 122 GGACAGCCGAGACTAGA 140

RESULT 31

US-10-357-930-45741/C
 ; Sequence 45741, Application US/10357930
 ; Publication No. US20040259086A1

GENERAL INFORMATION:

APPLICANT: Schlegel, Robert
 APPLICANT: Endege, Wilson

APPLICANT: Monahan, John

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 TITLE OF INVENTION: HUMAN PROSTATE CANCER

FILE REFERENCE: MRI-007BCN

CURRENT APPLICATION NUMBER: US/10/357, 930

PRIOR FILING DATE: 2003-02-04

PRIOR APPLICATION NUMBER: 09/785, 276

PRIOR FILING DATE: 2003-02-16

PRIOR APPLICATION NUMBER: 60/183, 319

PRIOR FILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: 60/189, 862

PRIOR FILING DATE: 2000-03-16

PRIOR APPLICATION NUMBER: 60/207, 454

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 60/211, 314

PRIOR FILING DATE: 2000-06-09

PRIOR APPLICATION NUMBER: 60/219, 007

PRIOR FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: 60/255, 281

PRIOR FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 62232

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 45741

LENGTH: 592

TYPE: DNA

ORGANISM: Homo sapiens

US-10-357-930-45741

Query Match 79.0%; Score 15.8; DB 8; Length 592;

Best Local Similarity 78.9%; Pred. No. 4.2e+02;

Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGACAGCCGAGACTGAC 19
 ||:|||||||:|
 Db 136 AAGTACAGCCAGACTAG 118

RESULT 32

US-10-767-701-25552
 ; Sequence 25552, Application US/10767701
 ; Publication No. US20040172684A1

GENERAL INFORMATION:

APPLICANT: Zhou, Yihua
 APPLICANT: Kovalic, David K.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

```
/ TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
/ FILE REFERENCE: 38-21(53535)B
/ CURRENT APPLICATION NUMBER: US/10/767,701
/ CURRENT FILING DATE: 2004-01-29
/ NUMBER OF SEQ ID NOS: 63128
/ SEQ ID NO 25552
/ LENGTH: 610
/ TYPE: DNA
/ ORGANISM: Sorghum bicolor
/ FEATURE:
/ OTHER INFORMATION: Clone ID: 30963281
/ US-10-767-701-25552

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 7; Length 610;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGUACAGCCAGGACTUACG 19
Db 334 AGGTCAGCGAGGACTTACG 352

RESULT 33
US-10-425-115-59643
/ Sequence 59643, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 59643
/ LENGTH: 678
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(678)
/ OTHER INFORMATION: unsure at all n locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MERT4577_154393C.1
/ US-10-425-115-59643

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 8; Length 678;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGUAACGCCAGGACTUACGA 20
Db 473 GGCACAGCCAGGACGACGA 491

RESULT 34
US-10-450-763-25544/c
/ Sequence 25544, Application US/10450763
/ Publication No. US20050196754A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc
/ TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
/ FILE REFERENCE: 790CIP3/US
/ CURRENT APPLICATION NUMBER: US/10/450,763
/ CURRENT FILING DATE: 2003-06-11
/ PRIOR APPLICATION NUMBER: PCT/US01/08631
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: 09/540,217
/ PRIOR FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: 09/649,167
```

```
/ PRIOR FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 60736
/ SOFTWARE: Custom
/ SEQ ID NO 25544
/ LENGTH: 693
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIMILAR
/ LOCATION: (355)..(690)
/ OTHER INFORMATION: 96% homologous to Escherichia coli Hisp-like nucleotide
/ OTHER INFORMATION: binding protein (phn), accession number J05260, Smith-Waterman Sco
/ OTHER INFORMATION: =528.
/ US-10-450-763-25544

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 9; Length 693;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGUAACGCCAGGACTUACGA 20
Db 186 GGCACAGCCAGGACTTAAGA 168

RESULT 35
US-10-027-632-113386/c
/ Sequence 113386, Application US/10027632
/ Publication No. US20020198371A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ TITLE OF INVENTION: Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 113386
/ LENGTH: 752
/ TYPE: DNA
/ ORGANISM: Human
/ US-10-027-632-113386

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 5; Length 752;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGUAACGCCAGGACTUACGA 20
Db 451 GGCACAGCCAGGACTTAAGA 433

RESULT 36
US-10-027-632-113387/c
/ Sequence 113387, Application US/10027632
/ Publication No. US20020198371A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
```

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; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113387
; LENGTH: 752
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-113387

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 6; Length 752;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGUACAGCCAGACTAAGA 20
Db 451 GGACAGCCAGACTAAGA 433

RESULT 37
US-10-027-632-113386/c
; Sequence 113386, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113386
; LENGTH: 752
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-113386

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 6; Length 752;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGUACAGCCAGACTAAGA 20
Db 451 GGACAGCCAGACTAAGA 433
```

```

Db 451 GGACAGCCAGACTAAGA 433

RESULT 38
US-10-027-632-113387/c
; Sequence 113387, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113387
; LENGTH: 752
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-113387

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 6; Length 752;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGUACAGCCAGACTAAGA 20
Db 451 GGACAGCCAGACTAAGA 433

RESULT 39
US-11-097-143-3449/c
; Sequence 3449, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
```

```
;; PRIOR APPLICATION NUMBER: 60/191,637
;; PRIOR FILING DATE: 2000-03-23
;; NUMBER OF SEQ ID NOS: 43008
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3449
;; LENGTH: 978
;; TYPE: DNA
;; ORGANISM: DROSOPHILA
US-11-097-143-3449

Query Match          79.0%; Score 15.8; DB 10; Length 978;
Best Local Similarity 78.9%; Pred. No. 4.2e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGUACAGCCAGACUACG 19
   |||:|||||:|||||:
Db 236 AGGTATGACGACGAGTACG 218

RESULT 40
US-10-389-647-172
;; Sequence 172, Application US/10389647
;; Publication No. US20040033549A1
;; GENERAL INFORMATION:
;; APPLICANT: GREENBERG, B. Peter
;; APPLICANT: SCHUSTER, Martin
;; APPLICANT: LOSTROH, Carol
;; TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA
;; FILE REFERENCE: UI2-038CP
;; CURRENT APPLICATION NUMBER: US/10/389,647
;; PRIOR FILING DATE: 2003-03-14
;; PRIOR APPLICATION NUMBER: 09/653730
;; PRIOR FILING DATE: 2000-09-01
;; PRIOR APPLICATION NUMBER: 60/153022
;; PRIOR FILING DATE: 1999-09-03
;; NUMBER OF SEQ ID NOS: 710
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 172
;; LENGTH: 1023
;; TYPE: DNA
;; ORGANISM: Pseudomonas aeruginosa
US-10-389-647-172

Query Match          79.0%; Score 15.8; DB 7; Length 1023;
Best Local Similarity 78.9%; Pred. No. 4.2e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGUACAGCCAGACUACG 19
   |||:|||||:|||||:
Db 166 AGCTACAGCCTGGACTACG 184

RESULT 41
US-09-866-050A-18
;; Sequence 18, Application US/09866050A
;; Publication No. US20030040471A1
;; GENERAL INFORMATION:
;; APPLICANT: Watson, James D.
;; APPLICANT: Strachan, Lorna
;; APPLICANT: Sleeman, Matthew
;; APPLICANT: Onrust, Rene
;; APPLICANT: Murison, James G.
;; APPLICANT: Kumble, Krishanand D.
;; TITLE OF INVENTION: Compositions Isolated From Skin Cells
;; TITLE OF INVENTION: and Methods for Their Use
;; FILE REFERENCE: 11000.1011c4U
;; CURRENT APPLICATION NUMBER: US/09/866,050A
;; CURRENT FILING DATE: 2001-05-24
;; NUMBER OF SEQ ID NOS: 725
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 18
;; LENGTH: 1057
;; TYPE: DNA
```

```
;; ORGANISM: Rat
US-09-866-050A-18

Query Match          79.0%; Score 15.8; DB 3; Length 1057;
Best Local Similarity 84.2%; Pred. No. 4.2e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGACUACGA 20
   |||:|||||:|||||:
Db 1022 GCTACAGCCAGACACGA 1040

RESULT 42
US-10-152-661-18
;; Sequence 18, Application US/10152661
;; Publication No. US20030022835A1
;; GENERAL INFORMATION:
;; APPLICANT: Watson, James D.
;; APPLICANT: Strachan, Lorna
;; APPLICANT: Sleeman, Matthew
;; APPLICANT: Onrust, Rene
;; APPLICANT: Murison, James G.
;; APPLICANT: Kumble, Krishanand D.
;; TITLE OF INVENTION: Compositions Isolated From Skin Cells
;; TITLE OF INVENTION: and Methods for Their Use
;; FILE REFERENCE: 11000.1011c5
;; CURRENT APPLICATION NUMBER: US/10/152,661
;; PRIOR FILING DATE: 2002-05-20
;; PRIOR APPLICATION NUMBER: 09/866,050
;; PRIOR FILING DATE: 2001-05-24
;; PRIOR APPLICATION NUMBER: 60/221,232
;; PRIOR FILING DATE: 2000-07-25
;; PRIOR APPLICATION NUMBER: 60/206,650
;; PRIOR FILING DATE: 2000-05-24
;; PRIOR APPLICATION NUMBER: 09/312,283
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: PCT/NZ99/00051
;; PRIOR FILING DATE: 1999-04-29
;; PRIOR APPLICATION NUMBER: 09/188,930
;; PRIOR FILING DATE: 1998-11-09
;; PRIOR APPLICATION NUMBER: 09/069,726
;; PRIOR FILING DATE: 1998-04-29
;; NUMBER OF SEQ ID NOS: 725
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 18
;; LENGTH: 1057
;; TYPE: DNA
;; ORGANISM: Rat
US-10-152-661-18

Query Match          79.0%; Score 15.8; DB 5; Length 1057;
Best Local Similarity 84.2%; Pred. No. 4.2e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGACUACGA 20
   |||:|||||:|||||:
Db 1022 GCTACAGCCAGACACGA 1040

RESULT 43
US-09-866-050A-447
;; Sequence 447, Application US/09866050A
;; Publication No. US20030040471A1
;; GENERAL INFORMATION:
;; APPLICANT: Watson, James D.
;; APPLICANT: Strachan, Lorna
;; APPLICANT: Sleeman, Matthew
;; APPLICANT: Onrust, Rene
;; APPLICANT: Murison, James G.
;; APPLICANT: Kumble, Krishanand D.
;; TITLE OF INVENTION: Compositions Isolated From Skin Cells
;; TITLE OF INVENTION: and Methods for Their Use
;; FILE REFERENCE: 11000.1011c4U
```

CURRENT APPLICATION NUMBER: US/09/866,050A
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 725
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 447
LENGTH: 1890
TYPE: DNA
ORGANISM: Rat
US-09-866-050A-447

Query Match 79.0%; Score 15.8; DB 3; Length 1890;
Best Local Similarity 84.2%; Pred. No. 4.1e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGACUACGA 20
DB 881 GCTACAGCCAGACACGA 899

RESULT 44

US-10-152-661-447
Sequence 447, Application US/10152661
Publication No. US20030022835A1
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Muirson, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE REFERENCE: 11000.1011c5
CURRENT APPLICATION NUMBER: US/10/152,661
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 09/866,050
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/221,232
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/206,650
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 09/312,283
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: PCT/NZ99/00051
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 09/188,930
PRIOR FILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: 09/069,726
PRIOR FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 725
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 447
LENGTH: 1890
TYPE: DNA
ORGANISM: Rat
US-10-152-661-447

Query Match 79.0%; Score 15.8; DB 5; Length 1890;
Best Local Similarity 84.2%; Pred. No. 4.1e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGACUACGA 20
DB 881 GCTACAGCCAGACACGA 899

RESULT 45

US-09-866-050A-230
Sequence 230, Application US/09866050A
Publication No. US20030040471A1
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna

APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Muirson, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE REFERENCE: 11000.1011c4U
CURRENT APPLICATION NUMBER: US/09/866,050A
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 725
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 230
LENGTH: 2004
TYPE: DNA
ORGANISM: Rat
US-09-866-050A-230

Query Match 79.0%; Score 15.8; DB 3; Length 2004;
Best Local Similarity 84.2%; Pred. No. 4.1e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGACUACGA 20
DB 995 GCTACAGCCAGACACGA 1013

RESULT 46

US-10-152-661-230
Sequence 230, Application US/10152661
Publication No. US20030022835A1
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Muirson, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE REFERENCE: 11000.1011c5
CURRENT APPLICATION NUMBER: US/10/152,661
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 09/866,050
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/221,232
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/206,650
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 09/312,283
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: PCT/NZ99/00051
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 09/188,930
PRIOR FILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: 09/069,726
PRIOR FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 725
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 230
LENGTH: 2004
TYPE: DNA
ORGANISM: Rat
US-10-152-661-230

Query Match 79.0%; Score 15.8; DB 5; Length 2004;
Best Local Similarity 84.2%; Pred. No. 4.1e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGACUACGA 20
DB 995 GCTACAGCCAGACACGA 1013

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RESULT 47
US-10-027-632-101774/c
; Sequence 101774, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101774
; LENGTH: 2407
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-101774

Query Match      79.0%; Score 15.8; DB 5; Length 2407;
Best Local Similarity 78.9%; Pred. No. 4.1e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db      1660 AGGUAAGCCAGGAGUACG 1642

RESULT 48
US-10-027-632-101774/c
; Sequence 101774, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101774
; LENGTH: 2407
; TYPE: DNA
; ORGANISM: Human
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US-10-027-632-101774

Query Match      79.0%; Score 15.8; DB 6; Length 2407;
Best Local Similarity 78.9%; Pred. No. 4.1e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy      1 AGGUAAGCCAGGAGUACG 19
Db      1660 AGGUAAGCCAGGAGUACG 1642

RESULT 49
US-10-282-122A-35246/c
; Sequence 35246, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA,034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35246
; LENGTH: 2412
; TYPE: DNA
; ORGANISM: Staphylococcus haemolyticus
US-10-282-122A-35246

Query Match      79.0%; Score 15.8; DB 7; Length 2412;
Best Local Similarity 78.9%; Pred. No. 4.1e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db      1017 AGGUAAGCCAGGAGUACG 999

RESULT 50
US-11-097-143-3448
; Sequence 3448, Application US/11097143
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; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: C0000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3448
; LENGTH: 3265
; TYPE: DNA
; ORGANISM: DROSOPHILA
; US-11-097-143-3448

Query Match      79.0%; Score 15.8; DB 10; Length 3265;
Best Local Similarity 78.9%; Pred. No. 4.1e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:35:44 ; Search time 1328.46 Seconds
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Title: US-10-800-926-3
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Sequence: 1 agnucacgacgcagacacga 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
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13: /cgn2_6/ptodata/1/pubpna/US18_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	20	100.0	20	US-11-127-654-379
2	18	90.0	5308	US-11-136-527-481
3	16.8	84.0	605	US-09-925-065A-693333
4	16.8	84.0	740	US-09-925-065A-73830
5	16.4	82.0	586	US-09-925-065A-369463
6	16	80.0	1734	US-11-136-527-603
7	16	80.0	90616	US-10-330-773-713
8	15.8	79.0	364	US-09-925-065A-132060
9	15.8	79.0	533	US-09-925-065A-290634
10	15.8	79.0	572	US-09-925-065A-290636
11	15.8	79.0	573	US-09-925-065A-813093
12	15.8	79.0	1098	US-10-933-182A-77115
13	15.8	79.0	1098	US-10-933-182A-77115
14	15.8	79.0	43256	US-10-330-773-713
15	15.4	77.0	363	US-09-925-065A-173502
16	15.4	77.0	538	US-09-925-065A-90145
17	15.4	77.0	538	US-09-925-065A-90146
18	15.4	77.0	593	US-09-925-065A-135672
19	15.4	77.0	610	US-09-925-065A-768047
20	15.4	77.0	2208	US-11-121-438-5

21	15.4	77.0	2944	US-10-750-185-56251	Sequence 56251, A
22	15.4	77.0	2944	US-10-750-623-56251	Sequence 56251, A
23	15.4	77.0	137671	US-11-121-086-47	Sequence 47, Appl
24	15.2	76.0	458	US-09-925-065A-591902	Sequence 591902, A
25	15.2	76.0	458	US-09-925-065A-226237	Sequence 226237, A
26	15.2	76.0	525	US-09-925-065A-20701	Sequence 20701, A
27	15.2	76.0	582	US-09-925-065A-502873	Sequence 502873, A
28	15.2	76.0	598	US-09-925-065A-191570	Sequence 191570, A
29	15.2	76.0	598	US-09-925-065A-544123	Sequence 544123, A
30	15.2	76.0	807	US-10-467-657-2197	Sequence 2197, Ap
31	15.2	76.0	828	US-10-467-657-2199	Sequence 2199, Ap
32	15.2	76.0	2049	US-09-925-065A-15531	Sequence 15531, A
33	15.2	76.0	3090	US-10-933-182A-4937	Sequence 4937, Ap
34	15.2	76.0	3090	US-10-933-182A-4937	Sequence 4937, Ap
35	15.2	76.0	58687	US-10-330-773-511	Sequence 511, Appl
36	15.2	76.0	100137	US-10-330-773-520	Sequence 620, Appl
37	15.2	76.0	101046	US-10-995-561-13330	Sequence 13330, A
38	15.2	76.0	118544	US-10-330-773-76	Sequence 76, Appl
39	15.2	76.0	1691140	US-11-091-018-1	Sequence 1, Appl1
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43	15	75.0	506	US-09-925-065A-793457	Sequence 793457, A
44	15	75.0	532	US-09-925-065A-361014	Sequence 361014, A
45	15	75.0	532	US-09-925-065A-361016	Sequence 361016, A
46	15	75.0	532	US-09-925-065A-361019	Sequence 361019, A
47	15	75.0	577	US-09-925-065A-178453	Sequence 178453, A
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49	15	75.0	578	US-09-925-065A-361018	Sequence 361018, A
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51	15	75.0	1025	US-09-925-065A-286697	Sequence 286697, A
52	15	75.0	1185	US-09-925-065A-41299	Sequence 41299, A
53	15	75.0	1803	US-10-750-185-38766	Sequence 38766, A
54	15	75.0	1803	US-10-750-623-38766	Sequence 38766, A
55	15	75.0	44617	US-10-330-773-928	Sequence 928, Appl
56	15	75.0	57860	US-10-330-773-659	Sequence 659, Appl
57	14.8	74.0	19	US-11-101-244-1186324	Sequence 1186324, A
58	14.8	74.0	19	US-11-083-784-1186324	Sequence 1186324, A
59	14.8	74.0	411	US-09-925-065A-440135	Sequence 440135, A
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61	14.8	74.0	502	US-09-925-065A-454207	Sequence 454207, A
62	14.8	74.0	513	US-09-925-065A-440046	Sequence 440046, A
63	14.8	74.0	537	US-09-925-065A-197434	Sequence 197434, A
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65	14.8	74.0	554	US-09-925-065A-955304	Sequence 955304, A
66	14.8	74.0	581	US-09-925-065A-954327	Sequence 954327, A
67	14.8	74.0	581	US-09-925-065A-339158	Sequence 339158, A
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69	14.8	74.0	583	US-09-925-065A-307356	Sequence 307356, A
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74	14.8	74.0	616	US-09-925-065A-751234	Sequence 751234, A
75	14.8	74.0	622	US-09-925-065A-602820	Sequence 602820, A
76	14.8	74.0	637	US-09-925-065A-861299	Sequence 861299, A
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78	14.8	74.0	711	US-10-750-185-33978	Sequence 33978, A
79	14.8	74.0	711	US-10-750-623-33978	Sequence 33978, A
80	14.8	74.0	857	US-09-925-065A-93302	Sequence 93302, A
81	14.8	74.0	857	US-09-925-065A-93303	Sequence 93303, A
82	14.8	74.0	857	US-09-925-065A-93304	Sequence 93304, A
83	14.8	74.0	857	US-09-925-065A-93305	Sequence 93305, A
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91	14.8	74.0	2056	US-11-091-883-314	Sequence 314, Appl
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C 390	13.8	69.0	3946	9	US-11-230-180-4	Sequence 4, Appl1
C 391	13.8	69.0	4050	7	US-10-932-182A-6036	Sequence 6036, Ap
C 392	13.8	69.0	4050	7	US-10-932-182A-6036	Sequence 6036, Ap
C 393	13.8	69.0	4285	8	US-10-947-249-175	Sequence 175, App
C 394	13.8	69.0	4370	8	US-10-750-185-35839	Sequence 35839, A
C 395	13.8	69.0	4370	8	US-10-750-623-35839	Sequence 35839, A
C 396	13.8	69.0	7944	8	US-10-821-234-451	Sequence 451, App
C 397	13.8	69.0	11062	12	US-11-128-061-566	Sequence 566, App
C 398	13.8	69.0	11062	12	US-11-128-049-566	Sequence 566, App
C 399	13.8	69.0	11261	12	US-11-177-504-1	Sequence 1, Appl1
C 400	13.8	69.0	11261	9	US-11-200-710-1	Sequence 10, Appl1
C 401	13.8	69.0	14121	12	US-11-124-020A-10	Sequence 3, Appl1
C 402	13.8	69.0	14121	12	US-11-123-656A-3	Sequence 474, App
C 403	13.8	69.0	21850	7	US-10-330-773-474	Sequence 62, Appl1
C 404	13.8	69.0	28672	7	US-10-893-483-62	Sequence 146, App
C 405	13.8	69.0	39700	7	US-10-330-773-146	Sequence 1, Appl1
C 406	13.8	69.0	43445	12	US-11-124-020A-1	Sequence 2, Appl1
C 407	13.8	69.0	43445	12	US-11-124-020A-2	Sequence 2892, Ap
C 408	13.8	69.0	46854	12	US-11-124-368A-2892	Sequence 63, Appl1
C 409	13.8	69.0	50484	7	US-10-893-483-63	Sequence 188, App
C 410	13.8	69.0	50833	7	US-10-330-773-188	Sequence 43, Appl1
C 411	13.8	69.0	72352	7	US-10-330-773-43	Sequence 105, App
C 412	13.8	69.0	109974	12	US-11-117-187-204	Sequence 13262, A
C 413	13.8	69.0	124285	7	US-10-893-483-105	Sequence 90, Appl1
C 414	13.8	69.0	141121	8	US-10-995-561-13262	Sequence 28, Appl1
C 415	13.8	69.0	172111	12	US-11-121-086-90	Sequence 664, App
C 416	13.8	69.0	172111	12	US-11-121-086-28	Sequence 54, Appl1
C 417	13.8	69.0	179487	7	US-10-330-773-664	Sequence 54, Appl1
C 418	13.8	69.0	189252	12	US-11-121-086-54	Sequence 13489, A
C 419	13.8	69.0	195998	8	US-10-995-561-13489	Sequence 9, Appl1
C 420	13.8	69.0	196200	12	US-11-121-086-9	Sequence 10, Appl1
C 421	13.8	69.0	199321	12	US-11-121-086-10	Sequence 119, App
C 422	13.8	69.0	228006	7	US-10-330-773-119	Sequence 111, App
C 423	13.8	69.0	254481	7	US-10-330-773-111	Sequence 677076, A
C 424	13.6	68.0	24	8	US-10-310-914A-677076	Sequence 357805, A
C 425	13.6	68.0	25	12	US-11-136-527-37805	Sequence 173501, A
C 426	13.6	68.0	336	7	US-10-932-182A-173501	Sequence 173501, A
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C 428	13.6	68.0	387	12	US-11-043-752-4275	Sequence 499, App
C 429	13.6	68.0	396	8	US-10-769-744-499	Sequence 607, App
C 430	13.6	68.0	431	12	US-11-096-191-607	Sequence 496543, A
C 431	13.6	68.0	441	6	US-09-925-065A-496543	Sequence 496543, A
C 432	13.6	68.0	444	6	US-09-925-065A-496544	Sequence 650636, A
C 433	13.6	68.0	444	6	US-09-925-065A-650636	Sequence 15458, A
C 434	13.6	68.0	455	6	US-09-925-065A-15458	Sequence 423887, A
C 435	13.6	68.0	471	6	US-09-925-065A-423887	Sequence 959, App
C 436	13.6	68.0	480	7	US-10-932-182A-959	Sequence 959, App
C 437	13.6	68.0	480	7	US-10-932-182A-959	Sequence 348077, A
C 438	13.6	68.0	485	6	US-09-925-065A-348077	Sequence 472268, A
C 439	13.6	68.0	485	6	US-09-925-065A-472268	Sequence 472268, A
C 440	13.6	68.0	510	6	US-09-925-065A-54398	Sequence 284463, A
C 441	13.6	68.0	514	6	US-09-925-065A-284463	Sequence 284463, A
C 442	13.6	68.0	519	6	US-09-925-065A-267826	Sequence 214374, A
C 443	13.6	68.0	526	6	US-09-925-065A-214374	Sequence 129787, A
C 444	13.6	68.0	527	6	US-09-925-065A-129788	Sequence 821038, A
C 445	13.6	68.0	527	6	US-09-925-065A-129788	Sequence 921809, A
C 446	13.6	68.0	529	6	US-09-925-065A-921809	Sequence 921809, A
C 447	13.6	68.0	541	6	US-09-925-065A-921809	Sequence 921809, A
C 448	13.6	68.0	541	6	US-09-925-065A-921825	Sequence 921825, A
C 449	13.6	68.0	541	6	US-09-925-065A-921826	Sequence 921826, A
C 450	13.6	68.0	541	6	US-09-925-065A-946735	Sequence 946735, A
C 451	13.6	68.0	541	6	US-09-925-065A-946735	Sequence 946735, A
C 452	13.6	68.0	541	6	US-09-925-065A-946742	Sequence 946742, A
C 453	13.6	68.0	541	6	US-09-925-065A-946743	Sequence 946743, A
C 454	13.6	68.0	545	6	US-09-925-065A-604819	Sequence 604819, A
C 455	13.6	68.0	552	12	US-11-136-527-3480	Sequence 3480, Ap
C 456	13.6	68.0	552	12	US-11-136-527-3480	Sequence 7576, Ap
C 457	13.6	68.0	554	6	US-09-925-065A-199532	Sequence 199532, A
C 458	13.6	68.0	554	6	US-09-925-065A-199532	Sequence 199532, A


```
970 13.2 66.0 24 8 US-10-310-914A-628616 Sequence 628616,
971 13.2 66.0 24 8 US-10-310-914A-779901 Sequence 779901,
972 13.2 66.0 25 7 US-10-932-182A-66721 Sequence 66721, A
973 13.2 66.0 25 7 US-10-932-182A-161588 Sequence 161588,
974 13.2 66.0 25 7 US-10-932-182A-178713 Sequence 178713, A
975 13.2 66.0 25 7 US-10-932-182A-66721 Sequence 66721, A
976 13.2 66.0 25 7 US-10-932-182A-161588 Sequence 161588,
977 13.2 66.0 25 7 US-10-932-182A-178713 Sequence 178713, A
978 13.2 66.0 25 7 US-10-932-982-48768 Sequence 48768, A
979 13.2 66.0 25 7 US-10-932-982-168304 Sequence 168304,
980 13.2 66.0 25 7 US-10-934-048A-113217 Sequence 113217,
981 13.2 66.0 25 12 US-11-121-849-140936 Sequence 140936,
982 13.2 66.0 25 12 US-11-121-849-150435 Sequence 150435,
983 13.2 66.0 25 12 US-11-121-849-176206 Sequence 176206,
984 13.2 66.0 25 12 US-11-121-849-178594 Sequence 178594,
985 13.2 66.0 25 12 US-11-121-849-380286 Sequence 380286,
986 13.2 66.0 25 12 US-11-121-849-524783 Sequence 524783,
987 13.2 66.0 25 12 US-11-136-527-321659 Sequence 321659,
988 13.2 66.0 25 12 US-11-136-527-357828 Sequence 357828,
989 13.2 66.0 82 8 US-10-310-914A-17485 Sequence 17485, A
990 13.2 66.0 201 8 US-10-995-561-40214 Sequence 40214, A
991 13.2 66.0 201 12 US-11-124-368A-1665 Sequence 1665, A
992 13.2 66.0 201 12 US-11-124-368A-13774 Sequence 13774, A
993 13.2 66.0 201 12 US-11-124-368A-14151 Sequence 14151, A
994 13.2 66.0 201 12 US-11-124-367A-27765 Sequence 27765, A
995 13.2 66.0 324 6 US-09-925-065A-39967 Sequence 39967, A
996 13.2 66.0 346 9 US-11-021-492-370 Sequence 370, App
997 13.2 66.0 414 6 US-09-925-065A-182610 Sequence 182610,
998 13.2 66.0 420 6 US-09-925-065A-259573 Sequence 259573,
999 13.2 66.0 424 6 US-09-925-065A-354759 Sequence 354759,
1000 13.2 66.0 424 6 US-09-925-065A-354760 Sequence 354760,
```

ALIGNMENTS

```
RESULT 1
US-11-127-654-379
; Sequence 379, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; TITLE OF INVENTION: INFLAMMATORY DISEASES
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 379
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-379
```

```
Query Match 100.0%; Score 20; DB 12; Length 20;
Best Local Similarity 90.0%; Pred. No. 0.44;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 AGGACAGCCAGGAGCAGCAGCA 20
|||:|||||:|||||:|||||:
Db 1 AGGACAGCCAGGAGCAGCAGCA 20
```

```
RESULT 2
US-11-136-527-481
```

```
; Sequence 481, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 481
; LENGTH: 5308
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-481
```

```
Query Match 90.0%; Score 18; DB 12; Length 5308;
Best Local Similarity 88.9%; Pred. No. 10;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 2 GGACAGCCAGGAGCAGCAGCA 19
|||:|||||:|||||:|||||:
Db 2734 GGACAGCCAGGAGCAGCAGCA 2751
```

```
RESULT 3
US-09-925-065A-693333/C
; Sequence 693333, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: PatSeqSO for Windows Version 4.0
; SEQ ID NO 693333
; LENGTH: 605
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-693333
```

```
Query Match 84.0%; Score 16.8; DB 6; Length 605;
Best Local Similarity 85.0%; Pred. No. 35;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 1 AGGACAGCCAGGAGCAGCAGCA 20
|||:|||||:|||||:|||||:
Db 398 AGGACAGCCAGGAGCAGCAGCA 379
```

```
RESULT 4
US-09-925-065A-73830
; Sequence 73830, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
```



```

; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73830
; LENGTH: 740
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-73830
```

```

Query Match      84.0%; Score 16, 8; DB 6; Length 740;
Best Local Similarity 80.0%; Pred. No. 36;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 AGTACAGCCAGGACGACGAC 20
DB      66 AGGTACAGCCAGGACGACGAC 85
```

```

RESULT 5
US-09-925-065A-369463
; Sequence 369463, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 369463
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-369463
```

```

Query Match      82.0%; Score 16, 4; DB 6; Length 586;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 AGTACAGCCAGGACGACGAC 18
DB      39 AGGTACAGCCAGGACGACGAC 56
```

```

RESULT 6
US-11-136-527-603
; Sequence 603, Application US/11136527
; Publication No. US20050287570A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 603
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-603
```

```

Query Match      80.0%; Score 16; DB 12; Length 1734;
Best Local Similarity 87.5%; Pred. No. 1,1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 GTACAGCCAGGACGACGAC 18
DB      1042 GTACAGCCAGGACGACGAC 1057
```

```

RESULT 7
US-10-330-773-573
; Sequence 573, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Melandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 573
; LENGTH: 90616
; TYPE: DNA
; ORGANISM: Mus musculus
; PEATRE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(90616)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-573
```

```

Query Match      80.0%; Score 16; DB 7; Length 90616;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 GTACAGCCAGGACGACGAC 18
DB      39970 GTACAGCCAGGACGACGAC 39985
```

```

RESULT 8
US-09-925-065A-132060/C
; Sequence 132060, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
```

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; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132060
; LENGTH: 364
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-132060

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 6; Length 364;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGGACUACGA 20
DB 93 GGTGACGCCAGGCGCTACGA 75

RESULT 9
US-09-925-065A-290634/c
; Sequence 290634, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 290634
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-290634

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 6; Length 533;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGUACAGCCAGGACUACG 19
DB 347 AAGTACAGCCAGGACTACG 329

RESULT 10
US-09-925-065A-290636/c
; Sequence 290636, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
```

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; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 290636
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-290636

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 6; Length 533;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGUACAGCCAGGACTACG 19
DB 347 AAGTACAGCCAGGACTACG 329

RESULT 11
US-09-925-065A-813093
; Sequence 813093, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 813093
; LENGTH: 572
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-813093

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 6; Length 572;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGACAGCCAGGACTACGA 20
DB 122 GGACAGCCAGGACTACGA 140

RESULT 12
US-10-932-182A-77115
; Sequence 77115, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHITIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
```

```

; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77115
; LENGTH: 1098
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-77115

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 7; Length 1098;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGUACAGCCAGACUACG 19
DB 726 AGGTACACTAGACTACG 744

RESULT 13
US-10-932-182A-77115
; Sequence 77115, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77115
; LENGTH: 1098
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-77115

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 7; Length 1098;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGUACAGCCAGACUACG 19
DB 726 AGGTACACTAGACTACG 744

RESULT 14
US-10-330-773-713
; Sequence 713, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 713
; LENGTH: 43256
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(43256)
```

```

; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-713

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 7; Length 43256;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGACUACGA 20
DB 27866 GGGACAGCCAGACTACCA 27884

RESULT 15
US-09-925-065A-173502
; Sequence 173502, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 173502
; LENGTH: 363
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-173502

Query Match
Best Local Similarity 77.0%; Score 15.4; DB 6; Length 363;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGUACAGCCAGACUUA 17
DB 41 ATGTACAGCCAGACTA 57

RESULT 16
US-09-925-065A-90145
; Sequence 90145, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
```

SEQ ID NO 90145
LENGTH: 538
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-90145

Query Match 77.0%; Score 15.4; DB 6; Length 538;
Best Local Similarity 82.4%; Pred. No. 1.9e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGAGACTCC 18
||:|||||:
Db 494 GGTAAGCCAGAGACTCC 510

RESULT 17
US-09-925-065A-90146
Sequence 90146, Application US/09925065A
Publication No. US20040181048A1

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 90146
LENGTH: 538
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-90146

Query Match 77.0%; Score 15.4; DB 6; Length 538;
Best Local Similarity 82.4%; Pred. No. 1.9e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGAGACTCC 18
||:|||||:
Db 494 GGTAAGCCAGAGACTCC 510

RESULT 18
US-09-925-065A-135672
Sequence 135672, Application US/09925065A
Publication No. US20040181048A1

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 135672
LENGTH: 593
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-135672

Query Match 77.0%; Score 15.4; DB 6; Length 593;
Best Local Similarity 82.4%; Pred. No. 1.9e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 UACAGCCAGAGACTAGCA 20
:|||||:
Db 70 TACAGCCAGAGACTAGCA 86

RESULT 19
US-09-925-065A-768047
Sequence 768047, Application US/09925065A
Publication No. US20040181048A1

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 768047
LENGTH: 610
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-768047

Query Match 77.0%; Score 15.4; DB 6; Length 610;
Best Local Similarity 82.4%; Pred. No. 1.9e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGAGACTCC 18
||:|||||:
Db 581 GGTAAGCCAGAGACTCC 597

RESULT 20
US-11-121-438-5
Sequence 5, Application US/11121438
Publication No. US20060014173A1

GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: PR/SET- Domain Containing Nucleic Acids,
Polypeptides, Antibodies and Methods of Use
FILE REFERENCE: P-11 5301
CURRENT APPLICATION NUMBER: US/11/121,438
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: US/10/200,012
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: US 09/910,478
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5
LENGTH: 2208
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: CDS
LOCATION: (250)...(1761)
US-11-121-438-5

Query Match 77.0%; Score 15.4; DB 12; Length 2208;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGGACUAC 18
DB 1001 GGTACAGCGAGGACTAC 1017

RESULT 21
US-10-750-185-56251

Sequence 56251, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFIELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 56251
LENGTH: 2944
TYPE: DNA
ORGANISM: Bovine
US-10-750-185-56251

Query Match 77.0%; Score 15.4; DB 8; Length 2944;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGUACAGCCAGGACUAC 17
DB 2293 AGGACAGCCAGGACTA 2309

RESULT 22
US-10-750-623-56251

Sequence 56251, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFIELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1

SEQ ID NO 56251
LENGTH: 2944
TYPE: DNA
ORGANISM: Bovine
US-10-750-623-56251

Query Match 77.0%; Score 15.4; DB 8; Length 2944;
Best Local Similarity 86.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGUACAGCCAGGACUAC 17
DB 2293 AGGACAGCCAGGACTA 2309

RESULT 23
US-11-121-086-47/c

Sequence 47, Application US/1121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: FOUTSSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 47
LENGTH: 137671
TYPE: DNA
ORGANISM: Homo sapiens
US-11-121-086-47

Query Match 77.0%; Score 15.4; DB 12; Length 137671;
Best Local Similarity 82.4%; Pred. No. 3.8e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 UACAGCCAGGACUACGA 20
DB 96035 TACAGCCAGGACTAGGA 96019

RESULT 24
US-09-925-065A-591902/c

Sequence 591902, Application US/0925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 591902
LENGTH: 458
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-591902

Query Match 76.0%; Score 15.2; DB 6; Length 458;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGCACTUACGA 20
|||:|||||:|||||:
DB 227 AGTTACAGCCAGCACTGACA 208

RESULT 25

US-09-925-065A-226237
; Sequence 226237, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 226237
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-226237

Query Match 76.0%; Score 15.2; DB 6; Length 487;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGCACTUACGA 20
|||:|||||:|||||:
DB 68 AGGTGACGCCAGGCGCTGCCA 87

RESULT 26

US-09-925-065A-20701
; Sequence 20701, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20701
; LENGTH: 525

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-20701

Query Match 76.0%; Score 15.2; DB 6; Length 525;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGCACTUACGA 20
|||:|||||:|||||:
DB 445 AGGCGCAGCCAGCACTTCCA 464

RESULT 27

US-09-925-065A-502873/c
; Sequence 502873, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 502873
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-502873

Query Match 76.0%; Score 15.2; DB 6; Length 582;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGCACTUACGA 20
|||:|||||:|||||:
DB 264 AGGTACAGCCAGCACAAAGA 245

RESULT 28

US-09-925-065A-191670
; Sequence 191670, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086

```
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 191670
/ LENGTH: 598
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-191670
```

```
Query Match          76.0%; Score 15.2; DB 6; Length 598;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 AGGUAACGCCAGACUACGA 20
        |||:|||||:|||||:|
DB      254 AGGTAGACGCCAGACTGCA 273
```

```
RESULT 29
US-09-925-065A-544123/c
/ Sequence 544123, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ PRIOR FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 544123
/ LENGTH: 598
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-544123
```

```
Query Match          76.0%; Score 15.2; DB 6; Length 598;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 AGGUAACGCCAGACUACGA 20
        |||:|||||:|||||:|
DB      495 AGGTGACGCCAGGCTTACA 476
```

```
RESULT 30
US-10-467-657-2197
/ Sequence 2197, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ PRIOR FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 2197
```

```
/ LENGTH: 807
/ TYPE: DNA
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2197
```

```
Query Match          76.0%; Score 15.2; DB 8; Length 807;
Best Local Similarity 75.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 AGGUAACGCCAGACUACGA 20
        |||:|||||:|||||:|
DB      6 AGTACTGCATGATACGA 25
```

```
RESULT 31
US-10-467-657-2199/c
/ Sequence 2199, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ PRIOR FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 2199
/ LENGTH: 828
/ TYPE: DNA
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2199
```

```
Query Match          76.0%; Score 15.2; DB 8; Length 828;
Best Local Similarity 75.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 AGGUAACGCCAGACUACGA 20
        |||:|||||:|||||:|
DB      793 AGTACTGCATGATACGA 774
```

```
RESULT 32
US-09-925-065A-15531
/ Sequence 1531, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ PRIOR FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 15531
/ LENGTH: 2049
/ TYPE: DNA
```



```

# PRIOR FILING DATE: 2002-09-25
# PRIOR APPLICATION NUMBER: 10/419,723
# PRIOR FILING DATE: 2003-04-18
# PRIOR APPLICATION NUMBER: 10/650,120
# PRIOR FILING DATE: 2003-08-27
# PRIOR APPLICATION NUMBER: 10/067,514
# PRIOR FILING DATE: 2002-02-04
# PRIOR APPLICATION NUMBER: 09/811,352
# PRIOR FILING DATE: 2001-03-19
# NUMBER OF SEQ ID NOS: 102
# SOFTWARE: FastSeq for Windows Version 4.0
# SEQ ID NO 1
# LENGTH: 1691140
# TYPE: DNA
# ORGANISM: Homo sapiens
# FEATURE:
# NAME/KEY: misc_feature
# LOCATION: (1)...(1691140)
# OTHER INFORMATION: n=a,T,c or G
US-11-091-018-1

```

Query Match	76.0%	Score 15.2;	DB 12;	Length 1691140;
Best Local Similarity	75.0%	Pred. No. 5.3e+02;		
Matches 15; Conservative	2;	Mismatches 3;	Indels 0;	Gaps 0;

```

Oy      1 AGGUACAGCCAGGACTUACGA 20
          |||:||||| |||: ||
Db      734050 AGGTACAGCCAGAAGTGGGA 734065

```

```

RESULT 40
US-11-175-859-84034
Sequence 84034, Application US/11175859
Publication No. US20060024715A1
GENERAL INFORMATION:
APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et al.
TITLE OR INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: PatentIn version 3.2
SEQ ID NO 84034
LENGTH: 50
TYPE: DNA
ORGANISM: homo sapien
US-11-175-859-84034

```

```

QY      1 AGGUA CAGCCAGGACUACGA 20
          ||| ||| ||| ||| : ||
Db      16256 AGGCACAGCCAGGACTGTGA 16237

```

QY 1 AGUAGAGCCAGACUA 17
| | : | | | : | | | : |
Db 19 ATGTACARCCAGACTA 35

```

RESULT 41
US-11-124-368A-16998
; Sequence 16998, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Carcilli
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection
; FILE REFERENCE: CL001574
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09

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; PRIOR APPLICATION NUMBER: US 60/566,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16998
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-368A-16998

Query Match
Best Local Similarity 75.0%; Score 15; DB 12; Length 201;
Pred. No. 2.8e+02;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGUAACGCCAGGACUA 17
Db 87 AGGTACAGCAGGAGSTA 103

RESULT 42
US-09-925-065A-439000
; Sequence 439000, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 439000
; LENGTH: 475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-439000

Query Match
Best Local Similarity 75.0%; Score 15; DB 6; Length 475;
Pred. No. 3.1e+02;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGUAACGCCAGGACU 16
Db 414 GGTACAGCAGGAGCT 428

RESULT 43
US-09-925-065A-793457
; Sequence 793457, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
```

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; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 793457
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-793457

Query Match
Best Local Similarity 75.0%; Score 15; DB 6; Length 506;
Pred. No. 3.1e+02;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGUAACGCCAGGACU 16
Db 422 GGTACAGCAGGAGCT 436

RESULT 44
US-09-925-065A-361014/C
; Sequence 361014, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 361014
; LENGTH: 532
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-361014

Query Match
Best Local Similarity 75.0%; Score 15; DB 6; Length 532;
Pred. No. 3.1e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGUAACGCCAGGAC 15
Db 291 AGGTACAGCAGGAGC 277

RESULT 45
US-09-925-065A-361016/C
; Sequence 361016, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
```

PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 361016
LENGTH: 532
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-361016

Query Match 75.0%; Score 15; DB 6; Length 532;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGAC 15
Db 291 AGGTACAGCCAGAC 277

RESULT 46
US-09-925-065A-361019/c
Sequence 361019, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 361019
LENGTH: 532
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-361019

Query Match 75.0%; Score 15; DB 6; Length 532;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGAC 15
Db 291 AGGTACAGCCAGAC 277

RESULT 47
US-09-925-065A-178453
Sequence 178453, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 178453
LENGTH: 577
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-178453

Query Match 75.0%; Score 15; DB 6; Length 577;
Best Local Similarity 76.5%; Pred. No. 3.1e+02;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGAC 17
Db 243 AGGTACAGCCAGAC 259

RESULT 48
US-09-925-065A-361017/c
Sequence 361017, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 361017
LENGTH: 577
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-361017

Query Match 75.0%; Score 15; DB 6; Length 577;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGAC 15
Db 252 AGGTACAGCCAGAC 238

RESULT 49
US-09-925-065A-361018/c
Sequence 361018, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:

```
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 361018
LENGTH: 577
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-361018
```

```
Query Match 75.0%; Score 15; DB 6; Length 577;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AGGACAGCCAGGAC 15
DB 252 AGGTACAGCCAGGAC 238
```

```
RESULT 50
US-09-925-065A-636833
Sequence 636833, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 636833
LENGTH: 638
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-636833
```

```
Query Match 75.0%; Score 15; DB 6; Length 638;
Best Local Similarity 93.3%; Pred. No. 3.2e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 AGGACAGCCAGGAC 15
DB 202 AGGTACAGCCAGGAC 216
```

Job completed: March 19, 2006, 05:42:58
Time: 1355.46 secs